

5	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	3.17
	461230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.16
	418000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.16
	444823	BE262989	Hs.12045	putative protein	3.15
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.15
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.15
	447801	H88923	Hs.270247	Homo sapiens cDNA FLJ11977 fis, clone HE	3.15
	424188	AW954552	Hs.142634	zinc finger protein	3.15
10	436941	AA860383	Hs.292791	ESTs	3.15
	400592			Target Exon	3.15
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.15
	450406	A1894913	Hs.279637	ESTs	3.15
	414161	AA138106	Hs.184852	KIAA1553 protein	3.15
15	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	3.14
	438538	AA832203	Hs.291955	ESTs	3.14
	441013	AI26252	Hs.126419	ESTs	3.14
	450431	AW136797	Hs.266041	ESTs	3.14
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	3.13
20	434768	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.13
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.12
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	3.12
	412673	AL042957	Hs.31845	ESTs	3.11
	420507	AF093408	Hs.96397	A kinase (PRKA) anchor protein 3	3.11
25	423419	R55336	Hs.23539	ESTs	3.11
	428925	AW242474	Hs.98960	ESTs	3.11
	426108	AA622037	Hs.166468	programmed cell death 5	3.10
	439398	AA284267	Hs.221504	ESTs	3.10
	449138	AW294215	Hs.195831	ESTs	3.10
30	441785	N58115	Hs.21137	AD024 protein	3.10
	458053	S57488	Hs.76252	endothelin receptor type A	3.10
	403610			C3001199:gl[7494834]pir[15308] hypothet	3.10
	421261	AI299139	Hs.17517	ESTs	3.10
	429274	AI379772	Hs.99206	ESTs	3.10
35	438243	AI581311		ESTs	3.10
	424800	AL036588	Hs.153203	MyoD family inhibitor	3.09
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.08
	418443	N59469	Hs.194225	ESTs	3.08
	421230	AW958439	Hs.105633	ESTs	3.07
40	427806	AA864330	Hs.166520	ESTs	3.07
	414706	AW340125	Hs.76889	KIAA0097 gene product	3.06
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.06
	445679	AI343868	Hs.301059	hypothetical protein FLJ12488	3.06
	434456	AW452621	Hs.116832	ESTs	3.05
45	433228	F28212	Hs.14953	KIAA1491 protein	3.05
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.05
	415227	AW821113	Hs.72402	ESTs	3.05
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	3.05
50	438869	AF076009		gb:Homo sapiens full length insert cDNA	3.05
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.04
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.04
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.04
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	3.04
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	3.04
55	435725	BE535787	Hs.113170	ESTs	3.03
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	3.03
	420598	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.02
	427953	AA417944	Hs.44331	ESTs	3.01
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.01
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	3.00
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cell	3.00
	434776	AA648988		gb:ns41f1.s1 NC1_CGAP_GCB1 Homo sapiens	3.00
	414132	AI801235	Hs.48480	ESTs	3.00
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
65	433493	AA594915	Hs.155087	ESTs	3.00
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	3.00
	453416	NM_003037	Hs.32970	signalling lymphocytic activation molecu	3.00

TABLE 53B

Key: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

75	Key	CAT Number	Accession
	432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA884939
	423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993605 BF926635 AA228938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
			BG215094 BG198867 BG196532 BG208220 BG212418
	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922596 BE061803
			AI352469 BE061601 BI062752 AW818206 BF887722
80	422828	227063_1	BE671981 BE503379 AI655440 AI337054 AI288920 AI242370 AI825182 AA758081 BF855141 BF081068
	418477	4172_1	BC022538 AI980847 BF478249 BG217995 BG212702 BG182057 AW588883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
			AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
	443068	18595_17	AW752763 AI032142 N30308 N22181 H93390 AW675632
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690873

5	427521	513212_1	AW973352 BF222929 AW016853 BF059130 A1651829 BE551767 AA550414 A1339359 BF059601 A1961162 A1341422 A1206248 A1206165 AA548736 AA768578 A1539081 AW025957 AA736837 N79575 AW594357 AA480892 AA764852 AA736937 AW954733 AA315005 AW856665 A1964001 A1634418 AW235545 A1824860 BF223710 AW139686 A1672051 A1655566 AW025712 N36327 BF222876 N34083 AA911045 N40303 AW835451 BF510715 BE673055 BE464111 AW590520 A1637939 AA404324 AW236441 A1650952 BF056796 AA974433 AA301270 AA301379 AA301366 AA683356 AW592804 A1150267 AF147390 R76593 R76594 AJ420453 AL526740 AW968449 AA459140 AA843893 A1568516 AW971760 AA430089 A1753216 AA854268 AA743075 A1864957 AA458920 A1566634 AA211796 BG616512 BE169275 BF983253 BF969462 AA766261 A1769894 AA135833 A1831542 N63376 AA274392 A1754486 AW605017 AW460072 AA464599 BE881875 A1061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135865 H04812 BF666746 D59356 BG678312 N56840 AA166861 AA917062 AA757369 AW592218 AL109688 R23665 R26578 BC009612 NM_Q03626 B1597616 AV761592 AV760377 AL601008 B1604131 BE454918 BG187760 BG181525 BG210634 BG192899 A1263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572536 A1143991 AA084581 AA033610 AV742510 AV735788 R08336 AA210987 D57294 AA214584 AA207006 D56572 AK025201 AA425472 A1694282 BG057305 AA907787 A1268170 A1694577 AJ420494 A1809865 BF058095 A1787773 A1160445 AL044114 AW665529 A1129239 AW297152 A1268215 A169807 A1699353 BE552356 N66509 AA736741 AA382655 AW075811 AV759188 B1259364 BF445142 BG232065 A1141758 A1631202 A1167566 A1208445 AA889823 BF982682 N90322 B1090882 BF208005 AW953918 AL044113 A1016793 AA382556 AW235763 AA927051 A1862075 BE886691 BE619282 AA906366 AA938956 A1910938 AW102570 AA907160 AA907120 AA737188 A1246890 AW977353 BG576155 BM005591 A1479075 A1025794 A1017957 AA448270 BE466812 AA853422 A1392649 BG952034 AA513384 BF840124 BE714620 AW969505 A1553633 BM453041 AA760783 BE218582 A1340046 AW166131 BF515854 A1630295 AA461307 A1090881 AW023059 AA156797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 BE072634 BE072653 AA830615 AA214736 AA331718 AA218925 AW962081 AA354237 BG570706 BG572749 AW806284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H58605 BE157601 AA113758 NM_Q00363 X54183 M64247 A1265781 A1760600 A1367238 BE140258 AW207185 A1857074 C03333 A1193911 C05024 C03193 A1950215 C05070 C05613 W17389 C06351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C09114 C03103 A1669979 A1652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339 AK056686 BG399272 AA187835 BF821903 AV660550 AV660556 AV660602 BG564397 BE379584 BF446861 A1653056 AW973709 A1653173 BG054997 A1266043 B1054879 A1658750 A182830 AW021142 A1472184 AW170066 A1082443 A1167821 D58940 B1492086 H74180 AW130886 A1348677 A1278577 AA761517 A1698203 AA115535 A1264790 AW205074 AA860452 AA554902 A1000715 D62102 BE544768 A1376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832 B1015205 A1761324 AW880937 AW880941 AA338252 AA338213 AK055748 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF959651 A1675065 BG001061 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038 AA933717 BF061897 AW628327 AA641788 AA400495 BE065183 A1144398 BE085367 BF377924 NM_Q58166 AF220030 AL043894 AW974257 AA625445 AU153502 A1650537 AW612116 A1672377 AW772451 BE892241 BE501740 AA718936 A1650276 A1654206 BE503226 A1651327 AW873562 AW271269 AW271565 A1873518 A1207150 A1338826 A1650258 A1628362 AA227117 A1207149 AW052076 A1470776 AA588100 AW235852 AA769791 A1701653 AK027664 A1984770 AU153469 BE222316 AA809539 BE220093 AA608112 B1054316 AF080229 AF080232 U87593 U87592 U87591 U87590 A1636743 A1633818 AW206802 A1583718 AF080231 AF080234 AF080233 A1535594 A1818326 AF080230 S46404 A1970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 A1672574 BE467547 A1680833 AW614951 N25986 N25695 H69001 U87596 BE573974 A197498 A1701526 AA703396 AW139734 H82278 N86048 BE219539 BE871865 A1624817 BE466611 A1206344 AA574387 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 A1887798 BF674385 AA204735 AW496808 AA204833 AA207156 B1004766 AA206282 A1355204 H77808 AW590511 T39328 T39310 T39303 T39284 BE893356 AA625304 A1765607 A1624898 R76600 AA069661 BG988885 R35783 BF086499 AA428755 A1245055 BC013389 BC017308 A1023543 AA191424 A1627700 A1669633 AW958485 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG265837 A1720344 BF541715 AA365086 AA172236 N50454 AA620999 T16375 AW958037 R42557 A1337047 AA946360 A1638005 AA459950 A1624915 A1638047 A1467856 A1521826 AA860305 A1832315 AW003092 AW271756 AW779380 AA609879 A1634791 A1493770 A1565211 Z41145 A1627952 AA303734 BE349457 AW196765 AA256527 BE089727 T65754 AA229658 AA229857 AK056650 AK056356 A1828212 A1742073 AW300558 BG058755 AA058343 A1554842 AW207438 BF509981 BF444964 AW026234 A1620104 AA973460 A1370934 N63066 AA493129 AW590888 A1682952 A1167202 AA831394 A1421915 A1222883 BF477519 A1208777 AA765849 A1676076 A1370922 A1339579 AA486224 AA453524 AW771805 A1492842 H54679 AA961022 AW023555 H06192 AA910222 A1660021 A1032525 A1375480 A1361860 A1032919 AA833589 BG057928 AA553913 AW235737 AA002124 AA813636 F04607 A1657699 AA648100 BE091446 AA486378 BE002022 H84627 B1059837 BF917659 BF917100 BF917043 BF917104 BF916878 BG290981 AW954251 AA757126 H11545 AA353384 N48448 AA379845 AA004943 AA379828 AA002123 BM470118 AL598847 AL598830 BG899239 R57470 BF939179 A1650642 A1758851 BF352505 W68422 W36297 H11435 AA937499 A1783996 R12500 A1819557 N39083 Z41819 H22849 AA004942 R09436 R02403 T90942 T85823 BG028683 A1248120 B1650480 AW779829 N22494 BE155042 BE155040 BE154987 BE155012 BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573 AW813110 BF771370 BF771371 AW813113 AW003381 B1862319 AA204955 BF240507 BG212143 AW205739 BF760647 BM129481 B1760482 AW300025 A1288591 AW236114 A1302852 A1038548 A1797207 AA534496 BG188194 AA921877 BG191845 BG182959 BE620243 BF217428 BC009514 BM463015 AL528077 BM051874 BG773269 BM314351 BM314660 AW628666 AA316207 A1623431 AA504153 AA314700 BG195449 BG614101 A599967 BF438599 AW864793 A1802889 BE815132 AW468888 A1672189 A1052004 BF112024 AA772335 AW275054 AA573845 A1144148 A1968683 AA846576 AA927355 H00424 AW873295 R88209 F29686 BE928871 AA846804 AA757581 A1050950 A1092024 AA838807
10	427486	684159_1	
	421974	864120_1	
	435514	132288_1	
	434639	14739_1	
	414136	30243_1	
15	415684	18695_18	
	437421	978554_1	
	439780	49082_1	
	453160	6028_5	
20	417886	1031334_1	
	412537	14066_1	
25	440801	2635916_1	
	436909	586835_1	
	429228	215430_1	
30	451050	11847_4	
	418235	886897_1	
	418378	1227421_1	
	450375	16559_3	
35	409517	4537_1	
40	442562	39593_1	
	451105	1145037_1	
	424281	892055_1	
	430183	17316_1	
45	427298	115241_1	
	444386	1490237_1	
	414725	19377_1	
50	433641	35983_1	
55	418768	2293204_1	
	409268	109625_1	
	415989	10194_1	
60	433979	2078469_1	
	420218	191547_1	
65	418866	245947_1	
	449587	25369_2	
70	445685	381678_1	
	413646	1525656_1	
	437834	294580_1	
75	454679	174325_1	
	440840	29686_1	
80	433023	3970_8	
	437440	2497201_1	

5	417553	258857_1	AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204599 W60115 N56751 N30878
	408065	101881_1	AI769345 R71250 AI363766 R22777 R17009 R27985 R28243
	418049	12052_4	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
	430968	1237115_1	AJ314647 NM_052888 BI494693 AA835065 AI634477 AJ336678 AI807698 BF477887 AF011147 Z39187 R38979 F02234 AA984711 BI222234
	400268	840_4	AV731417 R42405 H04996 T88498 R12489 R12577 R42405
10			AW972830 AA489820 AA527647 AA570362
			U69868 AA448366 X63105 BC016514 BE694436 AI555840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194555 AI870824 BE973573
			BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687
			BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AJ783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859
			AW167268 AI990460 AW300443 AA779660 AI620588 BF115024 BE504703 AW626332 AI922851 BE006636 AU156376 AI168279 AA809916
			AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA328388 AU160565 AU159374 AA687987 N58510 AI650450
			AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782
			AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW365516 AW391532
15	440605	10075_1	BE934857 BF925057 AW438446 R86245 AW179270 BE087782 BI832144
	427239	20459_2	BC017350 BC021031 AI220219 AI828751 AW134498 BE138642 AA894554 AI278594 AV747315 BE561749 BI085890 TB0117 H69682 N70904
			AV741999 H70098
			AL532360 BE794750 AA582905 AI015057 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
			AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
20			AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307558 AA876188 T29587 AI307493 AI255068 AI252868 AI252839
			AW074809 AI252926 AI252160 AI251662 AI251282 AI610913 AI270787 AI270156 AI252075 AW073459 AW072901 AW072495 AW071420
			AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138955 BE138502 AW073455 AI334733 AI064335 BE139260
			AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
			BF18773 BF718645 AW074866 BE857822
25	445093	175983_1	AJ207197 BF773544 AW195462
	456505	15472_2	BC017955 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312
	428612	1383189_1	AA770001 AA431112 AA432126
	437642	77594_1	AL079309 AA281819
	440129	2607882_1	AI732597 AA977633 AA865818
30	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
			AW840571
	438243	2532601_1	AJ581311 AA781682 AA781678
	438869	52134_1	AF075009 R63109 R63068
35	434776	118129_1	AW974599 AA548988 R98760

TABLE 53C

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt\_position: Indicates nucleotide positions of predicted exons.

45	Pkey	Ref	Strand	Nt_position
	408547	7711513	Minus	172780-174358
	404996	6007890	Plus	37999-38145,38652-38998,39772-39872,4055
	402199	8576116	Minus	84187-84744
	402145	8018280	Plus	113086-114800
50	401837	7630990	Minus	120993-121095,121660-121729
	403780	8076989	Plus	93160-93409
	402299	6693370	Plus	23367-25175
	401435	8217934	Minus	54508-55233
	401464	6682291	Minus	170688-170834
55	402098	8117697	Minus	44186-44330
	404287	2326514	Plus	53134-53281
	406367	9256126	Minus	58313-58489
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
	402178	8575912	Plus	391138-391711
60	403433	9719611	Minus	72225-72437
	402408	9798239	Minus	110326-110491
	405935	6758795	Minus	163112-163652
	406542	7711499	Plus	117335-118473
	402099	8117697	Plus	121553-121742,123265-123423
65	404068	3168621	Minus	18123-18766
	401644	8576138	Plus	82655-83959
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	401091	9958240	Plus	94760-94898
	400587	9887626	Plus	25435-25588,25668-25747
70	401148	2547238	Minus	22521-23053
	403432	9719611	Minus	68204-68392
	400592	9887642	Minus	24642-24815
	403610	8308286	Plus	157705-157860

TABLE 54A:

Pkey: Unique Eos probe set Identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of normal testis to normal adult tissues

R2: Ratio of "average" normal testis to "average" testicular cancer

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
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	401979			C17000767.gij11990770[amb]CAC19651.1  (A	10.08	43.3
	421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	10.35	36.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.74	32.0
5	441728	A1797395	Hs.169797	Homo sapiens BOULE (BOULE) mRNA, complet	10.54	24.5
	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	4.86	22.0
	415211	R64730.	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.93	19.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.94	18.5
	449108	A1140683	Hs.98328	hypothetical protein MGC13040	7.94	17.5
10	420437	AA992768	Hs.97633	A kinase (PRKA) anchor protein 4	16.75	15.6
	438632	AA724299	Hs.304020	ESTs, Weakly similar to CRTG_HUMAN CALRE	6.51	14.9
	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	4.96	14.6
	406409			Target Exon	3.98	14.3
	427060	AW378993	Hs.90286	ESTs	3.56	14.2
	427310	A1613480	Hs.47152	leklin 3	4.50	14.0
15	427166	AA431576	Hs.99154	ESTs	4.28	13.9
	427178	AA398868	Hs.97542	Homo sapiens testis-development related	10.19	13.7
	410694	AL137538	Hs.85500	Homo sapiens mRNA; cDNA DKFZp434N2019 (f	5.76	13.4
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.24	13.3
20	427441	AA412605	Hs.343879	SPANX family, member C	10.45	12.6
	438067	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORN1	18.57	12.3
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1058E13 on	5.18	12.3
	427293	AA705799	Hs.183714	ESTs	10.79	12.1
	444963	A1916973	Hs.213603	ESTs	3.18	12.1
25	428608	A1699329	Hs.99168	ESTs, Weakly similar to AF132972 1 CGI-3	15.40	11.8
	453178	AA496088	Hs.61648	ESTs	4.13	11.8
	428618	AA885360		Target CAT	7.53	11.5
	401741			Target Exon	10.41	11.5
	422086	AW182930	Hs.250182	ESTs	4.39	10.7
30	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	7.04	10.6
	442373	A1377758	Hs.164799	testes development-related NYD-SP17	8.23	10.3
	427455	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax Interact	3.03	10.1
	437248	AW448940	Hs.93090	ESTs	8.06	10.1
	428008	AA444162	Hs.99344	hypothetical protein PRD-NY3	3.68	10.0
35	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	9.70	9.8
	422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	11.85	9.7
	451610	AW118604	Hs.207126	ESTs	5.63	9.7
	410630	BE044582	Hs.266847	ESTs, Weakly similar to KIAA1214 protein	4.38	9.5
	426677	AW949858	Hs.97165	ESTs	6.58	9.3
40	437558	A1126471	Hs.124112	ESTs, Moderately similar to HSI2_HUMAN D	4.47	9.2
	423088	NM_006687	Hs.123530	actin-like 7A	15.07	8.9
	426476	NM_003296	Hs.2042	taste specific protein 1 (probe H4-1 p3	18.55	8.9
	421952	AA300800	Hs.98849	cystein light chain 2B (DNL2B)	13.93	8.8
	429877	W37337	Hs.103014	ESTs	6.97	8.7
45	413114	A1826838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	3.78	8.6
	412026	AA383618	Hs.73073	taste-specific ankyrin motif containing	22.03	8.5
	411844	A1807681	Hs.144858	ESTs, Weakly similar to T17257 hypotheti	7.34	8.3
	436868	AA974253	Hs.120319	Homo sapiens autoimmune infertility-rela	4.16	8.2
	426599	AW183574		ESTs	6.29	8.1
50	426683	A1073430	Hs.146775	ESTs, Weakly similar to T30993 hypotheti	10.89	8.0
	426930	AA393442		ESTs	5.06	8.0
	427836	AA416842	Hs.116176	ESTs	4.79	8.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	5.11	7.9
55	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	21.26	7.6
	434150	BE047007	Hs.116116	testis specific, 10	4.85	7.6
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	10.28	7.5
	422116	H84205	Hs.111850	mitochondrial capsule selenoprotein	9.12	7.5
	433724	A1827749	Hs.144924	serine/threonine protein kinase SSTK	22.24	7.4
	410187	AA860341	Hs.104680	ESTs	3.03	7.4
	419564	AF063356	Hs.283764	F-box only protein 24	6.43	7.4
60	456182	A1147998	Hs.155833	ESTs, Weakly similar to spliceosomal pro	9.90	7.3
	418865	T19204	Hs.185685	ESTs	7.14	7.3
	426646	AA382787	Hs.122713	ESTs	7.03	7.3
	420349	NM_016811	Hs.97174	potassium inwardly-rectifying channel, s	14.80	7.3
65	428624	A1125222	Hs.98712	hypothetical protein DKFZp434H0311	3.71	7.1
	420710	NM_007009	Hs.99875	zona pellucida binding protein	20.78	7.1
	434317	A1674095		ESTs	3.98	7.1
	443432	A1056863	Hs.339871	ESTs	3.46	7.0
	425709	AA383076	Hs.159274	outer dense fibre of sperm tails 1	23.21	7.0
70	426670	AA383047	Hs.310210	ESTs	6.92	7.0
	408613	AW242086	Hs.253967	ESTs	5.77	6.8
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	9.23	6.7
	434133	A1655275	Hs.236635	ESTs, Weakly similar to ATHUB actin beta	7.46	6.7
	427294	AA412594	Hs.126902	ESTs	3.44	6.7
75	427262	AA448509	Hs.128652	ESTs	5.66	6.5
	429851	AA459835	Hs.120573	hypothetical protein DKFZp434K1172	9.01	6.5
	406378			NM_021247*:Homo sapiens prolamine 3 (PRM	3.96	6.4
	425865	AA393491	Hs.183740	ESTs	9.15	6.4
	428665	NM_017481	Hs.189184	ubiquitin 3	11.07	6.4
80	439379	AA835002	Hs.125611	ESTs	5.06	6.3
	427620	BE467881	Hs.97489	ESTs, Weakly similar to B28096 line-1 pr	9.29	6.2
	458940	BE149824	Hs.132888	KIAA1674	3.11	6.2
	426620	AW450252		ESTs	12.27	6.2
	429516	A1653299	Hs.99354	ESTs, Weakly similar to hyperpolarizatio	9.15	6.1



	426736	AA431615	Hs.130722	ESTs	3.58	6.1
	427843	AC006822	Hs.180943	hypothetical protein R30953_1	6.34	6.1
	426639	A1799059	Hs.112807	ESTs	6.93	6.0
5	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein	3.04	6.0
	433795	A1216683	Hs.122599	ESTs, Weakly similar to ALU7_HUMAN ALU S	10.45	5.9
	441232	A1656050	Hs.7086	hypothetical protein MGC12435	4.27	5.9
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	6.87	5.8
	426955	AA393669	Hs.238094	ESTs	4.75	5.8
10	428918	AL036867	Hs.2324	protamine 2	38.40	5.8
	427851	AA846543	Hs.98257	ESTs	15.87	5.8
	428208	AA442327	Hs.104854	ESTs	6.34	5.7
	422207	A1828862	Hs.10964	ESTs	6.43	5.7
	431153	AW972342	Hs.77823	hypothetical protein FLJ21343	9.24	5.7
	419350	AC005328		Homo sapiens chromosome 19, cosmid R2668	14.94	5.6
15	427107	AA885586	Hs.180346	ESTs	6.25	5.6
	429461	A188219	Hs.39311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	3.92	5.6
	432512	NM_003284	Hs.3017	transition protein 1 (during Xistons to	22.03	5.6
	434451	AW445179	Hs.121438	ESTs	7.89	5.6
20	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1125 (f	11.26	5.5
	427214	AA442240	Hs.178213	ESTs	8.41	5.5
	458658	A1301117	Hs.122055	ESTs	4.35	5.5
	457034	AA398061	Hs.295587	Homo sapiens chromosome 21 segment HS21C	11.29	5.4
	423120	AW160551	Hs.124021	soggy-1 gene	8.86	5.4
25	438983	AF085884	Hs.20029	proacrosin binding protein sp32 precursor	22.69	5.4
	426619	A1357194	Hs.119284	ESTs	7.07	5.4
	440822	A1554897		Homo sapiens clone 19187 placenta expres	3.60	5.4
	416205	AA176396	Hs.169624	ESTs	10.26	5.4
	426712	AW173177	Hs.197755	hypothetical protein MGC5356	8.17	5.3
30	427840	A1216654	Hs.98251	ESTs	6.44	5.3
	439314	AA382413	Hs.178144	ESTs	8.35	5.3
	428943	BE551631	Hs.20969	ESTs	6.31	5.2
	409209	AA460180	Hs.73217	ESTs	7.85	5.2
	441710	A187683	Hs.127510	ESTs, Weakly similar to ENC1_HUMAN ECTOD	7.73	5.1
35	420571	AA442366	Hs.98952	Human DNA sequence from clone RP1-29G22	9.39	5.1
	428563	AA431816	Hs.98660	ESTs	14.94	5.1
	433994	AL042483	Hs.336499	ESTs	6.84	5.0
	441856	A1674774	Hs.128014	ESTs	3.74	5.0
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093	4.29	5.0
40	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	4.14	4.9
	430232	AA469940	Hs.105324	ESTs, Moderately similar to FRHUH ferrit	10.66	4.9
	421850	AW274576	Hs.121021	ESTs	12.27	4.9
	449438	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	4.50	4.9
	426699	AA383337	Hs.121269	ESTs	5.67	4.9
45	426627	AF012359	Hs.195685	ESTs	20.66	4.9
	427285	AA401664	Hs.97784	ESTs	4.72	4.8
	423693	AL133633	Hs.131779	Homo sapiens mRNA; cDNA DKFZp434E2118 (f	6.03	4.8
	457019	AA421844	Hs.12830	hypothetical protein	3.87	4.8
	405264			NM_030813: Homo sapiens suppressor of po	4.48	4.8
50	450606	A1668605	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	3.76	4.8
	421378	L77564	Hs.103978	serine/threonine kinase 22B (spermogene	7.35	4.8
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	8.66	4.7
	427423	BE267041	Hs.177925	exonuclease NEF-sp	19.27	4.7
	438756	AW081754	Hs.303923	hypothetical protein DKFZp434L1717	12.05	4.7
55	424197	AF096834	Hs.142989	germ cell specific Y-box binding protein	17.70	4.7
	423284	AC005704	Hs.126496	Homo sapiens chromosome 19, cosmid R3134	7.50	4.7
	432117	AL036195	Hs.2909	protamine 1	55.33	4.7
	424426	A178416	Hs.132888	KIAA1674	5.41	4.6
	437387	A1198374	Hs.28847	AD026 protein	5.04	4.6
60	420718	NM_002301	Hs.99881	lactate dehydrogenase C	9.18	4.6
	420768	A1468780	Hs.292503	ESTs, Weakly similar to T47142 hypotheti	5.70	4.6
	423577	M86808	Hs.131361	pyruvate dehydrogenase (liponitide) alpha	10.93	4.5
	436661	A1125270	Hs.128069	ESTs, Weakly similar to T19142 hypotheti	3.82	4.5
	427749	BE045979	Hs.98095	Homo sapiens cDNA: FLJ23052 fis, clone L	6.45	4.5
65	441830	AA363104	Hs.42954	hypothetical protein DKFZp564D0372	11.29	4.5
	427877	AW138725	Hs.178067	ESTs	4.09	4.5
	426623	AA382826	Hs.132793	ESTs	26.62	4.5
	429965	AL040379	Hs.99551	Homo sapiens cDNA FLJ11789 fis, clone HE	13.25	4.5
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.88	4.4
70	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosom	3.46	4.4
	421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	4.69	4.4
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	19.15	4.4
	426710	BE041517	Hs.143893	ESTs	5.57	4.4
	428710	A1850919	Hs.126780	ESTs, Weakly similar to T12519 hypotheti	11.86	4.4
75	438641	AW138484	Hs.190653	ESTs	6.19	4.4
	420614	AL110281	Hs.99364	putative transmembrane protein	6.88	4.4
	422705	NM_006686	Hs.119287	actin-like 7B	9.73	4.4
	421805	AL042716	Hs.130947	hypothetical protein DKFZp434N1415	5.89	4.4
	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610712, mRNA,	6.77	4.3
80	426738	AA421097	Hs.291902	ESTs	3.49	4.3
	440403	AW665135	Hs.130531	ESTs	6.97	4.3
	456085	A1184560	Hs.130362	ESTs, Weakly similar to A47582 B-cell gr	6.30	4.3
	439594	A1245026	Hs.111099	hypothetical protein MGC10974	7.85	4.3
	428909	A1190714	Hs.98945	ESTs	7.78	4.3

	426735	T78716	Hs.120446	ESTs	5.10	4.3
	430653	AW188039	Hs.131813	ESTs	5.29	4.3
	443038	AI968058	Hs.209206	ESTs, Weakly similar to S38782 actin bai	7.29	4.2
5	428677	AI657119	Hs.120036	troponin I, cardiac	10.73	4.2
	424220	AK000869	Hs.143251	hypothetical protein	9.13	4.2
	426299	H93373	Hs.168222	acrosomal vesicle protein 1	4.87	4.2
	426871	AA913840	Hs.98903	ESTs	3.76	4.2
	410163	AF151977	Hs.59260	NTT5 protein	7.29	4.2
10	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.29	4.2
	427757	AI142295	Hs.129794	ESTs	3.57	4.1
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	11.13	4.1
	401682			C16000122*gi5689527[db][BAA83047.1] (A	6.37	4.1
	403783			NM_031956.Homo sapiens NYD-SP14 protein	3.74	4.0
15	421611	AA459841	Hs.97309	ESTs	11.51	4.0
	404271			ENSP00000244792*-Phosphoglycerate kinase	4.02	4.0
	441900	AW027571	Hs.7973	hypothetical protein DKFZp434G156; KIAA1	8.86	4.0
	423000	AF049615	Hs.122959	Huntingtin Interacting protein M	3.60	4.0
	423118	AL035460	Hs.124009	Human DNA sequence from clone RPS-860F19	4.84	4.0
20	420419	AA397798	Hs.11614	HSPC085 protein	4.07	3.9
	435897	AF269223	Hs.128322	I-complex 11 (a murine top homolog)	23.29	3.9
	428516	R38137	Hs.156469	ESTs, Moderately similar to KIAA0940 pro	5.28	3.9
	427179	AA400690	Hs.97543	ESTs	6.18	3.9
	426609	AL040604	Hs.99344	hypothetical protein PRTD-NY3	10.07	3.9
25	452679	AA131657	Hs.23830	ESTs	5.24	3.9
	441443	BE466999	Hs.129293	ESTs	4.60	3.9
	427709	AI631811	Hs.180403	STRIN protein	3.82	3.9
	435484	AA682756	Hs.98051	ESTs	5.10	3.9
	426555	AA389291	Hs.130767	Homo sapiens cDNA: FLJ23653 fls, clone 1.	4.61	3.8
30	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	7.14	3.8
	421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214 salivary	5.20	3.8
	427086	AA436131	Hs.188781	ESTs	5.76	3.8
	420475	AW408407	Hs.187018	ESTs	3.99	3.8
	441357	AI240184	Hs.343487	ESTs	4.63	3.8
35	438643	AA757628	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	8.04	3.8
	441806	AI024442	Hs.346385	ESTs	5.48	3.8
	413209	AW083791	Hs.21263	suppressor of potassium transport defect	9.02	3.8
	414544	AA149285	Hs.115659	hypothetical protein MGC5521	10.15	3.8
	427251	AI026844	Hs.98843	ESTs, Highly similar to GRA2_HUMAN GLYC	7.69	3.8
40	437982	N93465	Hs.121764	ESTs, Weakly similar to testicular tekli	3.46	3.7
	442589	BE409869		protein kinase, cAMP-dependent, regulato	4.50	3.7
	425841	BE262961	Hs.99052	ESTs	8.26	3.7
	410350	AA446395	Hs.62595	chromosome 9 open reading frame 9	7.64	3.7
	440487	AI203685	Hs.135763	ESTs	5.90	3.7
45	419455	AW172570	Hs.14600	ESTs	4.23	3.7
	436588	AA759233		ESTs	5.04	3.7
	421610	AA393188	Hs.90034	hypothetical protein FLJ21916	5.53	3.7
	441982	AI216902	Hs.48802	ESTs	4.79	3.6
	427288	AI139000	Hs.97792	hypothetical protein DKFZp434I099	5.17	3.6
50	414439	W45387	Hs.100007	regulatory factor X, 2 (influences HLA c	4.43	3.6
	401798			Target Exon	4.83	3.6
	433395	AF039442	Hs.160881	Homo sapiens colon cancer antigen NY-CO-	3.17	3.6
	438054	AI476330	Hs.234934	ESTs	3.56	3.6
	426658	AA387912	Hs.115366	Human DNA sequence from clone RP4-803K15	7.26	3.6
55	431986	AA536130		Novel human gene mapping to chromosome 20	6.13	3.6
	427872	AA835058	Hs.9622	Human DNA sequence from clone RP1-261G23	4.04	3.6
	437886	AA813689	Hs.123436	ESTs, Weakly similar to KIAA1205 protein	4.69	3.6
	420431	AB007131		Homo sapiens cDNA FLJ12825 fls, clone NT	4.24	3.5
	409467	Z22780	Hs.307358	cyclin, basic: protein of sperm head cyt	5.13	3.5
60	422770	AL117544	Hs.120021	DKFZP434I092 protein	8.02	3.5
	437399	AI808626	Hs.121188	ESTs, Weakly similar to T29922 hypotheti	5.03	3.5
	428448	AA625766	Hs.98609	ESTs, Weakly similar to A Chain A, Coagu	4.30	3.5
	426705	AL042749	Hs.97714	ESTs	10.45	3.5
	427312	AA400657	Hs.136283	ESTs	4.47	3.5
65	423329	AF054910	Hs.127111	laklin 2 (testicular)	4.40	3.5
	439290	AI638094	Hs.236896	ESTs	3.29	3.4
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	6.18	3.4
	420500	AC005261	Hs.98338	serine/threonine kinase 13 (neuronal PL1-	6.24	3.4
	441168	AI198850	Hs.131654	DMRT-like family B with proline-rich C-t	10.39	3.4
70	420482	X57655	Hs.98243	serine protease inhibitor, Kazal type, 2	20.38	3.4
	425985	AI208684	Hs.163960	Homo sapiens heat shock transcription fa	5.02	3.4
	444968	AW628509	Hs.148653	ESTs	5.10	3.4
	429210	AA448011	Hs.131918	ESTs	4.22	3.4
	442970	R28215	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	4.20	3.4
75	422782	AL133054	Hs.120369	hypothetical protein DKFZp434H2215	4.72	3.4
	436601	AA969884		ESTs	4.84	3.4
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	7.83	3.4
	415705	U06632	Hs.966	collin	6.30	3.4
	435587	AF215924	Hs.97899	putative allantoinase	3.48	3.3
	427572	AA417291	Hs.97978	hypothetical protein MGC4766 similar to	3.54	3.3
80	427541	AI798983	Hs.82921	solute carrier family 35 (CNP-staic aci	10.33	3.3
	429404	NM_005738	Hs.201672	ADP-ribosylation factor-like 4	3.57	3.3
	415014	AW954064	Hs.24951	ESTs	4.03	3.3
	420547	AF155140	Hs.98738	gonadotrophin-regulated testicular RNA hs	10.76	3.3

5	412092	H43229	Hs.125201	ESTs, Weakly similar to I38022 hypotheli	5.27	3.3
	441579	AW468847	Hs.127194	ESTs	7.13	3.3
	420619	AF130256	Hs.99430	testis zinc finger protein	5.19	3.3
	425388	AB014595	Hs.155976	cullin 4B	3.07	3.3
	426638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.52	3.3
10	429938	BE295804	Hs.226377	phosphate cytidylyltransferase 2, ethanol	3.03	3.3
	453017	R84301	Hs.31387	DKFZP564J0123 protein	3.30	3.3
	424466	AL040420	Hs.148250	Homo sapiens mRNA; cDNA DKFZp434N1535 (f	4.81	3.3
	442084	HB1173	Hs.34596	ESTs	4.78	3.3
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	4.63	3.3
15	434183	AW104257	Hs.123426	ESTs, Weakly similar to SN1L_HUMAN PROBA	5.73	3.3
	428093	AW594506	Hs.104830	ESTs	6.95	3.3
	433982	AA724720	Hs.112941	ESTs	5.11	3.2
	428821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (fr	4.04	3.2
	408415	AW418788		ESTs, Weakly similar to S43569 R01H10.6	3.49	3.2
20	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.77	3.2
	402867			Target Exon	3.19	3.2
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	3.69	3.2
	436114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	14.29	3.2
	427748	AA421041		ESTs	4.57	3.2
25	422794	AJ011733	Hs.120857	synaptogyrin 4	4.23	3.2
	417488	AL046052	Hs.321046	hypothetical protein FLJ11743	3.57	3.2
	440115	R41808		ESTs, Weakly similar to B Chain B, Solut	4.67	3.2
	437143	AW204056	Hs.8917	ESTs	4.16	3.2
	417473	M55268	Hs.82201	casein kinase 2, alpha prima polypeptide	4.02	3.2
30	426594	AA884317	Hs.97130	ESTs	3.45	3.2
	428733	AA346824	Hs.191996	Homo sapiens organic cation transporter	6.29	3.2
	440884	AI382142	Hs.132104	ESTs	8.48	3.2
	427141	AW628007	Hs.97643	testis-specific protein TSP-NY	5.60	3.2
	431534	AI137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp434F0919 (f	5.10	3.2
35	438670	AI275803	Hs.123428	ESTs	4.08	3.2
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fls, clone L	4.26	3.2
	452251	R37132	Hs.65009	ESTs	4.01	3.1
	444141	AW629475	Hs.8977	ESTs, Weakly similar to RED1_HUMAN DOUBL	4.89	3.1
	428254	AK000542	Hs.183362	hypothetical protein FLJ20535	5.23	3.1
40	421621	AL045589	Hs.180197	ESTs	7.09	3.1
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	3.57	3.1
	457138	AW140059	Hs.98579	ESTs	13.17	3.1
	428524	AA429772		ESTs	4.40	3.1
	428726	AA432195	Hs.98694	ESTs	6.47	3.1
45	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fls, clone TH	4.07	3.1
	428076	AA420979	Hs.234895	ESTs, Weakly similar to Lysozyme [H.sapi	5.97	3.1
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.45	3.1
	424450	AL137526	Hs.147472	dyncin intermediate chain 2	6.01	3.1
	433963	AI218808	Hs.187778	ESTs	5.68	3.1
50	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.20	3.1
	440933	AI208217		ESTs	3.44	3.1
	441854	AA215990	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.s	4.03	3.1
	423313	NM_014269	Hs.128838	a disintegrin and metalloproteinase doma	6.36	3.1
	428630	AA431270	Hs.140646	ESTs	3.59	3.1
55	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R2	5.63	3.0
	434720	AI208541	Hs.189180	ESTs, Weakly similar to cytochrome c-lik	6.04	3.0
	436328	AI201145	Hs.122042	Human DNA sequence from clone RP4-576H24	7.10	3.0
	429293	AI767879	Hs.99214	ESTs	5.69	3.0
	427255	AA400082	Hs.343593	ESTs, Weakly similar to TD54_HUMAN TUMOR	5.37	3.0
60	440713	AA904448	Hs.126368	ESTs	6.28	3.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	7.88	3.0
	423216	NM_015896	Hs.167380	BLU protein	6.68	3.0
	444844	AW070834	Hs.144794	ESTs	5.00	3.0
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.75	3.0
65	427829	AI188225		ESTs	7.36	3.0
	426879	AI889340	Hs.115437	hypothetical protein MGC3048	7.24	3.0
	427362	AA625582	Hs.97762	EST	4.38	3.0
	441973	T80072	Hs.10688	ESTs, Weakly similar to HRIHFB2157 [H.sa	4.06	2.9
	428989	AF104260	Hs.194712	pint (Drosophila)-like 1	4.45	2.9
70	438735	M76676		ESTs	3.81	2.9
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	11.37	2.9
	427585	AA609661	Hs.190582	ESTs, Moderately similar to WASP-family	6.26	2.9
	427306	AI478743	Hs.229275	ESTs	3.00	2.9
	418725	AL117637	Hs.306094	DKFZP434I225 protein	7.13	2.9
75	456748	AW137749	Hs.125902	ubiquitin specific protease 2	3.48	2.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.80	2.9
	433836	AA610065	Hs.179548	ESTs	3.33	2.9
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	3.22	2.9
	437426	AW136558	Hs.125246	ESTs	4.49	2.9
80	405528			C2002547:gi14507721 ref NP_003310.1  tit	6.03	2.9
	442977	AW291731	Hs.144080	ESTs	4.23	2.9
	433330	AW207084	Hs.132816	hypothetical protein MGC14601	13.24	2.8
	424275	AW673173	Hs.144505	DKFZP566F0548 protein	5.60	2.8
	428657	AA770016	Hs.121182	ESTs	3.64	2.8
	410202	AB023213	Hs.60177	KIAA0996 protein	3.00	2.8
	428080	AI198658	Hs.98330	ESTs	4.09	2.8
	427252	AA400089	Hs.97757	hypothetical protein FLJ13031	4.34	2.8

	458255	AW140126	Hs.132357	ESTs	3.23	2.8
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.95	2.8
	440582	AA993337	Hs.129082	ESTs	5.29	2.8
5	435566	AI457958	Hs.80464	hepatitis B virus x-interacting protein	3.28	2.8
	433771	AI028794	Hs.112684	ESTs	3.36	2.8
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.30	2.8
	426703	AI221893	Hs.121549	ESTs	3.93	2.8
	430251	AA609245	Hs.181451	ESTs	4.04	2.8
10	427184	AI969351	Hs.180471	ESTs	6.78	2.8
	439909	AW450062	Hs.187134	ESTs, Moderately similar to AF263742 1 g	3.65	2.8
	448885	AW003686	Hs.30325	ESTs, Highly similar to AF200923 1 test	3.34	2.7
	450340	AA442322	Hs.60288	ESTs	5.39	2.7
	428100	AW665592	Hs.190413	ESTs	5.32	2.7
15	449333	AI203021		ESTs	4.35	2.7
	429861	AI989571	Hs.99510	ESTs	3.28	2.7
	426622	AI044400	Hs.25371	ESTs, Weakly similar to A37232 mucin, tr	5.38	2.7
	427256	AI042436	Hs.97723	ESTs	4.08	2.7
	408407	AF214680	Hs.44685	C3HC4-like zinc finger protein	3.27	2.7
20	403328			Target Exon	4.26	2.7
	436264	AA707457	Hs.120014	ESTs	3.58	2.7
	427104	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial ci	3.68	2.7
	426640	AI200961	Hs.98104	ESTs	4.80	2.7
	426789	AW296167	Hs.91930	ESTs	4.23	2.7
25	435274	AA887547	Hs.150905	ESTs	4.25	2.7
	426612	AA922067	Hs.184185	ESTs	7.17	2.7
	435110	N42688	Hs.81001	F-box only protein 25	4.85	2.7
	433792	AA778661		ESTs	4.06	2.7
30	423278	AI117627	Hs.126289	Homo sapiens mRNA; cDNA DKFZp434B115 (fr	3.04	2.7
	427284	AA400298	Hs.144696	ESTs	5.81	2.6
	423375	Z94277	Hs.127689	type 1 protein phosphatase inhibitor	3.38	2.6
	422362	Z46967	Hs.115460	calicin	4.72	2.6
	439993	T18864	Hs.144924	serine/threonine protein kinase SSTK	5.03	2.6
	409364	AI480252	Hs.137368	ESTs	7.22	2.6
35	419224	NM_012189	Hs.314452	fibrous sheathin II	13.88	2.6
	428915	AI041278	Hs.87908	Snf2-related CBP activator protein	4.73	2.6
	427181	AI183653	Hs.27888	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.21	2.6
	442122	AI932330		ESTs	3.07	2.6
40	424812	AF059252	Hs.153299	DCM-3 (C. elegans) homolog Z	3.80	2.6
	430856	AI183529	Hs.2706	glutathione peroxidase 4 (phospholipid h	3.19	2.6
	427234	AA398867	Hs.104875	ESTs	3.43	2.6
	423005	AL080148	Hs.123004	DKFZP434B204 protein	3.53	2.6
	428214	AA936282	Hs.120397	ESTs	4.14	2.6
	452613	AA461599	Hs.23459	ESTs	7.78	2.6
45	410380	AL133068	Hs.62880	novel protein similar to mouse MOV10	3.45	2.6
	452637	AW247390	Hs.77735	hypothetical protein FLJ11618	3.43	2.6
	401712			Target Exon	4.61	2.6
	429186	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	5.90	2.6
50	438124	AA778610	Hs.122045	ESTs	3.43	2.6
	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	3.60	2.6
	410279	BE271977	Hs.61809	hypothetical protein FLJ14117	4.36	2.6
	428625	W87565	Hs.18566	ESTs	5.29	2.6
	433439	AA431176	Hs.133230	ribosomal protein S15	3.50	2.6
	433760	AW592321		ESTs	3.26	2.6
55	431219	AI190773	Hs.127204	ESTs, Weakly similar to similar to CR16,	5.10	2.5
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	8.07	2.5
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.56	2.5
	445158	AI992108	Hs.127206	ESTs	3.80	2.5
	440860	R10482	Hs.132876	ESTs	4.26	2.5
60	452420	BE664871	Hs.29463	centrin, EF-hand protein, 3 (COC31 yeast	3.95	2.5
	433281	N48673	Hs.146037	hypothetical protein DKFZp434C135	5.68	2.5
	429869	AI269514	Hs.129802	ESTs	3.49	2.5
	433949	AI674766	Hs.112877	ESTs	5.15	2.5
	427688	AA298760	Hs.180181	hypothetical protein FLJ14904	10.46	2.5
65	414708	AA393379	Hs.97415	ESTs, Weakly similar to T33068 hypotheti	3.87	2.5
	408485	AW274294	Hs.144092	ESTs, Weakly similar to A Chain A, Sacch	6.10	2.4
	412889	AA290712	Hs.82407	CXC chemokine ligand 16	5.64	2.4
	426956	AA393673		ESTs, Weakly similar to ALU5_HUMAN ALU S	4.68	2.4
	429152	AA447209	Hs.99099	Homo sapiens NYD-SP28 mRNA, complete cds	4.34	2.4
70	426247	U92982	Hs.98834	ESTs	5.40	2.4
	427589	T19219	Hs.97978	hypothetical protein MGC4766 similar to	3.40	2.4
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2 (testis)	5.85	2.4
	453353	U33055	Hs.32959	G protein-coupled receptor kinase 2 (Dro	4.82	2.4
	413372	H55532		tubulin, alpha 2	9.32	2.4
75	411737	AW160339	Hs.71791	hypothetical protein	5.26	2.4
	453868	NM_014433	Hs.35984	rhomboid tumor deletion region protein 1	3.05	2.4
	427098	AA398181	Hs.97602	ESTs	3.21	2.4
	427185	AA428708	Hs.99336	ESTs, Weakly similar to T15446 hypotheti	4.27	2.4
	426808	AA364109	Hs.177950	ESTs	7.80	2.4
80	444790	AB030506	Hs.11955	B9 protein	3.32	2.4
	426718	AA383656	Hs.126413	ESTs	4.20	2.4
	411441	AL042355	Hs.70202	WD repeat domain 10	6.14	2.4
	450862	AI983364	Hs.7740	oxysterol binding protein-like 1	4.97	2.3
	427054	AA421240	Hs.97570	ESTs	3.10	2.3

5	438633	AI663327	Hs.123501	ESTs	3.46	2.3
	427199	AW015836	Hs.292919	ESTs	4.31	2.3
	440182	AA868919	Hs.250110	ESTs	3.03	2.3
	435517	AA928626	Hs.130177	ESTs	3.64	2.3
	448309	BE044261	Hs.149774	ESTs	3.52	2.3
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	4.23	2.3
	433829	AI190715	Hs.102021	ESTs	6.08	2.3
	429485	AW197086	Hs.99338	ESTs	3.14	2.3
10	423058	AW964568	Hs.111591	ESTs	3.36	2.3
	433822	AI218609	Hs.112772	ESTs	3.83	2.3
	442268	BE278064	Hs.8179	hypothetical protein, clone 2746033	3.00	2.3
	434298	AA860390	Hs.116290	ESTs	3.71	2.3
	440720	AW662776	Hs.336943	Human DNA sequence from clone RP11-60H7	3.08	2.3
15	427554	AW246578	Hs.179615	hypothetical protein FLJ10058	3.39	2.3
	414251	AL042306	Hs.97689	VASA protein	11.25	2.3
	430254	AI809520		ESTs	3.27	2.3
	437418	AI478964	Hs.59459	ESTs	3.43	2.2
	437522	AA983844	Hs.121383	ESTs	4.15	2.2
20	422808	AA449014	Hs.121025	chromosome 11 open reading frame 5	3.09	2.2
	436595	AA725655	Hs.120480	ESTs	5.26	2.2
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	6.78	2.2
	421625	AA405386	Hs.178004	ESTs	3.22	2.2
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	5.51	2.2
25	428174	AA813321	Hs.126778	ESTs	3.09	2.2
	409735	AL035295	Hs.56175	H.sapiens gene from PAC 106H8, similar t	3.11	2.2
	444467	AI150368		ESTs	3.81	2.2
	433832	AA918018	Hs.172516	ESTs	6.94	2.2
	440036	AW593295	Hs.210956	ESTs	5.87	2.2
30	415240	AA161411	Hs.58668	chromosome 21 open reading frame 57	3.66	2.2
	432538	BE258332	Hs.278362	male-enhanced antigen	3.58	2.1
	440882	AI205777	Hs.129538	ESTs	3.83	2.1
	436605	AI187742		ESTs	3.41	2.1
	422990	AF036520	Hs.122764	BRCA1 associated protein	5.66	2.1
35	432174	AW590264	Hs.132806	ESTs	3.05	2.1
	409267	NM_012453	Hs.52515	transducin (beta)-like 2	5.46	2.1
	423021	AL036111	Hs.292767	ESTs	3.87	2.1
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	5.25	2.1
40	433812	AA725026	Hs.57165	ESTs, Weakly similar to T31611 hypothet	3.62	2.1
	456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	4.38	2.1
	437249	AA432202	Hs.103147	hypothetical protein FLJ21347	3.38	2.1
	426038	AA368101	Hs.99052	ESTs	3.03	2.1
	427065	AA397903	Hs.236635	ghz18912.r1 Soares_testis_NHT Homo sap	3.23	2.1
45	428824	W23624	Hs.173059	ESTs	3.07	2.1
	428224	X54017	Hs.183088	acrosin	3.18	2.1
	436954	AA740151	Hs.130425	ESTs	3.20	2.1
	444470	AA412196	Hs.13740	ESTs	4.27	2.1
	457579	AB030816	Hs.38761	HRAS-like suppressor	5.30	2.1
50	427686	AA417083	Hs.104789	ESTs	3.49	2.1
	439273	AW139099	Hs.269701	ESTs	3.83	2.1
	434318	AW207552	Hs.116328	ESTs, Weakly similar to A39554 transcrip	4.01	2.1
	427015	AA397520		ESTs	4.28	2.1
	421598	AW830942	Hs.106061	RD RNA-binding protein	3.30	2.1
55	427235	AA398959	Hs.148271	ESTs	3.07	2.1
	434520	AA205273	Hs.177011	hypothetical protein	3.19	2.0
	456051	T85626	Hs.78239	hypothetical protein FLJ20808	3.11	2.0
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	8.41	2.0
	451807	W52854		hypothetical protein FLJ23293 similar to	3.52	2.0
60	448984	AW751955	Hs.22753	hypothetical protein FLJ23318	4.73	2.0
	420484	W32963	Hs.98289	VRK3 for vaccinia related kinase 3	3.86	2.0
	414181	AK000476	Hs.75798	hypothetical protein	3.33	2.0
	424558	AF036847	Hs.150490	FK506-binding protein 6 (36kD)	7.70	2.0

TABLE 548

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

70	Pkey	CAT Number	Accession
	428618	2568_1	BC017898 BI826643 BG715794 BG722697 BI460787 BG773459 H52859 AI852853 AI890773 AW655193 AW340601 AA913806 AI337099 BE045942 AW572790 AW515852 H15004 AA909115 BI485310 BI482024 BI581578 BI463075 BG722527 R86003 BG623286 H15003 BI562131 BG435272
	428599	10110_1	BE736800 BM471423 AL557221 BG763302 BF742196 BF991016 BG200112 BF920027 BG576409 BG332214 BI830957 AI827504 AW183574 AI805171 AI126491 AA448257 AI090641 AW183329 AA994873 AI203683 BE041513 AA382280 AA382261 AL554887 BE273483
75	426930	1310779_1	AI809889 AA393442 AI150574 AI200886 AI221892 AA608977 AA813213
	434317	599587_1	AI209094 AI377740 AW117382 AW182289 AI674095 AW188019 AA897352 AA931314 AA923336 AW665317 AA629314 AA776691 AA908846 AA974625 AA884357 AI808590
	428620	142987_1	AL042392 AI147451 AA758821 AW450252 AA399310 AI656343 AI836668 AW515660 AI190733 AI025812 AA723645 AA709253 AA725709 AA398244 AA382463 AI138637
80	419350	13086_1	AI218809 BC014609 BG724383 AI024358 AA904573 AI138595 AA858685 AI768931 BI828436 BG717350 BG719800 AW182303 AA448181 BI828670 BI827131 BI830254 BI824155 BI831745 T19190 BI830415
	440822	532606_1	BG207582 BG192113 AA977616 AW274024 AI554897 AI221379 AA969158 AA908867 AI873494 AI015039
	421938	863689_1	AA412383 AA300575 BG773248 AA412243 AA405951

	442589	33097_2	NM_004157 X14968 BG480486 BE409869 BG723898 BG476313 AU121626 BE386516 AI959297 AW172340 AA896658 R23436 AJ015037 BE250558 BF590945 AW385993 BF983000 AA070235 AL556082 M78388 AW504473 AW370139 BG913697 BE899096 BG827945 BE741233 AI015465 AW370169 BE297350 AA093249	
5	436688	2470836_1	AI122828 AA909991 AA759233	
	431986	76926_1	AL591713 BF197609 AI985084 AW448916 AI243277 AI449630 AL449629	
	420431	29290_1	AW241405 AW205071 AI671586 AI652354 AI638465 AW590359 AW662771 AW594067 BE502532 AI218894 BE466416 BF056295 AI247366	
	436601	10131_1	AI990484 AI917746 AW665925 AI216456 AW182169 AA969884 AA723888 AI018419	
	408416	4581_6	BI602176 BI603138 BI459895 BI756030 AW418788 AA883999 AA724858 AI480311 AW196355 AI004813 AI651117 BE814363 AW589856	
10	427748	1372622_1	AA448124 AA447962 BI461165 AA405629	
	440115	34_3	AI208966 AA421041 AA815377 AA411964	
	428524	1382184_1	BF980396 R51074 BF979863 AI539370 BM128735 AA993397 AI611039 AW593985 R41808	
	440933	960517_1	AI208080 AA442862 AA429772	
15	427829	1373537_1	AI125404 AW593312 AI247364 AI208217 AA910021 AI015307	
	438735	10316_1	AI190292 AI188225 AA416673 AA416596 AA952888 AA872172 AA906874	
	449333	36378_1	M76676 NM_022571 BG772522 BF516449 AI537485 AW517245 BF762536 AA634446 AW196331 AI203036 BG722281	
			AK056320 AL522040 BI793043 AW071691 AI433882 AA855414 AA702684 BI792794 H96879 R52351 AA211126 AA442875 N25725 AA482563	
			N33446 N25222 Z41110 N26507 N73447 N24077 N20492 AW275550 H99619 AL518306 AL522041 AW959849 AL518307 AA725907 AI855113	
			AI309906 F10184 BM451081 BE257595 BG721625 BI828509 BG700470 F12568 Z45396 BI829288 AA364618 AA364851 AA421448 T74231	
20	433792	2204621_1	R52350 AA482415 AI203021 T88948 AI566842	
	442122	2684549_1	AI024286 AA768898 AA778661 AA868972 AA609524	
	433760	584982_1	AI932330 AI190707 AI376782 AA976847	
	428956	657337_1	AA809179 AW592321 AA758262 AI214437 AW072537 AA781937	
25	413372	32896_1	BI831486 AW190479 AI472793 AA460217 AA459937 BF082576 AA393673 AA398702	
			NM_006001 L11645 AI205604 AI207994 AI187362 AA709190 BI462421 BG772170 BG722772 AA436991 BG771655 BI553260 BF126025	
			BF125857 BI462670 BG724164 BI562424 BG721662 BI559662 BG722455 BI596415 BG717561 BG722138 BG773507 BG720572 C03867 AI016802	
			AL042663 AA770436 AA435720 T19365 AA626698 AA759057 AI208021 BF507844 AI208058 AA412719 AA426374 AI208775 AA977217 AA758055	
	430254	13102_1	F34585 AA180062	
30	444467	1008400_1	9G700885 AA868017 AW347119 AA971332 AI688794 Z20462 AI08145 AW665263 AA884952 AA906136	
	436605	1008207_1	AW663704 AI150368 AI216464	
	427016	683123_1	AI125340 AI125684 AI377949 AI125470 AI218351 AW665355 AI243952 AW663454 AI240603 AI187742 AA884214 AA723933	
	451807	17758_2	AA857437 AI968733 AI968938 AA992784 AA397520 AW236244	
			BM479185 AL552795 AL577722 BF038886 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 AI806539 AW449522 AA993634	
			AI827626 AA904788	
35	TABLE 54C			
	Key:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of		
40	Strand:	human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
45	Key	Ref	Strand	Nt_position
	401979	2828778	Minus	75693-75851,76977-77112
	406409	9256364	Minus	141101-141256
	401741	2982169	Plus	195686-196823,200241-200381
	406378	9256142	Minus	125408-126800
	405284	7329374	Plus	28556-28584
50	401692	3540172	Plus	26355-26510
	403783	8081824	Plus	128412-128635
	404271	9828129	Minus	56392-57645
	401788	6730720	Plus	22831-23448
	402857	9801539	Plus	13402-14133
55	405528	9531957	Minus	22418-22687
	403328	8468086	Minus	120428-120703
	401712	6682593	Minus	76410-76527,76692-76829,78737-78866,8024
60	TABLE 55A:			
	Key:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
65	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues		
70	Key	ExAccn	UnigeneID	Unigene Title
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal
	423961	D13866	Hs.136348	perlecan(OSF-2os)
	412948	BE243313	Hs.334851	UIM and SHS protein 1
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithel)
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)
75	414438	AI879277	Hs.76136	thioredoxin
	406658	AI920365	Hs.77961	major histocompatibility complex, class
	446899	NM_005397	Hs.16426	podocalyxin-like
	411573	AB029000	Hs.70823	KIAA1077 protein
	432730	AI065520	Hs.131358	ESTs
80	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothel
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
	447526	AL048753	Hs.303549	small inducible cytokine A2 (monocyte ch
	418174	L20688	Hs.83556	Rho GDP dissociation inhibitor (GDI) bet

5	406866	AW515336	Hs.29797	ribosomal protein L10	23.66
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	23.60
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	23.60
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptide	22.35
	417426	NM_002291	Hs.82124	laminin, beta 1	21.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	21.55
	439180	AI393742	Hs.199057	v-erb-b2 avian erythroblastic leukemia v	21.50
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	21.50
10	406669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	20.90
	412636	NM_004415		desmoplakin (DPI, DPII)	20.90
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIb	20.30
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	19.46
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	19.30
	406648	AA563730	Hs.277477	major histocompatibility complex, class	19.10
15	412247	AF022375	Hs.73793	vascular endothelial growth factor	17.45
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	17.40
	424800	AL035588	Hs.153203	MyoD family inhibitor	17.20
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	16.90
20	415314	N88802	Hs.5422	glycoprotein M6B	16.80
	406656	M16714	Hs.89643	major histocompatibility complex, class	16.75
	426285	AW367283		zinc finger protein 6 (CMPX1)	16.25
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	16.00
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	15.85
25	417088	M54915	Hs.81170	p1m-1 oncogene	15.60
	449338	H73444	Hs.394	adrenomedullin	15.61
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	15.33
	414420	AA043424	Hs.76095	immediate early response 3	15.30
	425543	R23313	Hs.334895	ribosomal protein L10a	15.10
30	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	15.00
	420754	W79431	Hs.346911	ribosomal protein L22	14.92
	410397	AF217517	Hs.63042	DKFZp564J157 protein	14.86
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	14.70
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	14.60
35	406786	AW161678	Hs.111334	femlin, tight polypeptide	14.57
	422105	AI929700	Hs.111660	endosulfina alpha	14.57
	422714	AS018335	Hs.119387	KIAA0792 gene product	14.25
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.05
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.00
40	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	14.00
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	13.95
	410185	BE294068	Hs.737	immediate early protein	13.85
	409038	T97490	Hs.60002	small inducible cytokine subfamily A (Cy	13.60
	410611	AW954134	Hs.20924	KIAA1628 protein	13.60
45	448588	AI970276	Hs.156905	KIAA1676	13.40
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	13.10
	420962	NM_005804	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.00
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	13.00
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	13.00
50	454413	AI653672	Hs.40092	PNAS-123	12.90
	415221	W07418	Hs.78225	annexin A1	12.89
	425535	AB007937	Hs.168287	KIAA0468 gene product	12.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	12.45
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.40
55	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	12.19
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	12.12
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	12.07
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	11.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	11.80
60	430542	AI557486	Hs.119122	ribosomal protein L13a	11.51
	424670	W61215	Hs.116651	epithelial V-like antigen 1	11.50
	432409	AA805638	Hs.130732	KIAA1575 protein	11.50
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	11.44
	425996	W67330		hypothetical protein AL110115	11.40
65	449981	AW265634	Hs.133100	ESTs	11.40
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	11.25
	407179	AA206465		thymosin, beta 4, X chromosome	11.21
	412823	R28898	Hs.74170	metallothionein 1E (functional)	11.10
	429978	AA249027		ribosomal protein S6	11.10
70	450377	AB033091		KIAA1265 protein	11.10
	418609	AB028624	Hs.85639	ATP synthase, H transporting, mitochondr	11.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	11.00
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	11.00
	451106	BE382701	Hs.25960	N-MYC oncogene	10.93
75	426552	BE297680	Hs.170328	moesin	10.91
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	10.90
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	10.80
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	10.80
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rhodokin, clone	10.75
80	423673	BE003064	Hs.1695	matrix metalloproteinase 12 (macrophage	10.70
	435056	AW023337	Hs.5422	glycoprotein M6B	10.70
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	10.70
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	10.65
	420676	AI434780	Hs.4248	vav 2 oncogene	10.60

	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	10.60
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	10.50
	436075	BE090176	Hs.179902	transporter-like protein	10.30
5	450139	AK001838		serum/glucocorticoid regulated kinase	10.30
	427691	AW194426	Hs.20726	ESTs	10.26
	424201	L33075	Hs.1742	HQ motif containing GTPase activating pr	10.15
	448412	AJ219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	10.10
	440528	BE313555	Hs.7252	KIAA1224 protein	10.06
10	423184	NM_004428	Hs.1624	ephrin-A1	10.05
	450847	NM_003155	Hs.25590	stanniocalcin 1	9.90
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.90
	438876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mito	9.90
	421395	D90084	Hs.1023	pyruvate dehydrogenase (liponamide) alpha	9.89
15	435918	AF263538	Hs.86232	growth differentiation factor 3	9.89
	411251	R19774	Hs.22835	HHGP protein	9.80
	406791	AJ220684	Hs.347939	hemoglobin, alpha 2	9.75
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	9.75
	425580	L11144	Hs.1907	galanin	9.60
20	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	9.60
	413813	M98956	Hs.75561	larotocarcinoma-derived growth factor 1	9.60
	434280	BE005398		gb:CM1-BN0116-150400-189-002 BN0116 Homo	9.60
	417944	AJ077186	Hs.82985	collagen, type V, alpha 2	9.53
	409863	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	9.51
25	428864	AK001666	Hs.185095	similar to SALL1 (sal (Drosophila))-like	9.42
	416926	H03109	Hs.263395	HT018 protein	9.41
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	9.40
	428066	AI634046	Hs.157313	ESTs	9.40
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.39
30	410325	AB023154	Hs.62284	KIAA0937 protein	9.30
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.30
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	9.29
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp647M072 (fr	9.24
	447211	AL161981	Hs.17787	KIAA1554 protein	9.22
35	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	9.20
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p85), ly	8.93
	421379	Y15221	Hs.103882	small inducible cytokine subfamily B (Cy	8.90
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.90
	422241	Y00052	Hs.170121	protein tyrosine phosphatase, receptor t	8.90
40	449335	AW150717	Hs.345728	STAT Induced STAT inhibitor 3	8.84
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	8.80
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	8.70
	428215	AW963419	Hs.155223	stanniocalcin 2	8.70
	446827	AI973016	Hs.15725	hypothetical protein SBB48	8.60
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	8.60
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	410023	AB017169	Hs.57929	sliT (Drosophila) homolog 3	8.50
	445245	AB032973	Hs.12461	LCHN protein	8.50
	448776	BE302454	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.40
50	463856	AA804789	Hs.19447	PDZ-LIM protein mystique	8.35
	410143	AA188168		KIAA1191 protein	8.35
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.30
	433208	AW002834	Hs.24095	ESTs	8.30
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.25
55	432559	AW452948	Hs.257631	ESTs	8.20
	450581	AF081513	Hs.25195	TGF-beta 4	8.10
	450157	AW961578	Hs.60178	ESTs	8.10
	444795	AI193356	Hs.160316	ESTs	8.10
	400288	X06258	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	8.05
60	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	8.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	8.00
	419970	AW612022		ESTs	8.00
	411975	AI916058	Hs.144583	ESTs	7.95
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.90
65	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	437103	AW139408	Hs.152940	ESTs	7.90
	432636	AA340864	Hs.278962	claudin 7	7.87
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.84
70	418682	H13139	Hs.92282	paked-like homeodomain transcription fa	7.80
	407137	T97307		gb:ye53n05.s1 Soares fetal liver spleen	7.80
	450147	AW373713	Hs.146324	CGI-145 protein	7.75
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.70
	449571	AW016812	Hs.200266	ESTs	7.70
	429355	AW973253	Hs.292689	ESTs	7.70
75	446488	AB037782	Hs.15119	KIAA1361 protein	7.70
	414774	X02419	Hs.77274	plasminogen activator, urokinase	7.69
	424244	AI186431	Hs.296638	prostate differentiation factor	7.67
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	7.65
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	7.65
80	451812	X81889	Hs.152151	plakophilin 4	7.65
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	7.60
	452674	AK001061	Hs.30925	hypothetical protein FLJ10199	7.60
	422746	NM_004484	Hs.119651	glypican 3	7.60
	414020	NM_002884	Hs.75703	small inducible cytokine A4 (homologous	7.57



5	447874	BE270640	Hs.19192	cyclin-dependent kinase 2	7.57
	426889	BE245550	Hs.171825	basic helix-loop-helix domain containing	7.55
	444933	NM_018245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.53
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	7.50
	425246	A085561	Hs.155321	serum response factor (c-fos serum respo	7.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	7.47
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.44
	401466			vesicle-associated membrane protein 4	7.43
10	435080	A1831760	Hs.155111	hypothetical protein FLJ14428	7.40
	413686	A169213	Hs.71404	ESTs	7.40
	408805	AF025374	Hs.46465	T-cell, immune regulator 1	7.40
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.30
	444838	AV651680	Hs.208558	ESTs	7.30
15	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	7.28
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	7.20
	452924	AW580939	Hs.97199	complement component C1q receptor	7.15
	436398	H87136	Hs.5174	ribosomal protein S17	7.15
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.10
20	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.10
	447735	AA775268	Hs.5127	Homo sapiens cDNA: FLJ23020 fis, clone L	7.10
	401192			Target Exon	7.08
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	7.08
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	7.00
25	449567	A1990790	Hs.188614	ESTs	7.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to t38022 hypot	7.00
	450506	NM_004480	Hs.418	fibroblast activation protein, alpha	7.00
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	7.00
	431427	AK004001	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	6.90
30	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	6.87
	442492	AA528489	Hs.234518	ribosomal protein L23	6.84
	417365	D50883	Hs.82028	transforming growth factor, beta recepto	6.80
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	6.80
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	6.80
35	436684	NM_001290	Hs.4980	LIM domain binding 2	6.80
	442685	AB033017	Hs.8594	KIAA1191 protein	6.79
	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	6.77
	411789	AF245505	Hs.72157	Adipon	6.76
	441565	AW553575	Hs.303125	p53-induced protein PIGPC1	6.75
40	440268	BE270030	Hs.338959	Homo sapiens, clone IMAGE:3677185, mRNA	6.74
	444207	A1565004		cathepsin D (lysosomal aspartyl) protease	6.72
	408912	AB011084	Hs.48924	KIAA0512 gene product: ALEX2	6.70
	429600	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	6.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.70
45	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	6.70
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	6.70
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.70
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	6.66
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	6.65
50	406858	A1865720	Hs.29797	ribosomal protein L10	6.65
	435748	AA689756	Hs.117335	ESTs	6.63
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	6.62
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65857 alpha-1C-	6.62
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.61
55	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.60
	442379	NM_004613	Hs.8285	transglutaminase 2 (C polypeptide, prote	6.55
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	6.50
	450294	H42587	Hs.238730	hypothetical protein MGC10823	6.45
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.45
60	418707	U97502	Hs.67497	butyrophilin, subfamily 3, member A2	6.43
	402145			Target Exon	6.43
	414652	AL036058	Hs.76807	major histocompatibility complex, class	6.42
	436860	H12751	Hs.5327	PRO1914 protein	6.40
	438982	BE046694		gb:hn41c11.x1 NCL CGAP_RDF2 Homo sapiens	6.40
65	435837	AA830893	Hs.119769	ESTs	6.40
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	6.40
	446173	BE565849	Hs.14158	copine III	6.39
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	6.36
	412093	BE242591	Hs.14947	ESTs	6.34
70	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.30
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.30
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.30
	447519	U46258	Hs.339665	ESTs	6.30
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.30
75	434423	NM_006769	Hs.3844	LIM domain only 4	6.30
	434524	AA635931	Hs.249716	ESTs	6.30
	441970	AW959918	Hs.73737	ESTs	6.30
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	6.30
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	6.25
80	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	6.23
	407284	A1539227	Hs.214039	hypothetical protein FLJ23556	6.20
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.20
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	6.20
	417315	A1080042	Hs.180450	ribosomal protein S24	6.20

	418840	AI821614	Hs.185831	ESTs	6.20
	410668	BE379794	Hs.159651	hypothetical protein	6.16
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.13
5	413840	AJ301558		RNA binding motif protein, X chromosome	6.13
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	6.12
	450944	AA554989		sudD (suppressor of bimD6, Aspergillus n	6.10
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	6.10
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.10
10	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	6.10
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	6.10
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.09
	435812	AA700439	Hs.188490	ESTs	6.06
15	432805	X94630	Hs.3107	CD97 antigen	6.06
	441283	AA927570	Hs.131704	ESTs	6.06
	417632	R20855	Hs.5422	glycoprotein M6B	6.00
	435905	AW997484	Hs.5003	KIAA0450 protein	6.00
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	5.99
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.95
20	410698	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	5.95
	425291	AA354572		gb:EST62857 Jurkat T-cells V Homo saplen	5.95
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14295 fis, clone PL	5.93
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	5.90
25	447217	BE465754	Hs.17778	neuropilin 2	5.90
	417228	AL134324	Hs.7312	ESTs	5.86
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13616 fis, clone PL	5.86
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.84
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.84
30	414483	R25513	Hs.10683	ESTs	5.82
	428570	AA430321	Hs.293945	ESTs	5.81
	443194	A954968		matrix Gla protein	5.80
	429582	AI569058	Hs.22247	ESTs	5.80
	414405	AI362533		KIAA0306 protein	5.80
35	428342	AI739188		Homo sapiens cDNA FLJ13458 fis, clone PL	5.80
	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 (H.sapi	5.80
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	5.80
	442821	BE391929	Hs.8752	transmembrane protein 4	5.77
	434511	R28982	Hs.18106	ESTs	5.76
40	408745	AW511970	Hs.279860	tumor protein, translationally-controlled	5.70
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	5.70
	453115	AW772041	Hs.18439	ESTs, Moderately similar to JC5238 galac	5.70
	406857	AA613726	Hs.29797	ribosomal protein L10	5.69
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	5.68
45	444273	AI903474	Hs.230	fibromodulin	5.65
	441623	AA316805		desmoglein 2	5.63
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone G	5.63
	440099	AL080058	Hs.6909	DKFZP564G202 protein	5.60
	434096	AW862958	Hs.75825	pleiomorphic adenoma gene-like 1	5.60
50	417621	AV654694	Hs.82316	Interferon-induced, hepatitis C-associat	5.60
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	5.60
	438278	BE408248	Hs.57988	hypothetical protein FLJ22357 similar to	5.58
	430451	AA836472	Hs.297939	cathepsin B	5.57
	406699	L08505	Hs.182979	ribosomal protein L12	5.53
55	458965	AA010319	Hs.60389	ESTs	5.50
	430592	AJ224864	Hs.9688	leukocyte membrane antigen(LRC1)	5.50
	433655	AL036559	Hs.3463	ribosomal protein S23	5.50
	428471	X57348	Hs.184510	stratfin	5.42
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	5.40
60	417849	AW291587	Hs.82733	nidogen 2	5.40
	408989	AW361666	Hs.49500	KIAA0745 protein	5.40
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	5.40
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	5.40
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	5.40
65	406819	AA908472		gb:cg82a10.s1 NCL_CGAP_Ov8 Homo sapiens	5.39
	416655	AW968813	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.36
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.34
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.34
	427968	AI857607	Hs.181301	cathepsin S	5.32
70	429307	AU076592	Hs.198951	jun B proto-oncogene	5.30
	424950	AA602917	Hs.156974	ESTs	5.30
	410619	BE512730	Hs.65114	keratin 18	5.30
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	6.27
	425430	BE185921	Hs.98073	ESTs, Moderately similar to Z195_HUMAN Z	5.27
75	411165	NM_000169	Hs.59089	galactosidase, alpha	5.26
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	5.26
	435631	BE254088	Hs.29647	uncharacterized hematopoietic stem/proge	5.24
	418905	BE539574		actinin, alpha 4	5.23
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	5.22
80	440703	AL137663	Hs.7378	Homo sapiens mRNA: cDNA DKFZp434G227 (fr	5.20
	430814	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	5.20
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	5.20
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.20
	407254	AW129401	Hs.181166	eukaryotic translation elongation factor	5.20

	409604	AW444448	Hs.49124	ESTs	5.20
	432581	AU076465	Hs.278441	KIAA0015 gene product	5.16
	430556	AW967807	Hs.13797	ESTs	5.16
5	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5.16
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	5.15
	454227	AW963897	Hs.44743	KIAA1435 protein	5.15
	429357	AB007867	Hs.278311	plexin B1	5.12
	452191	AU076408	Hs.28309	UDP-glucose dehydrogenase	5.11
10	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis, clone NT	5.11
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	5.10
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	5.10
	421878	AA299852	Hs.111498	Homo sapiens cDNA FLJ11643 fis, clone HE	5.10
	424875	AI87945	Hs.199310	ESTs	5.10
15	427641	AI270591	Hs.146116	ESTs	5.10
	442806	AW294522	Hs.149991	ESTs	5.10
	442495	AI184717		ESTs	5.10
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.10
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	5.09
20	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.07
	418117	AI922013	Hs.83496	linker for activation of T cells	5.06
	431824	AW972842		gb:EST384937 MAGE resequences, MAGI. Homo	5.06
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	5.06
	410570	AI133086	Hs.64593	ATP synthase, H transporting, mitochondr	5.03
25	431805	NM_014053	Hs.270594	FLVCR protein	5.00
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	5.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	5.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	5.00
	443834	H73972	Hs.134460	ESTs	5.00
30	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	5.00
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	4.97
	422200	AA080895	Hs.347969	cytochrome c oxidase subunit IV	4.95
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	4.94
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	4.94
35	452063	R53185	Hs.32366	ESTs, Weakly similar to TWIST_HUMAN TWIST	4.93
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.93
	429558	AI391454	Hs.207251	nucleolar autoantigen (55kD) similar to	4.92
	432588	X92715	Hs.3057	zinc finger protein 74 (Cof52)	4.92
	433162	AI025842		ESTs	4.92
40	406797	AI432224		ribosomal protein L6	4.91
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	4.90
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	4.90
	447197	R36075		gb:zh88b01.s1 Soares placenta Nb2HP Homo	4.90
	447832	AI433357		ESTs	4.90
45	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	4.90
	413593	AA206248		gb:zz78c12.r1 Stralagene hNT neuron (937	4.90
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	4.90
	441224	AU076964	Hs.7763	calumenin	4.90
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	4.90
50	424871	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.90
	417308	H60720	Hs.81892	KIAA0101 gene product	4.90
	438763	AI583207	Hs.99029	CCAA7/enhancer binding protein (C/EBP),	4.89
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.89
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (alfin)	4.88
55	421748	NM_014718	Hs.107809	KIAA0728 gene product	4.87
	427486	AA974433		fibroblast growth factor 4 (heparin secr	4.86
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	4.82
	406867	AA157857	Hs.182265	keratin 19	4.81
	449378	AW664026	Hs.59892	ESTs	4.81
60	427202	BE272922	Hs.173936	Interleukin 10 receptor, beta	4.80
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	4.80
	448906	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.80
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	4.79
65	441321	H17182	Hs.7771	B-cell associated protein	4.75
	448896	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr	4.75
	447232	AW499834	Hs.327	Interleukin 10 receptor, alpha	4.73
	449317	AW293413	Hs.132906	19A24 protein	4.73
	436372	AW972301	Hs.310286	ESTs	4.71
70	422082	AA016188	Hs.111244	hypothetical protein	4.70
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	4.70
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	4.70
	446659	AI335361	Hs.226376	ESTs	4.70
	414829	AA321668	Hs.77436	pleckstrin	4.70
75	418036	Z37976	Hs.83337	latent transforming growth factor beta b	4.70
	417677	NM_016055	Hs.82389	CGI-118 protein	4.70
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.70
	423766	AA303799	Hs.300141	ribosomal protein L39	4.70
	432407	AA221036	Hs.13273	gb:z03f12.r1 Stralagene NT2 neuronal pr	4.69
80	453485	BE620712	Hs.33026	hypothetical protein PP2447	4.67
	452973	H88409	Hs.40527	ESTs	4.67
	427816	AA159248	Hs.180909	peroxiredoxin 1	4.67
	406794	AI890243		ribosomal protein L6	4.66
	449476	AI348027	Hs.108557	hypothetical protein PP1057	4.65

	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.64
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	4.62
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	4.61
5	417535	AA203669	Hs.191482	ESTs	4.61
	421818	AW992976	Hs.50098	NM_002469:Homo sapiens NADH dehydrogenas	4.61
	408491	AI088063	Hs.7682	ESTs	4.60
	426398	AI249368	Hs.98558	ESTs	4.60
	410295	AA741357		ndogen (enactin)	4.60
10	407198	H91679		gbcyv04a07.s1 Soares fetal liver spleen	4.60
	440327	R12581	Hs.191146	ESTs	4.60
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.60
	426141	C05686	Hs.293972	ESTs	4.60
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	4.59
15	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.58
	416987	D86957	Hs.80712	KIAA0202 protein	4.57
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.57
	416581	H66276	Hs.108288	ESTs	4.56
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	4.56
20	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	4.56
	413663	BE247585	Hs.75462	BTG family, member 2	4.55
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity 1, rec	4.54
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	4.53
	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	4.52
25	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	4.51
	440774	AI420611	Hs.153034	ESTs	4.51
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	4.51
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	4.51
	449267	AI638640	Hs.220624	ESTs	4.51
30	432605	NM_002104	Hs.3065	granzyme K (serine protease, granzyme 3;	4.50
	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50
	436823	AW748865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	4.50
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.50
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	4.50
35	415526	N76535	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	406623	X69392	Hs.91379	ribosomal protein L26	4.49
	456642	AW451623	Hs.109752	putative c-Myc-responsive	4.47
	406653	AA574074	Hs.77981	major histocompatibility complex, class	4.47
	408307	AI761786	Hs.204674	ESTs	4.46
40	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.46
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.45
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	4.45
	406870	AA075144		gb:zm96f06.s1 Stratagene ovarian cancer	4.45
	446291	BE397753	Hs.14523	interferon, gamma-inducible protein 30	4.44
45	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	4.44
	428773	BE256238	Hs.193163	bridging integrator 1	4.43
	427640	AF058293	Hs.180015	D-dopa-chromatolomease	4.43
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	4.43
	412265	AA101325	Hs.88154	hypothetical protein FLJ12457	4.43
50	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	4.42
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	4.41
	424858	AI568170	Hs.96886	ESTs	4.41
	408380	AF123050	Hs.44532	diubiquitin	4.40
	411960	R77776	Hs.18103	ESTs	4.40
55	428782	X12830	Hs.193400	Interleukin 8 receptor	4.40
	408380	AI806090	Hs.44344	hypothetical protein FLJ20534	4.40
	456629	AW691985		histone deacetylase 3	4.40
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	4.40
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	4.39
60	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	4.39
	427779	AA906997	Hs.180780	TERA protein	4.38
	422340	AW296219	Hs.116325	RAB7, member RAS oncogene family-like 1	4.37
	413276	Z24725	Hs.75280	mitogen inducible 2	4.36
	452651	AI218918	Hs.30200	KIAA0854 protein	4.35
65	453467	AI535997	Hs.30089	ESTs	4.35
	435961	BE293127	Hs.283722	GTT1 protein	4.35
	415691	AW963979	Hs.24723	ESTs	4.34
	435968	AW161481	Hs.111577	Integral membrane protein 3	4.34
	420099	D80011	Hs.95140	KIAA0189 gene product	4.33
70	412522	R48881	Hs.102991	hypothetical protein FLJ13956	4.33
	457073	AA233210	Hs.179943	ribosomal protein L11	4.31
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.31
	420732	AA789133	Hs.63525	ESTs	4.30
	432731	R31178	Hs.287820	fibronectin 1	4.30
75	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.30
	408784	AW971350	Hs.63386	ESTs	4.30
	441982	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	4.30
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.30
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	4.30
80	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.30
	413677	AW503116	Hs.301819	zinc finger protein 146	4.29
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.28
	406896	AI610447	Hs.48778	nban protein	4.26
	433550	AA989061	Hs.177376	ESTs	4.26

	406230		Target Exon	4.25	
	435655	AW105663	Hs.6947	HSPC069 protein	4.25
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.24
5	437386	W52452		ribosomal protein L10	4.24
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	4.23
	447341	AF106941	Hs.18142	arestin, beta 2	4.22
	410423	AW402432	Hs.63488	protein tyrosine phosphatase, non-recept	4.22
	409453	AI885516	Hs.95612	ESTs	4.22
10	428453	AB011110	Hs.184367	GTPase activating protein-like	4.22
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.21
	416072	AL110370	Hs.79000	growth associated protein 43	4.20
	450937	R49131	Hs.26267	ATP-dependant Interferon response protei	4.20
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.20
15	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	4.20
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	4.20
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.20
	431560	BE244136	Hs.260238	hypothetical protein FLJ10842	4.20
	439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN [H]	4.20
20	409245	AA361037		RNA isopenitlypyrophosphate transferas	4.18
	437296	AA350994	Hs.20281	KIAA1700	4.17
	406877	AA226392	Hs.179943	ribosomal protein L11	4.17
	419652	AL157485	Hs.91973	hypothetical protein	4.15
	406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.15
25	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	4.14
	448782	AL050295		KIAA0758 protein	4.14
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	4.14
	422960	AW890487		cadherin 13, H-cadherin (heart)	4.13
	432841	M83425	Hs.62	protein tyrosine phosphatase, non-recept	4.12
30	415657	AA856115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	4.11
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.11
	419726	U50330	Hs.1274	bone morphogenetic protein 1	4.11
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	4.10
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.10
35	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.10
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	4.10
	457415	AK000010	Hs.258798	hypothetical protein FLJ20003	4.10
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	4.10
	427509	M82505	Hs.2161	complement component 5 receptor 1 (C5a1	4.10
40	444633	AF111713	Hs.286218	junctional adhesion molecule 1	4.10
	441384	AA447849	Hs.288680	Homo sapiens cDNA: FLJ22182 fis, clone H	4.09
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.09
	422310	AA318822	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.08
	439815	AA206079	Hs.6693	hypothetical protein FLJ20420	4.07
45	417930	H81136	Hs.334604	Homo sapiens mRNA for KIAA1870 protein,	4.06
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.06
	424484	R68537	Hs.17962	ESTs	4.06
	417035	AA192465	Hs.22988	Homo sapiens clone IMAGE:451939, mRNA se	4.06
	412627	BE391959	Hs.74276	chloride intracellular channel 1	4.06
50	414890	BE281095	Hs.77573	uridine phosphorylase	4.05
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.05
	450687	AA011518	Hs.271778	ESTs, Weakly similar to I36022 hypotieti	4.05
	444224	AV648599	Hs.199438	ESTs	4.05
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
55	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.04
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.04
	408745	AW936356	Hs.300925	ESTs, Weakly similar to A46010 X-linked	4.03
	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.01
	410597	W16518	Hs.278518	amyloid beta (A4) precursor-like protein	4.01
60	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	4.01
	426398	BE266390	Hs.169718	calponin 2	4.01
	417777	AJ823763	Hs.7065	ESTs, Weakly similar to I78885 serine/th	4.01
	446979	AI654443	Hs.197683	ESTs	4.00
	418000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	4.00
65	426547	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.00
	436394	AA531187	Hs.126705	ESTs	4.00
	409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	4.00
	414802	AW630088	Hs.78550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	4.00
	446013	AJ360167	Hs.152774	ESTs	4.00
70	452404	AW450675	Hs.212709	ESTs	4.00
	444736	AA533491	Hs.23317	hypothetical protein FLJ14681	4.00
	438590	AA811465	Hs.123375	ESTs	4.00
	451838	AW005866	Hs.193969	ESTs	4.00
	449832	AA694264	Hs.60049	ESTs	4.00

TABLE 55B

Key: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Key CAT Number Accession





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AI336371 AI989381 AI131425 AI147483 AI311637 AW338638 AI141649 AA709414 AI187177 AA780854 AI333805 AA045312 AI623918 AI349421  
 W63763 W70299 AA557276 AA299007 N98212 W74064 N24823 T64892 AA054724 W73059 AI869152 N93462 N71889 AI537432 R71628  
 AA303089 AI498550 T60941 AV706417 AW067848 AI150577 AW338118 AI336313 AA826256 AI139518 AA662948 AA902723 AI970175 W68682  
 AI089380 AI148372 H99951 AW183001 AI270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914  
 AI862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547  
 N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 AI249109  
 BG015794 BE158357 BE158353 BE158358 BE158360 BE158352 BE158351 BE158355  
 AA075144  
 AW891955 AW604749 BE080872 R15559 BE177623 AW883520 AW945343 AI246157 T07082 AW805679 W95278 AA135796 W32615 AW995418  
 AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239  
 BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW382791 AW604759 AW666589 AW604768 N44337 AI378548  
 AW890438 AA077172 AI288633 AA229639 AA091945 AW945454 AA063629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399  
 AW885686 BE244086 BE005035 AW861913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW861939  
 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI246811 BE179917 BE002200  
 AW607506 AW392889 AW894560 AW381360 AI904206 AW863633 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW801420  
 AI695314 BE083790 AW858568 AW945650 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW688979 AW794240 AW945566  
 AI688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW604582 AW806778 AW838449  
 BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099  
 BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878862 AW894887 BE082356 AW898211 AW804286 AW610312 AI904717  
 AW610318 AW996909 AW610286 AW801923 AW880003 AI762171 AW062582 AW368713 AW062593 AW176663 AW842064 AW842069  
 AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577  
 AI908628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835566 AW606765 AW606770 AW835578 AW606758 AW806778 AI907484  
 BE172621 AW605768 AW999517 AW844165 BE171738 AW751683 AW810493 BE177484 BE177487 AA090510 AW844117 BE173367 AW999578  
 AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA810287 AW176676 AW076672 BE172639 AW893232 AA329629  
 BE089008 BE178350 BE178214 BE063291 AW820236 AW999653 BE089486 BE173126 BE171775 BE185787 AA558280 AI174840 AW999112  
 BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998872  
 AA767189 AW042722 H50699 AA768399 AA767764 AI087888 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945  
 AW118215 AI970480 AI627641 AW236081 AA574090 AI827652 AI661913 AI759993 N69591 N69276 BE467722 AW392780 BE172467 H92861  
 AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H67220 AW374781  
 BM476606 BI545004 BI834836 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AJ734997 AA931168 AA429766  
 N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI689031 N98464 AI820039 AI459034 AV652512 AA822990  
 BE857200 AA932998 AA740573 AI826264 AA865683 AI344650 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895  
 AA535689 BF806025 BF806061 BF805885 BF746099 BF746097 AI309259 AI597603 BF806066 AI090653 AI129205 AI248410 H72993 AW615341  
 BF805990 BF805982 AA933819 T34373 T35604 H56242 AA548145 T35607 BF806691 N94015 AV703438 BG774276 H82341 R76371  
 AK056682 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145  
 AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA298632 AI137857  
 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R68856 H01374 BI257369 BI259830  
 AW808845 BM468252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024  
 BF093281 AW021929 H22650 AA459715 BG496341 BE697763 BI254208 BG498543 H42946 BI059780 BI086741 H87896 H87599 BF691752  
 BE768511 BG940948 W37195 BF372041 BE883786 BF372082 BF367329 BF908744 AW966003 AV714014 BI492868 BI495144 AA921845  
 AI693426 AI652147 AI435448 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897  
 AW655247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245  
 AA884954 AI125702 AI382834 AA931835 AI358631 AW439905 AI027633 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667  
 AA948472 AI818214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D66771 AA095911 BE222062  
 D56772 AW372285 BM054985 D12485 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI482848  
 H16217 H21980 H22651 H88179 H87354 H44062 H25185 H44128  
 AB018301 AL050295 BF513128 AW385080 AI551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118788 AI453845  
 AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039548 AI002491 AI240412 Z25099 AA995178 AW050649  
 AW026140 AI796309 AI584012 BE166686 AI787991 AI309041 AA724059 AI895284 AI245085 T63971 Z40627 BE166681 BG570071 BF921915  
 BI562702 BG506502 AV658058 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281 BG540263 BG538901 N95226 AI3566752  
 AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361  
 N73937 AA127680 AW044037 AI086437 AA384077 BF941499 T93764 BG003285  
 BF090249 AW954847 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119  
 AA319610 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260

TABLE 55C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401466	6682292	Plus	28745-29023
401192	9719502	Minus	69559-70101
402474	7547176	Minus	53528-63828, 55755-55920, 57530-57757
402145	8018280	Plus	113086-114800
406230	4760409	Plus	71716-72515

TABLE 56A:

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigena Title: Unigene gene title  
 R1: Ratio of seminomatous testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigenelD	Unigena Title	R1
414438	AI879277	Hs.76136	thioredoxin	47.30



	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	44.80
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.10
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	34.90
5	417088	M54915	Hs.81170	pim-1 oncogene	31.10
	430542	A1557486	Hs.119122	ribosomal protein L13a	29.60
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	29.10
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	28.15
	406820	A1223958	Hs.108124	ribosomal protein S4, X-linked	28.13
10	433800	A1034381	Hs.135150	lung type-I cell membrane-associated gly	28.10
	406658	A1920965	Hs.77961	major histocompatibility complex, class	27.85
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	27.70
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	27.20
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.30
15	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	25.80
	429978	AA249027		ribosomal protein S6	25.40
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	24.60
	440207	A1371978	Hs.128326	ESTs	24.50
	425543	R23313	Hs.334895	ribosomal protein L10a	24.30
20	442682	BE379584		delichyl-diphosphooligosaccharide-protei	24.10
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	24.05
	413063	AL036737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	24.00
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	22.90
	420367	AA259090	Hs.257028	ESTs	22.90
25	408956	AW515336	Hs.29797	ribosomal protein L10	22.77
	417139	M89043	Hs.81328	nuclear factor of kappa light polypeptid	22.75
	412636	NM_004415		desmoplakin (DPI, DP1)	22.40
	420678	A1434780	Hs.4248	vav 2 oncogene	22.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	21.40
30	446827	A1973016	Hs.15725	hypothetical protein SBBI48	21.20
	410315	A1638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	21.10
	420754	W79431	Hs.346911	ribosomal protein L22	20.98
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	20.90
	440440	Z28925	Hs.7188	semu domain, immunoglobulin domain (Ig)	20.80
35	428490	A1971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	19.60
	422714	AB018335	Hs.119387	KIAA0792 gene product	19.15
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.00
	413787	AL352558		tyrosine 3-monooxygenase/tryptophan 5-mo	18.50
40	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.50
	430265	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.00
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	17.90
	448588	A1970276	Hs.156905	KIAA1678	17.70
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	17.50
45	428782	X12630	Hs.193400	interleukin 6 receptor	17.40
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	17.20
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	17.15
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	17.10
	440528	BE313555	Hs.7252	KIAA1224 protein	17.06
50	410143	AA188169		KIAA1191 protein	17.05
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.90
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	16.70
	429183	AB014604	Hs.197955	KIAA0704 protein	16.70
	450937	R49131	Hs.26267	ATP-dependent interferon response protel	16.60
55	449571	AW016812	Hs.200266	ESTs	16.50
	432730	A1066520	Hs.131358	ESTs	16.20
	428295	AW367283		zinc finger protein 6 (CMPX1)	16.15
	439180	A1393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	15.90
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	15.80
60	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	15.80
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	15.50
	428928	BE408838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	14.90
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	14.90
65	406656	M16714	Hs.89643	major histocompatibility complex, class	14.85
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	14.71
	450377	AB033091		KIAA1265 protein	14.70
	426998	W67330		hypothetical protein AL110115	14.60
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	14.60
70	427691	AW184426	Hs.20728	ESTs	14.42
	429614	A1371172	Hs.211539	hypothetical protein MGC4248	14.35
	451106	BE382701	Hs.25980	N-MYC oncogene	14.21
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.13
	436860	H12751	Hs.5327	PRO1914 protein	13.90
75	446899	NM_005397	Hs.16426	podocalyxin-like	13.90
	450000	A1952797	Hs.10888	hypothetical protein FLJ21709	13.75
	408380	AF123050	Hs.44532	diubiquitin	13.70
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	13.40
	427521	AW973352		ESTs	13.30
80	410598	A1817130	Hs.9185	Homo sapiens cDNA FLJ13698 fs, clone PL	13.25
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.23
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fs, clone OV	13.23
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	12.70
	426552	BE297860	Hs.170328	moesin	12.69

5	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.55
	436398	H87136	Hs.5174	ribosomal protein S17	12.50
	418151	AA664238	Hs.83583	actin related protein 2/3 complex, subun	12.30
	453020	AL182039	Hs.31422	Homo sapiens mRNA: cDNA DKFZp434M229 (fr	12.30
	410275	U85558	Hs.61795	transcription factor AP-2 gamma (activat	12.28
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	12.25
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	12.25
	416938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	12.20
10	419384	AA490866	Hs.39429	ESTs	12.20
	410186	BE294068	Hs.737	Immediate early protein	12.15
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	12.05
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.00
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	11.90
15	406989	AW361666	Hs.49500	KIAA0746 protein	11.80
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	11.80
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone 1.	11.80
	410325	AB023154	Hs.62264	KIAA0957 protein	11.70
	445817	NM_003542	Hs.13340	histone acetyltransferase 1	11.70
20	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p85), ly	11.61
	445863	R12234	Hs.13386	Homo sapiens clone 25028 mRNA sequence	11.60
	454413	AI653672	Hs.40092	PNAS-123	11.60
	418460	M26315	Hs.85258	CDB antigen, alpha polypeptide (p32)	11.40
	428065	AI634046	Hs.157313	ESTs	11.40
25	432805	X94630	Hs.3107	CD97 antigen	11.36
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.35
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	11.30
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-in	11.30
	405963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	11.11
30	402474			NM_004078:Homo sapiens cathepsin S (CTSS	11.00
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALJ7_HUMAN ALU S	11.00
	406786	AW161678	Hs.111334	ferritin, light polypeptide	10.95
	428227	AA321849	Hs.2248	small inducible cytokine subfamily B (Cy	10.90
	444656	AI277924	Hs.145199	ESTs	10.90
35	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	10.85
	440774	AI420611	Hs.153934	ESTs	10.82
	408669	AI493581	Hs.78146	platelet/endothelial cell adhesion molec	10.80
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	10.80
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.80
40	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	10.70
	437374	AL359571	Hs.44054	nuclein (GSK3B interacting protein)	10.65
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	10.60
	450719	AI098837	Hs.21349	ESTs, Weakly similar to R88B_HUMAN RAS-R	10.43
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.40
45	446682	AW205632	Hs.211198	ESTs	10.40
	447211	AL181961	Hs.17767	KIAA1554 protein	10.31
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	10.30
	422105	AI929700	Hs.111680	endosulfine alpha	10.21
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	10.20
50	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	10.20
	452651	AI218918	Hs.30209	KIAA0854 protein	10.15
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	10.11
	426996	AW988934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	10.10
	427761	AA412205	Hs.140986	ESTs	10.10
55	443623	AK001575	Hs.9536	hypothetical protein FLJ10713	9.90
	402145			Target Exon	9.82
	413886	AI469213	Hs.71404	ESTs	9.80
	446488	AB037782	Hs.15119	KIAA1351 protein	9.80
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	9.80
60	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	9.80
	407179	AA206465		thymosin, beta 4, X chromosome	9.72
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	9.70
	430068	AA464964		gb:cc80f10.s1 Soares ovary tumor NbHOT H	9.70
	446795	AI797713	Hs.156471	ESTs	9.70
65	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	9.65
	451864	N20370	Hs.69547	ESTs	9.65
	419490	NM_006144	Hs.80708	granzyme A (granzyme 1, cytotoxic T-lymp	9.60
	419504	AA974411	Hs.18672	ESTs	9.60
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.60
70	409208	Y00093		Integrin, alpha X (antigen CD11C (p150),	9.52
	424950	AA802917	Hs.158974	ESTs	9.50
	447534	AW953935	Hs.288656	ESTs	9.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	9.41
	423573	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.40
75	422960	AW890487		cadherin 13, H-cadherin (heart)	9.33
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	9.32
	408784	AW971350	Hs.63386	ESTs	9.30
	417407	AA923278	Hs.290505	ESTs, Weakly similar to protease JH.sapi	9.30
	432409	AA806538	Hs.130732	KIAA1575 protein	9.30
80	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	9.30
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.22
	408161	AW852912	Hs.300383	hypothetical protein MGC3032	9.20
	434280	BE006398		gb:CM1-BND116-150400-189-h02 BND116 Homo	9.20
	434624	AA635931	Hs.249716	ESTs	9.20

	450294	H42587	Hs.238730	hypothetical protein MGC10823	9.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.10
	434442	AA737415		ESTs	9.10
5	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.03
	447519	U46258	Hs.339665	ESTs	9.00
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	8.98
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	8.90
	436823	AW748865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	8.90
	442806	AW294522	Hs.149991	ESTs	8.90
10	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H	8.89
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	8.81
	406437	AW957744	Hs.278469	lacrimal proline rich protein	8.80
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	8.80
15	431187	AW971146	Hs.293187	ESTs	8.80
	421098	A1697901	Hs.192425	ESTs	8.70
	445528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	8.70
	446108	AL036596	Hs.42322	A kinase (PKA) anchor protein 2	8.70
	401091			decay accelerating factor for complement	8.62
20	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	438089	W06391		nuclear receptor subfamily 1, group 1, m	8.60
	431958	X63529	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	8.60
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFp547W072 (fr	8.59
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	8.56
25	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.50
	414829	AA321568	Hs.77436	pleckstrin	8.50
	430162	AW450843	Hs.346348	ESTs	8.50
	448412	A219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	8.50
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.45
30	407833	AW955632	Hs.56666	ESTs, Weakly similar to S19560 proline-r	8.43
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	8.40
	433208	AW002834	Hs.24095	ESTs	8.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.38
	425284	AF155568		NS1-associated protein 1	8.33
35	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.33
	408360	A1806090	Hs.44344	hypothetical protein FLJ20534	8.30
	426827	AW067805	Hs.172665	methylene tetrahydrofolate dehydrogenase	8.30
	453716	AA037675	Hs.152675	ESTs	8.30
	418840	A1821614	Hs.185831	ESTs	8.20
40	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	8.20
	449556	AA002008	Hs.188833	ESTs	8.20
	425535	AB007837	Hs.158287	KIAA0468 gene product	8.17
	409483	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.13
	432559	AW452848	Hs.257631	ESTs	8.10
45	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.10
	420099	D80011	Hs.95140	KIAA0189 gene product	8.01
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.00
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.00
	434423	NM_006769	Hs.3844	LIM domain only 4	8.00
50	437886	BE284111	Hs.31314	retinoblastoma-binding protein 7	8.00
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.92
	433655	AL038559	Hs.3463	ribosomal protein S23	7.89
	435968	AW161481	Hs.111577	integral membrane protein 3	7.89
	434511	R28982	Hs.18106	ESTs	7.88
55	423523	AW298828	Hs.193580	ESTs	7.86
	409327	L41182	Hs.53563	collagen, type IX, alpha 3	7.84
	411960	R77776	Hs.18103	ESTs	7.80
	434159	AW135214	Hs.191828	ESTs	7.80
	447500	A1381900	Hs.159212	ESTs	7.80
60	406698	L06505	Hs.182979	ribosomal protein L12	7.75
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	7.68
	428759	A1590401	Hs.21213	ESTs	7.66
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.62
	422689	AW858865		glt:RC3-CT0297-280100-013-d03 CT0297 Homo	7.60
65	444795	A1193356	Hs.160316	ESTs	7.60
	406663	U24683		immunoglobulin heavy constant mu	7.59
	442821	BE391929	Hs.8752	transmembrane protein 4	7.56
	412347	AW970026	Hs.73818	ubiquitin-cytochrome c reductase hinge p	7.52
	407252	AA659037	Hs.163780	ESTs	7.50
70	414405	A1362533		KIAA0306 protein	7.50
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.50
	429999	A1761902	Hs.99597	ESTs	7.50
	441436	AW137772	Hs.185980	ESTs	7.50
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.50
75	420943	A1718702	Hs.279930	major histocompatibility complex, class	7.46
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.43
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.42
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	7.41
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	7.40
80	408912	A9011084	Hs.48924	KIAA0512 gene product, ALEX2	7.40
	419839	U24577	Hs.83304	phospholipase A2, group VII (platelet-ac	7.40
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	7.40
	437469	AW753112	Hs.15514	hypothetical protein MGC3280	7.40
	432598	A1341227	Hs.157106	ESTs	7.38

	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.34
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.30
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.30
5	437103	AW139408	Hs.152940	ESTs	7.30
	442495	AI184717		ESTs	7.30
	445929	AK896680	Hs.323401	dpy-30-like protein	7.30
	446013	AI360167	Hs.152774	ESTs	7.30
10	436075	BE090176	Hs.179902	transporter-like protein	7.20
	450139	AK001838		serum/glucocorticoid regulated kinase	7.20
	423905	AW578960	Hs.135150	lung type-I cell membrane-associated gly	7.17
	406819	AA908472		gb:op82a10.s1 NCL CGAP_Ov8 Homo sapiens	7.16
	407719	AW863866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.12
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	7.10
15	413886	AW958264	Hs.103832	similar to yeast Upk3, variant B	7.10
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	7.10
	424677	U08414		zinc finger protein 137 (clone pHZ-30)	7.10
	427254	AL121523	Hs.97774	ESTs	7.10
20	427307	AF117947	Hs.174796	PDZ domain-containing guanine nucleotide	7.10
	438980	AW502384		gb:UL-HF-BR0p-aka-12-0-ULr1 NHL_MGC_5	7.10
	451129	BE072881		gb:RC2-BT0548-200300-012-s09 BT0548 Homo	7.10
	441878	AI801859	Hs.127982	ESTs	7.09
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.04
25	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	7.00
	417315	AI080042	Hs.180450	ribosomal protein S24	7.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.00
	429281	AA830866	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.00
	445245	AB032973	Hs.12481	LCHN protein	7.00
30	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.00
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	6.97
	410397	AF217517	Hs.63042	DKFZp564J157 protein	6.96
	418686	AW959433	Hs.326290	hypothetical protein FLJ12581	6.96
	445924	W30661	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	6.95
35	418134	AA397769	Hs.86617	ESTs	6.90
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	6.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	6.90
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypothel	6.88
	451838	AW005866	Hs.193969	ESTs	6.88
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	6.87
	453485	BE620712	Hs.33026	hypothetical protein PP2447	6.85
	401466			vesicle-associated membrane protein 4	6.84
	457073	AA233210	Hs.179943	ribosomal protein L11	6.83
	412093	BE242691	Hs.14947	ESTs	6.83
45	442492	AA528489	Hs.234518	ribosomal protein L23	6.83
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14298 fis, clone PL	6.83
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	6.82
	416401	N80139	Hs.268916	ESTs	6.80
	426501	AW043782	Hs.293616	ESTs	6.80
50	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	6.80
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	6.80
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.80
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.79
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	6.77
55	425277	NM_001241	Hs.155478	cyclin T2	6.72
	425246	AI055581	Hs.155321	serum response factor (c-fos serum respo	6.70
	428728	NM_016525	Hs.191381	hypothetical protein	6.70
	430289	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	6.70
	433735	AA608955	Hs.109653	ESTs	6.70
60	430556	AW967807	Hs.13797	ESTs	6.69
	417535	AA203569	Hs.191482	ESTs	6.69
	418117	AI922013	Hs.83496	linker for activation of T cells	6.67
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.65
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	6.62
65	447341	AF106941	Hs.18142	arrestin, beta 2	6.61
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	6.60
	442460	NM_014135	Hs.8345	PRO0641 protein	6.60
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	6.59
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.57
70	415221	W07418	Hs.78225	annexin A1	6.56
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.54
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	6.51
	421684	BE281591	Hs.105768	hypothetical protein FLJ10511	6.50
	441224	AU076964	Hs.7753	calumenin	6.50
75	443749	R38828	Hs.143463	ESTs	6.50
	448094	H24387	Hs.32061	ESTs, Weakly similar to 138022 hypothel	6.50
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	6.40
	418259	AA215404		ESTs	6.40
	421633	AF121860	Hs.106260	sorting nexin 10	6.40
80	435937	AA830893	Hs.119769	ESTs	6.40
	445612	N94126	Hs.12969	hypothetical protein	6.40
	451553	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.40
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.40
	422693	BE300073	Hs.279860	tumor protein, translationally-controlled	6.39

5	434817	AA082118	Hs.102737	goliath protein	6.38
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	6.35
	425410	AA310874	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.34
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.33
	435812	AA700439	Hs.188490	ESTs	6.31
	401113			solute carrier family 22 (organic cation	6.30
	408418	AW963897	Hs.44743	KIAA1435 protein	6.30
10	412220	BE360058	Hs.36787	chromodomain helicase DNA binding protei	6.30
	426780	BE242284	Hs.172199	adenylate cyclase 7	6.30
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	6.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	6.30
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	6.30
	449576	AW014631	Hs.225068	ESTs	6.30
15	449333	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	6.30
	432841	M83425	Hs.52	protein tyrosine phosphatase, non-recept	6.27
	411975	A1916058	Hs.144583	ESTs	6.26
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	6.25
	433162	A1025842		ESTs	6.23
20	449322	A1638616	Hs.196566	ESTs	6.22
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	6.20
	440327	R12581	Hs.181146	ESTs	6.20
	442832	AW206560	Hs.253569	ESTs	6.20
	456382	AW973003	Hs.179909	hypothetical protein FLJ22995	6.20
25	427968	A1857607	Hs.181301	cathepsin S	6.18
	414682	AL036058	Hs.78807	major histocompatibility complex, class	6.16
	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	6.16
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	6.15
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.15
30	445493	A1915771		metallothionein 1E (functional)	6.15
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.14
	427477	AW973119	Hs.178391	ribosomal protein L44	6.14
	422499	A1268666	Hs.19631	ESTs, Weakly similar to I38022 hypot	6.13
	443441	AW291196	Hs.92195	ESTs	6.12
35	413677	AW503116	Hs.301819	zinc finger protein 146	6.11
	406797	A1432224		ribosomal protein L6	6.10
	406857	AA613726	Hs.29797	ribosomal protein L10	6.10
	410387	A1277357	Hs.47094	ESTs	6.10
	410503	AW975746	Hs.188662	KIAA1702 protein	6.10
40	441962	AW972642	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	6.10
	425762	BE244076	Hs.158578	AT-hook transcription factor AKNA	6.08
	406877	AA226392	Hs.179943	ribosomal protein L11	6.07
	407784	AW139585	Hs.12708	ESTs	6.05
	418297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.05
45	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	6.01
	412949	A1471639	Hs.71913	ESTs	6.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	6.00
	435756	AA184666	Hs.33665	ESTs	6.00
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.00
50	441623	AA315805		desmoglein 2	5.98
	416926	H03109	Hs.263395	HTD18 protein	5.96
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subun	5.95
	441244	BE612935	Hs.184052	PP1201 protein	5.95
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.95
55	430604	H52761		Homo sapiens, clone MGC:12617, mRNA, com	5.94
	422310	AA316822	Hs.98370	cytochrome P450, subfamily IIS, polypept	5.92
	406605	AF025374	Hs.46465	T-cell, immune regulator 1	5.91
	433891	AA613792		gb:mo97h03.s1 NCI_CGAP_P12 Homo sapiens	5.90
	406542			C19000728*gi12585552[sp]Q9Y2Q1[Z257_HU	5.90
60	406858	A1865720	Hs.29797	ribosomal protein L10	5.90
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.90
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	5.90
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.90
	455263	AW981702		Homo sapiens cDNA FLJ14028 fis, clone HE	5.90
65	441321	H17182	Hs.7771	B-cell associated protein	5.88
	429083	Y08397	Hs.227817	BCL2-related protein A1	5.87
	406806	AW086535		ribosomal protein, large, P0	5.87
	416987	D86957	Hs.80712	KIAA0202 protein	5.86
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	5.83
70	428773	BE256238	Hs.193163	bridging integrator 1	5.83
	406794	A1890243		ribosomal protein L6	5.82
	457752	A1821270	Hs.285843	Homo sapiens cDNA FLJ14384 fis, clone HE	5.82
	435511	AA683336	Hs.189046	ESTs	5.81
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.80
75	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	5.80
	412528	A1123478	Hs.32112	ESTs	5.80
	424875	A1187945	Hs.199310	ESTs	5.80
	426981	AL044675	Hs.173081	KIAA0530 protein	5.80
	447711	AA59554	Hs.161286	ESTs	5.80
80	449961	AW265634	Hs.133100	ESTs	5.80
	415759	AK000978	Hs.79741	hypothetical protein FLJ10116	5.80
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5236 galactosy	5.79
	422773	AB028862	Hs.301552	KIAA1039 protein	5.78
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	5.78

5	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.77
	449317	AW293413	Hs.132906	19A24 protein	5.75
	425787	AA363867	Hs.155029	ESTs	5.73
	414890	BE281085	Hs.77573	uridine phosphorylase	5.72
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne)	5.71
10	435961	BE293127	Hs.283722	GTT1 protein	5.71
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	5.70
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	5.70
	437457	AA767900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	5.70
	446659	A1335361	Hs.226376	ESTs	5.70
15	457250	AAB11987	Hs.125779	ESTs	5.70
	414150	AA136026		gb:zn88d07.r1 Stratagene lung carcinoma	5.68
	439924	A1885897	Hs.125293	ESTs	5.67
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.66
	451812	X81889	Hs.152151	plakophilin 4	5.65
20	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	5.63
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	5.63
	424326	NM_014479	Hs.145298	ADAM-like disintegrin protease, dacylin	5.60
	431770	BE221880	Hs.268555	5'-3' exoribonuclease 2	5.60
	436511	AA721252	Hs.291502	ESTs	5.60
25	446630	AW364793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	5.60
	406623	X69392	Hs.81379	ribosomal protein L26	5.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.57
	416047	BE438894	Hs.78991	DNA segment, numerous copies, expressed	5.56
	437296	AA350994	Hs.20281	KIAA1700	5.56
30	453985	N44545	Hs.251865	ESTs	5.56
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	5.55
	448877	A1583696	Hs.253313	ESTs	5.53
	435748	AA689756	Hs.117335	ESTs	5.52
	420732	AA789133	Hs.53525	ESTs	5.51
35	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	5.50
	430815	AA488953		gb:aa55e05.r1 NCL_CGAP_GCB1 Homo sapiens	5.50
	435716	A1433540		gb:li69g05.x1 NCL_CGAP_Kid11 Homo sapien	5.50
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	5.50
	449625	NM_014253		odt (odd Ozten-m, Drosophila) homolog 1	5.50
40	456497	AW957956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	5.50
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associ	5.50
	433701	AW445023	Hs.15155	ESTs	5.49
	427640	AF056293	Hs.180015	D-dopachrome tautomerase	5.47
	420552	AK000492	Hs.98806	hypothetical protein	5.45
45	449338	H73444	Hs.394	adrenomedullin	5.42
	427176	AW381568	Hs.40334	ESTs	5.42
	409945	AW015935	Hs.122642	ESTs	5.40
	421568	W85858	Hs.99804	ESTs	5.40
	423961	D13666	Hs.136348	perlestin(OSF-2os)	5.40
50	440719	AA150869	Hs.25267	ATP-dependant Interferon response protei	5.40
	443035	Z45822	Hs.8908	Homo sapiens clone 24889 mRNA sequence	5.40
	456659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	5.40
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	5.40
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	5.39
55	422163	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
	439815	AA206079	Hs.6683	hypothetical protein FLJ20420	5.37
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	5.37
	457465	AW301344	Hs.122908	DNA replication factor	5.37
	412935	BE267046	Hs.75064	tubulin-specific chaperone c	5.36
60	409486	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	5.35
	430283	BE391688		RAB7, member RAS oncogene family	5.33
	406814	AA642947	Hs.119122	ribosomal protein L13a	5.33
	409019	AW385412		myosin regulatory light chain 2, smooth	5.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	5.30
65	412623	E28898	Hs.74170	metallothionein 1E (functional)	5.30
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	5.30
	418702	BE268368	Hs.86945	ESTs, Weakly similar to A46010 X-linked	5.30
	419926	AW800892	Hs.93796	DKFZP586D2223 protein	5.30
	422900	AA641201	Hs.222051	ESTs	5.30
70	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein Interac	5.30
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.30
	427774	AA276583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	5.30
	430177	AW969233	Hs.302746	MSTP028 protein	5.30
	430835	A1240006	Hs.192326	ESTs	5.30
75	433009	AA761668		gb:rz24c08.s1 NCL_CGAP_GCB1 Homo sapiens	5.30
	438776	AL360140	Hs.176006	Homo sapiens mRNA full length insert cDN	5.30
	447082	T85314	Hs.54629	thioredoxin-like	5.30
	415995	NM_004573		phospholipase C, beta 2	5.29
	424578	AK001973	Hs.150890	hypothetical protein	5.27
80	441303	AW293081	Hs.241801	ESTs	5.27
	427818	AA159248	Hs.180909	peroxiredoxin 1	5.27
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.26
	450273	AW298464	Hs.24743	hypothetical protein FLJ20171	5.24
	444708	AW971049	Hs.11774	protein (peptidyl-prolyl) cis/trans isome	5.23
	415121	D60871	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	5.21
	458079	AT968670	Hs.54277	DNA segment on chromosome X (unique) 992	5.21
	405086			NM_006662*:Homo sapiens Sn2-related CBP	5.20

5	413401	AJ361861	Hs.118659	ESTs	5.20
	418459	R85436	Hs.268814	ESTs	5.20
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.20
	426496	D31765	Hs.170114	KIAA0061 protein	5.20
	431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp554F133 (fr	5.20
10	434372	AA631373		gbcnp86c01.s1 NCL_CGAP_Try1 Homo sapiens	5.20
	436812	AW298067		gbc:U1-H-BWD-ajp-g-08-0-U1.s1 NCL_CGAP_Su	5.20
	441390	A1692550	Hs.131175	ESTs	5.20
	449419	R34910	Hs.119172	ESTs	5.20
	453127	A1696671	Hs.294110	ESTs	5.20
15	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.20
	417750	A1267720	Hs.260523	synovial sarcoma, translocated to X chro	5.19
	451614	AA847992	Hs.137003	ESTs	5.18
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	5.16
	405799	AA908548		gbcog83g12.s1 NCL_CGAP_Ov8 Homo sapiens	5.16
20	413963	R84282	Hs.75643	nuclear factor (erythroid-derived 2), 45	5.15
	422293	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	5.14
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	5.12
	414768	AW376989	Hs.259855	elongation factor-2 kinase	5.12
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	5.12
25	430478	NM_014349	Hs.241535	apolipoprotein L, 3	5.11
	420151	AA255931	Hs.186704	ESTs	5.11
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	5.10
	419317	AA236282	Hs.172318	ESTs	5.10
	424699	AW206227	Hs.287727	hypothetical protein FLJ23132	5.10
30	428403	A1393040	Hs.326159	leucine rich repeat (in FLJ) Interactin	5.10
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	5.10
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	5.10
	436137	A1056769	Hs.133612	ESTs	5.10
	440948	AW188311	Hs.128619	ESTs	5.10
35	448497	BEB13269	Hs.21893	hypothetical protein DKFZp761N0624	5.09
	416655	AW988613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.09
	417228	AL134324	Hs.7312	ESTs	5.09
	424868	A1568170	Hs.96886	ESTs	5.08
	418905	BE59674		actinin, alpha 4	5.08
40	427726	AJ359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fs, clone L	5.07
	442618	R56222	Hs.28514	ESTs	5.06
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.06
	406813	AW276131		ribosomal protein L13a	5.06
	454128	AL031269	Hs.41639	programmed cell death 2	5.05
45	440709	AW797724	Hs.130350	ESTs	5.05
	436372	AW972301	Hs.310286	ESTs	5.05
	446173	BE565849	Hs.14158	copine III	5.05
	453330	A1285081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	5.04
	418876	AA740616		gb:ny97f11.s1 NCL_CGAP_GCB1 Homo sapiens	5.03
50	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	5.00
	410570	A1133095	Hs.84593	ATP synthase, H transporting, mitochondr	5.00
	410800	BE280421	Hs.94499	ESTs	5.00
	431451	AA761378	Hs.192013	ESTs	5.00
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
55	435655	AW106583	Hs.6947	HSPC069 protein	5.00
	435919	AJ052189	Hs.114104	ESTs	5.00
	436394	AA531187	Hs.126705	ESTs	5.00
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fs, clone PL	5.00
	442232	AJ357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	5.00
60	442685	AB033017	Hs.8594	KIAA1191 protein	5.00
	444454	BE018316	Hs.11183	sorting nexin 2	5.00
	444670	HS8373	Hs.332938	hypothetical protein MGC5370	5.00
	447197	R35075		gbcyh88b01.s1 Soares placenta Nb2HP Homo	5.00
	450113	AJ683098	Hs.200868	ESTs, Moderately similar to ALU7_HUMAN A	5.00
65	450511	R07423	Hs.85092	thyroid hormone receptor Interactor 11	5.00
	450887	AA011518	Hs.271778	ESTs, Weakly similar to B8022 hypofitell	5.00
	452055	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	5.00
	457068	X69391		ribosomal protein L8	5.00
	406793	AW264291	Hs.5662	guanine nucleotide binding protein (G pr	4.97
70	439864	AJ720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.96
	420298	A1199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.94
	440638	AJ376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	4.92
	400261			Eos Control	4.91
	414420	AA043424	Hs.76095	Immediate early response 3	4.90
75	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.90
	434866	AF151103	Hs.112259	T cell receptor gamma locus	4.90
	449057	AB037784	Hs.22941	KIAA1363 protein	4.90
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.90
	451598	N28102	Hs.118078	ESTs	4.90
80	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	4.88
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.88
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.86
	447150	A1439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	4.86
	418453	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.85
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	4.85
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	4.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	4.84

	406781	AA639388		gb:ncq88b06.s1 NCI_CGAP_Co9 Homo sapiens	4.83
	449810	AB008681	He.23994	activin A receptor, type IIB	4.82
	410323	AJ241708	He.296322	Homo sapiens cDNA: FLJ22844 fis, clone K	4.81
	444652	BE513613	He.11538	actin related protein 2/3 complex, subun	4.81
5	422340	AW286219	He.115325	RAB7, member RAS oncogene family-like 1	4.81
	400424	AJ276316	He.287374	zinc finger protein 304	4.80
	411573	AB029000	He.70823	KIAA1077 protein	4.80
	421045	BE144608	He.55533	ESTs	4.80
10	425235	AA353113	He.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.80
	430387	AW372884	He.240770	nuclear cap binding protein subunit 2, 2	4.80
	438590	AA811465	He.123375	ESTs	4.80
	442071	BE048433	He.276043	ESTs	4.80
	449567	AI990790	He.188614	ESTs	4.80
15	453213	AA062650	He.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	4.80
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	4.78
	437802	AI475995	He.122910	ESTs	4.77
	409461	AA382169	He.54483	N-myc (and STAT) interactor	4.77
	421932	W51778	He.323949	kangal 1 (suppression of tumorigenicity	4.74
20	428453	AB011110	He.164367	GTPase activating protein-like	4.74
	413441	AI929374	He.75367	Src-like-adaptor	4.74
	446560	AK001567	He.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	4.73
	435541	AA687361	He.221318	ESTs	4.71
	410557	AA085803	He.192997	ESTs, Moderately similar to I7885 serin	4.70
25	412766	BE544475	He.54347	ESTs	4.70
	415526	N76536	He.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.70
	418973	AA233056	He.191518	ESTs	4.70
	421433	AI829192	He.22380	ESTs	4.70
	432925	AA878324	He.254750	ESTs	4.70
30	438869	AF076009		gb:Homo sapiens full length Insert cDNA	4.70
	442233	AW667149	He.28439	ESTs, Weakly similar to I38022 hypotheti	4.70
	447196	D61523	He.283435	ESTs	4.70
	448552	AW973653	He.20104	hypothetical protein FLJ00062	4.70
	444681	AJ243937	He.288316	chromosome 6 open reading frame 9	4.66
35	414598	AI084221	He.135150	lung type-I cell membrane-associated gly	4.66
	447817	BE620775	He.4866	Homo sapiens cDNA FLJ14387 fis, clone HE	4.65
	416062	AA724811	He.334791	Homo sapiens cDNA FLJ14609 fis, clone NT	4.65
	406881	X66975	He.172550	polypyrimidine tract binding protein (he	4.64
	424582	AF026849	He.150922	BGS1 (yeast homolog)-like	4.64
40	411165	NM_000169	He.69089	galactosidase, alpha	4.63
	436905	AW997484	He.5003	KIAA0456 protein	4.63
	445776	NM_001310	He.13313	cAMP responsive element binding protein-	4.62
	424730	NM_003358	He.23703	ESTs, Moderately similar to CEGT_HUMAN C	4.62
	414747	U30872	He.77204	centromere protein F (350/400kD, mitosis	4.62
45	410668	BE379794	He.159651	hypothetical protein	4.61
	406774	AW518383	He.177592	ribosomal protein, large, P1	4.60
	406648	AA563730	He.277477	major histocompatibility complex, class	4.60
	407961	W77762	He.79015	antigen identified by monoclonal antibod	4.60
	415682	A347128	He.191870	ESTs	4.60
50	417621	AV654694	He.82316	interferon-induced, hepatitis C-associated	4.60
	419970	AW612022		ESTs	4.60
	420012	AW957965	He.99014	Homo sapiens, clone IMAGE:3632168, mRNA	4.60
	431574	AW572659	He.261373	hypothetical protein dJ434014.3	4.60
	432586	AA568548		ESTs	4.60
55	437438	AL359620	He.14217	hypothetical protein DKFZp762P2111	4.60
	441355	AI822034	He.137097	ESTs	4.60
	444539	AI955765	He.146907	ESTs, Weakly similar to 2004369A chromos	4.60
	458965	AA010319	He.60389	ESTs	4.60
	406855	M21533	He.277477	major histocompatibility complex, class	4.60
60	414915	NM_002462	He.76391	myxovirus (influenza) resistance 1, homo	4.60
	414821	M63835	He.77424	Fc fragment of IgG, high affinity Is, re	4.59
	423766	AA303799	He.300141	ribosomal protein L39	4.59
	451351	AW056261	He.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	450043	AA895899	He.24332	CGI-26 protein	4.56
65	447742	AF113925	He.19405	caspase recruitment domain 4	4.54
	433339	AF019226	He.8036	glioblastoma overexpressed	4.54
	426395	BE151985		hypothetical protein FLJ23316	4.53
	418300	AI433074	He.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	4.53
	423799	AW026300	He.132906	19A24 protein	4.53
70	445093	AZ07197		ESTs	4.52
	428044	AA093322	He.301404	RNA binding motif protein 3	4.52
	453968	AA847843	He.62711	High mobility group (nonhistone chromoso	4.51
	414194	BE175494	He.75811	N-acylsphingosine amidohydrolase (acid c	4.50
	427747	AW411425	He.180655	serine/threonine kinase 12	4.50
75	406745	AW511970	He.279860	tumor protein, translationally-controlled	4.50
	407013	U35637	He.83870	gb:Human nebulin mRNA, partial cds	4.50
	407198	H91679		gb:yr04a07.s1 Soares fetal liver spleen	4.50
	414546	AA353776	He.901	CD48 antigen (B-cell membrane protein)	4.50
	429687	AI675749	He.211608	nucleoporin 153kD	4.50
	436566	BE545586	He.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	4.50
80	437634	AW283046	He.255158	ESTs	4.50
	438971	W32474	He.301748	RAP2A, member of RAS oncogene family	4.50
	442485	BE092285	He.29724	hypothetical protein FLJ13187	4.50
	445873	AA250970	He.251948	poly(A)-binding protein, cytoplasmic 1-I	4.50



5	450497	H64159	Hs.15328	ESTs	4.50
	417497	AW402482	Hs.82212	CD53 antigen	4.50
	447667	AL117611	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (f	4.49
	413856	D13639	Hs.75586	cyclin D2	4.49
	419556	U29615	Hs.91093	chitinase 1 (chitinotriosidase)	4.49
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.48
	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.48
	446021	BE389213	Hs.286	ribosomal protein L4	4.47
10	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.46
	412819	T25829	Hs.24048	FK506 binding protein precursor	4.46
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.45
	401846			NM_000988*:Homo sapiens ribosomal protei	4.44
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	4.43
15	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	4.43
	436623	AI417073	Hs.107285	ESTs	4.42
	412146	M92444	Hs.73722	APEX nuclease (multifunctional DNA repai	4.42
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	4.42
	416754	H07145	Hs.6799	ESTs, Weakly similar to T12483 hypotheti	4.41
20	436671	AW137159	Hs.183291	ESTs	4.40
	410079	U94362	Hs.58589	glycogenin 2	4.40
	420150	AA648712	Hs.29798	KIAA1712 protein	4.40
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.40
	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, non	4.40
25	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	4.40
	430280	AA361258	Hs.237868	Interleukin 7 receptor	4.40
	438330	AW450572	Hs.257316	ESTs	4.40
	438962	BE046594		gbcln41c11.x1 NCLCGAP_RDF2 Homo sapiens	4.40
	444794	AI419991	Hs.145225	ESTs	4.40
30	445100	AW186205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	4.40
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	4.40
	449832	AA694264	Hs.60049	ESTs	4.40
	452404	AW450675	Hs.212709	ESTs	4.40
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.39
35	425097	NM_014247		PDZ domain containing guanine nucleotide	4.37
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.37
	405742	AI468091	Hs.279860	tumor protein, translationally-controlled	4.36
	425095	AW014160	Hs.182585	KIAA1276 protein	4.34
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity 1, rec	4.34
40	442333	AI650877	Hs.129302	ESTs	4.33
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.32
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.32
	437386	W52452		ribosomal protein L10	4.31
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	4.30
45	408875	NM_015434	Hs.48804	DKFZP434B168 protein	4.30
	409604	AW444448	Hs.49124	ESTs	4.30
	418866	T65754		gbcyc1f007.s1 Stratagene lung (937210) H	4.30
	419423	D26488	Hs.90315	KIAA0007 protein	4.30
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	4.30
50	422797	AB033064	Hs.236463	KIAA1238 protein	4.30
	428457	AK002121	Hs.184465	hypothetical protein FLJ11259	4.30
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	4.30
	434551	BE387182	Hs.280658	ESTs, Highly similar to A35661 DNA excis	4.30
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	4.30
55	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	4.30
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.30
	452994	AW962597	Hs.31305	KIAA1547 protein	4.30
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.30
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.29
60	440910	H97875	Hs.117974	ESTs	4.29
	406853	AA514553	Hs.252259	hypothetical protein FLJ23059	4.28
	432295	BE091049	Hs.343665	ribosomal protein S15a	4.28
	400244			Eos Control	4.28
	413518	BE149455	Hs.75415	beta-2-microglobulin	4.28
65	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.27
	406746	AA580995	Hs.279860	tumor protein, translationally-controlled	4.26
	400395	AF111167		v-fos FBJ murine osteosarcoma viral onco	4.26
	443229	AI057129	Hs.133396	ESTs	4.26
	450201	T97838	Hs.25722	ESTs	4.25
70	409636	AA305729	Hs.18272	amino acid transporter system A1	4.25
	422082	AA016188	Hs.111244	hypothetical protein	4.24
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	4.24
	453902	BE502341	Hs.3402	ESTs	4.24
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	4.22
75	404854			Target Exon	4.21
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.20
	400440	X83957	Hs.83870	nebulin	4.20
	415049	N67334	Hs.50158	ESTs	4.20
	418304	AA215702		gbczr97g10.r1 NCLCGAP_GCB1 Homo sapiens	4.20
80	423180	AF068502	Hs.125031	choline/ethanolaminephosphotransferase	4.20
	424584	AW752714	Hs.5174	ribosomal protein S17	4.20
	429412	NM_005235	Hs.2407	POU domain, class 2, associating factor	4.20
	438141	AW946871		gbcRC2-ET0022-080500-012-d02 ET0022 Homo	4.20
	438607	AW080237	Hs.252884	ESTs	4.20

5	451952	AL120173	Hs.301663	ESTs	4.20
	455397	AW936332		gb:QV4-DT0021-281299-070-g01 DT0021 Homo	4.20
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287 similar to	4.19
	453247	T80198	Hs.111806	ESTs	4.19
	430451	AA836472	Hs.297939	calthapsin B	4.19
	414283	AW960011	Hs.154993	ESTs	4.18
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.18
	450746	D82673	Hs.278589	general transcription factor II, I	4.16
10	444797	AB018333	Hs.12002	KJAA0790 protein	4.18
	445718	H79791	Hs.15227	ESTs	4.15
	425783	AI026740	Hs.1948	ribosomal protein S21	4.15
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family, member	4.15
	406710	AI708347	Hs.184014	ribosomal protein L31	4.15
15	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	4.14
	422343	AI628633	Hs.346823	gb:ly77d05.x1 NCJ_CGAP_Kid11 Homo sapien	4.13
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	4.13
	406724	C14071	Hs.234518	ribosomal protein L23	4.12
	449475	AJ348027	Hs.108557	hypothetical protein PP1057	4.12
20	413828	L19067		v-rel avian cellcarcinoembryofectoma viral	4.11
	416819	U77735	Hs.80205	plm-2 oncogene	4.11
	436674	AA725002	Hs.272018	low molecular mass ubiquitinone-binding pr	4.11
	405266			Target Exon	4.10
	408895	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	4.10
25	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	4.10
	420851	AA281062	Hs.28493	hypothetical protein FLJ20142	4.10
	423096	AA732684	Hs.278428	progesterone induced protein	4.10
	428328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypothetl	4.10
	429355	AW973253	Hs.292689	ESTs	4.10
30	433308	AA582718	Hs.291650	ESTs	4.10
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.10
	450850	AA648886	Hs.151999	ESTs	4.10
	453785	AJ368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.10
	406864	AA613706	Hs.252259	ribosomal protein S3	4.10
35	410768	AF038185	Hs.55187	Homo sapiens clone 23700 mRNA sequence	4.09
	415612	AI98267	Hs.110613	KJAA0421 protein	4.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.08
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	4.08
	441374	AA043696	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	4.08
40	443415	AI065523	Hs.133472	ESTs	4.08
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	4.07
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.07
	400233			Eos Control	4.06
	421959	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.06
45	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	4.06
	424795	AW102850	Hs.153177	ribosomal protein S28	4.05
	446231	NM_002163	Hs.14453	interferon consensus sequence binding pr	4.05
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fls, clone H	4.05
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfam1	4.05
50	409061	AI204994	Hs.7874	Homo sapiens cDNA: FLJ21435 fls, clone C	4.03
	413891	BE271020		tumor suppressor deleted in oral cancer-	4.03
	414004	AA737033	Hs.7155	ESTs, Moderately similar to Z115357A TYK	4.02
	417035	AA192455	Hs.22958	Homo sapiens clone IMAGE:451938, mRNA se	4.02
	410584	AB011112		KJAA0540 protein	4.01
55	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.00
	423645	AI215632	Hs.147487	ESTs	4.00
	430048	T65064	Hs.73605	ESTs	4.00
	431113	AK000673	Hs.274337	hypothetical protein FLJ20666	4.00
	434170	AA626509	Hs.122329	ESTs	4.00
60	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fls, clone NT	4.00
	435391	AA704588	Hs.58534	ESTs	4.00
	446768	AV660306	Hs.110286	ESTs	4.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.00
	451831	NM_001674	Hs.460	activating transcription factor 3	4.00

TABLE 56B

Pkey: Unique Eos probe set identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE968931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358889 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709128 BE673807 AI923886 AA947032 AI276126 AI185720 AW510698 AA987230 BE467708 AW898628 AW898644 AI146984 AW043642 AI288245 AI186832 AI635262 AI139455 AI298739 AI813954 AI024768 BE694445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF476318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699468 D52477 D55017 BF956933 BG523583 AV646254 AA463522 BI003244 AI299190 W40188 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552







438141	1173217_1	AA776849 AW946871 AW946782 AW946955
455397	1163608_1	AW936332 AW936341
413828	9463_1	BC011603 BG479117 AU124990 BG829759 AU143705 BG701663 BG699781 AU131718 BE515064 AU121812 BG898850 AL558461 BM151887
5		AU128758 BM263692 AU099013 AU241350 UB8316 AW058398 AW469340 BF683967 A470140 AU150993 AA633376 AW150821 AA536142
		AU148749 A1520647 AU151769 AU163404 AW070666 A457758 AU153077 N99966 AW050940 BG055674 AA506657 AW301529 A1918646
		A1611235 A1266081 A1334542 AW071277 A1312434 AW303114 A1436544 A1436466 R22972 A1472987 N77896 AW072883 AA318683 D19761
		AW050566 A1312433 AA328444 R72435 AA430721 A1142589 AA582290 AU148896 AA721233 AW628132 R93935 AA100710 B1520773 A1934172
		BG222461 H85359 AW074639 AA017117 B1028412 AL582142 AA43547 AA586793 AA777535 AA693844 A1018661 AA577422 AA522800
		BF064818 AA102378 AA757993 AA687769 R55540 AA505784 B1820705 B1787939
10	410704	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877482 BE166927 BE166932 AW877523
		BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166966 BE166913 BE166919 AW877456 AW877537 BE076866
		AW840571
15	400233	11259_1
		BC004324 NM_001020 BC007977 M60854 BM050628 BG829809 BE385504 BG744451 B1826914 BE440007 B1260566 BE395117 BE388334
		BE255792 B1194169 B1668218 B1194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM424171 B1826267 AW958606 BG831252
		BE392943 BE394033 B1858915 B1668334 BE621019 BG706995 BE791985 BF967484 B1193635 BG761858 BM466537 BG747165 BG827488
		A1133550 BM011511 B1227282 BG489212 BG478388 BE727789 B1160880 BG831707 BG324692 BM470427 B1083889 BG831605 BG754114
		BG420536 BF308210 BE384213 BG832271 BG828032 BG481541 BF205675 BE899041 BE271558 B1193607 B1159866 BG473786 BG591778
		B1194428 B117210 BG768326 BG759507 BF975645 BF343857 BM020598 BG831082 BG829943 BG829501 BF306567 BE562511 BM050145
		BM017978 B1193934 B1160764 B1160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 B1192794 BG831002 BG830459
20		BG764737 BG761808 BG481705 BG104314 BM464565 B1261500 BG831857 BG831884 BG828652 BG765030 BG760419 BG760268 BG749762
		BG480900 BG419627 BG248771 BF975542 BM042233 B1161149 BG831302 BG830033 BG829626 BM050064 B1193014 B1161360 BG822729
		BG110091 BG106500 B1258369 BG831882 BM458301 BM019513 B1161350 B114178 BG481869 BG474870 BF974048 BF971122 BE741405
		BE395269 BG832027 BG831469 BG490895 BM413838 BG943529 BG831012 BG829471 BG886284 BG337576 BG396551 BF206677 B1258301
		B1160946 BG105893 BF183072 BM459542 B1193881 BG832043 BG831323 B1194545 B1160968 BG755930 BG708018 BE743865 BM465145
25		BG831227 BG774290 BF683451 BE907161 BM045391 B1194396 B1161269 BG747091 BG546643 BF984863 B1160206 B1226402 B1226336
		AW328236 BG339458 BF972634 BE809808 B1160988 B1160251 BG828764 BG828860 BG758360 BF568228 B1181828 B1457127 BG831491
		BG759864 A1830010 BF568381 BE907238 B1161172 B1118773 BG827153 BG825088 BG335419 BG109404 A192058 BE906364 BE408564
		BM045000 BG339617 BG282794 BG335767 BE907263 BF568821 BG829961 BG479305 BG260397 A1922228 BE301975 AW516055 BG480919
30		BG480626 AW198817 BG336261 BE806157 BE395717 BE391427 B1192954 BG829757 BG476379 BE301636 BE394727 BE257695 BE906344
		AA433577 BE894416 BE886992 BE409223 BF034756 BE904077 BG830888 BE909153 BE907998 BE395767 A1871751 BE744523 B1192663
		BG831689 A1000225 BE743836 BE272515 AA628078 BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297
		BE391448 BE390780 BE388821 BE258477 BE905870 BE901567 BE898633 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542
		BE744156 BE394125 BE742207 BE395265 BE382942 BE894336 BE378222 BE806926 BE904650 BE393704 BE820999 BE515162 BE378753
35		BE272370 BE907458 BE612801 BE392484 BE907638 BE907353 BE910491 BE909798 BE905331 AW248173 A1683576 BE908826 BE620180
		BF037570 BE908312 BE615015 BE256977 BE746875 BE394133 BE391478 BE910068 BE907185 BE742109 AA995746 BE561195 BE908825
		BE906472 BE906509 BE906017 BE910442 BE514657 B1261969 BE741707 BE392216 BM042793 BF570283 B1262119 BE395707 BE378298
		AW327827 BE394422 BF689178 BE263240 A1700512 BG830290 BF669308 BF569158 B1194687 BE390831 BG745096 A1681675 BE395674
		AA136372 BE279892 AA442822 BE384898 AA313519 A1878866 AA305904 F33366 BE394852 F299153 F33618 A133637 AA300009 F34063
40	413891	823_1
		F29455 AU099691 A1905085 A1908856 AA343249 BE388691 AW404260 AA379888 F29022 BF089981 F31013 F24305
		BE271020 A1925430 A1806151 AW129911 AA828002 AW003639 BE042625 A1287859 AW778973 A1621173 A1991000 AA846016 AW150029
		AW169748 AA649945 A1470921 BF434211 AW513748 AW451232 A1933739 A1249448 A1040580 A1655280 A1637976 AW194345
		AW611897 A1367197 BF064039 F29658 A1537342 BF583207 AW879538 AA973211 A1674328 AW879559 BF061961 AA481914 AA426632
		AA426653 AA480106 AW243290 BF513102 BF346057 A1763358 AW003726 A1139045 A1570748 AW237602 T57482 BE807212 A1969311
		AA133045 F23464 AA576416 T15590 A1650891 A1850958 A1983931 AW515101 A1650820 H81989 AA508473
45	410584	35319_1
		BF828833 A1968217 A1651409 A1760574 A1147562 AW001418 A1146791 A1650589 A1952939 A1432373 A1964094 A1963870 A1420438 A1336803
		AA809634 BF590826 AA741075 B1712639 AL134637 BM264338 AA527993 A1887208 A1439038 A1684987 A1631698 A1567126 A1637622 A1651931
		A1867525 A1783674 A1638281 A1825752 A1339187 A1653411 A1341372 A1673213 A1673191 AW779768 A1627934 A1921836 A1741834 A1382284
		A1741624 A1401569 AW190430 AW196390 A1829182 A1523816 A1760522 BE505014 A1917343 BG818909 AW009307 AA927544 AA825621
		AA829400 AA527307 A1887999 A1865022 AA865063 AA653458 AA463816 AA836167 AA505879 AA421004 AA252628 A1380678 AW195980
50		AA649133 A1742276 AW015700 AA595019 AA877835 A1701658 AA729793 AA535004 AA926792 AA505113 AA603726 W68390 N90130 AA489481
		AA830462

TABLE 56C

Pkey:	Unique number corresponding to an Eos probe set
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402474	7547175	Minus	53526-53628,55755-55920,57530-57157
402145	8018280	Plus	113086-114800
401091	9958240	Plus	94780-94898
401466	6682292	Plus	28740-29023
401113	9966541	Minus	19419-19959
406542	7711498	Plus	117335-118473
405088	8072509	Plus	73684-73841,74081-74217,74510-74779,7492
401846	7712190	Minus	82775-82823,82912-83022
404854	7143420	Plus	14260-14537
405266	4156171	Minus	63337-63552

TABLE 57A: 703 genes upregulated in testicular cancer relative to normal body tissues

Table 57A lists about 703 genes upregulated in testicular cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu3 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
5	Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
	UniGene Title:	UniGene gene title
	R1	95th percentile of testicular cancer AIs divided by the 50th percentile of normal tissues AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
10	Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1	
		424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase); matrix metalloproteinase 9 (gelatinase B; 31.23
		440119; AA865455; Hs.125331; ESTs, Moderately similar to unknown [H.sapiens]; ESTs, Moderately similar to unknown [H.s; 27.37
15		421241; X91817; Hs.102866; transketolase-like 1; transketolase-like 1; 26.89
		431840; AA534908; Hs.2860; POU domain, class 5, transcription factor 1; POU domain, class 5, transcription factor; 25.03
		435918; AF263536; Hs.86232; growth differentiation factor 3; growth differentiation factor 3; 19.88
		432686; AW204069; Hs.351118; ESTs, Weakly similar to unnamed protein product [H.sapiens]; ESTs, Weakly similar to unnamed protein; 17.74
		419556; U29615; Hs.91093; chitinase 1 (chitinobiosidase); chitinase 1 (chitinobiosidase); 17.64
20		452838; U65011; Hs.30743; preferentially expressed antigen in melanoma; preferentially expressed antigen in melanoma; 17.06
		417886; AA214584; ; ESTs; ESTs; 15.96
		412266; AA101325; Hs.86154; hypothetical protein FLJ12457; hypothetical protein FLJ12457; 15.93
		425572; AB011076; Hs.158307; undifferentiated embryonic cell transcription factor 1; undifferentiated embryonic cell transcript; 15.82
		423905; AW579960; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 15.11
25		419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; ubiquitin carrier protein E2-C; 15.08
		427584; BE410283; Hs.179718; v-myb avian myeloblastosis viral oncogene homolog-like 2; v-myb avian myeloblastosis viral oncogene; 14.17
		418696; AW959433; Hs.326290; hypothetical protein FLJ12581; hypothetical protein FLJ12581; 13.58
		416819; U77735; Hs.80205; pim-2 oncogene; pim-2 oncogene; 13.20
		414034; UB9277; Hs.305885; early development regulator 1 (homolog of polyhomeotic 1); early development regulator 1 (homolog o; 12.93
30		464077; AC005952; Hs.37082; insulin-like 3 (Leydig cell); insulin-like 3 (Leydig cell); 12.90
		432730; AIO66520; Hs.131358; ESTs; ESTs; 12.84
		446293; AJ420213; Hs.148722; LIM domain transcription factor LIM-1 (hLIM-1) mRNA; LIM domain transcription factor LIM-1 (h; 12.74
		423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; calcium channel, voltage-dependent, alpha; 12.46
		450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta 4; 12.42
35		450719; AIO98337; Hs.21349; ESTs, Weakly similar to RBBB_HUMAN RAS-RELATED PROTEIN RAB-8B [H.sapiens]; ESTs, Weakly similar to RBBB_HUMAN RAS-R; 12.26
		431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precursor; granin-like neuroendocrine peptide precu; 11.96
		431364; BE046956; Hs.251673; DNA (cytosine-5)-methyltransferase 3 beta; DNA (cytosine-5)-methyltransferase 3 be; 11.91
		402199; ; Target Exon; Target Exon; 11.85
		424578; AK001973; Hs.150690; hypothetical protein; hypothetical protein; 11.81
40		416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholipase A2, group IID; 11.67
		439979; AV600291; Hs.62633; hypothetical protein FLJ10430; hypothetical protein FLJ10430; 11.57
		410048; W76467; Hs.343874; proline oxidase homolog; proline oxidase homolog; 11.42
		442573; H93366; Hs.7567; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 11.42
		414812; X72756; Hs.77367; monokine induced by gamma interferon; monokine induced by gamma interferon; 11.38
45		421917; AB028943; Hs.109445; KIAA1020 protein; KIAA1020 protein; 11.15
		440009; AK000317; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; NALP2 protein; PYRIN-Containing APAF1-I; 10.92
		414683; S78298; Hs.76888; hypothetical protein MGC12702; hypothetical protein MGC12702; 10.91
		423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage elastase); matrix metalloproteinase 12 (macrophage; 10.74
		433800; AIO34361; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 10.68
50		429120; AK001673; Hs.196530; hypothetical protein FLJ10811; hypothetical protein FLJ10811; 10.48
		444371; BE540274; Hs.239; forkhead box M1; forkhead box M1; 10.46
		441553; AA281219; Hs.121296; ESTs; ESTs; 10.37
		426534; U58096; Hs.2061; testis specific protein, Y-linked; testis specific protein, Y-linked; 10.28
		441878; AIO01868; Hs.127982; ESTs; ESTs; 10.06
55		432117; AL036195; Hs.2909; protamine 1; protamine 1; 10.01
		425427; AIO52662; Hs.317432; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 9.97
		416201; AA467752; Hs.195161; ESTs; ESTs; 9.97
		410929; H47233; Hs.30643; ESTs; ESTs; 9.91
60		427486; AA974433; Hs.352432; fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene); fibroblast growth factor 4 (heparin secr; 9.81
		427239; BE270447; Hs.356512; ubiquitin carrier protein; ubiquitin carrier protein; 9.68
		402680; ; Target Exon; Target Exon; 9.68
		409208; Y00093; Hs.172631; Integrin, alpha X (antigen CD11C (p150), alpha polypeptide); Integrin, alpha X (antigen CD11C (p150); 9.46
		443426; AF088158; Hs.9329; chromosome 20 open reading frame 1; chromosome 20 open reading frame 1; 9.42
		440207; A1371978; Hs.128328; ESTs; ESTs; 9.41
65		433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; clone HQ0310 PRO0310p1; 9.41
		447634; AW953935; Hs.288655; ESTs; ESTs; 9.33
		442333; AIO50877; Hs.129302; ESTs; ESTs; 9.28
		421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425); Homo sapiens mRNA; cDNA DKFZp434B0425 (f; 8.24
		423458; AIO24212; Hs.351113; ESTs; ESTs; 9.23
70		431958; X83629; Hs.2877; cadherin 3, type 1, P-cadherin (placental); cadherin 3, type 1, P-cadherin (placenta; 9.23
		422938; NM_001809; Hs.1594; centromere protein A (17kD); centromere protein A (17kD); 9.21
		411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor; 9.21
		425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); topoisomerase (DNA) II alpha (170kD); 9.18
		428684; AK001666; Hs.189095; similar to SALL1 (sal (Drosophila)-like; similar to SALL1 (sal (Drosophila)-like; 9.17
75		428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabotropic glutamate family GPCR; retinoic acid induced 3 (RAIG1); metabo; 9.11
		447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient, yeast, homolog)-like 2; MAD2 (mitotic arrest deficient, yeast, h; 9.11
		422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 9.10
		449722; BE280074; Hs.23960; cyclin B1; cyclin B1; 8.86
80		441580; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vt; 8.86
		440983; M20661; Hs.7694; solute carrier family 2 (facilitated glucose transporter), member 3; solute carrier family 2 (facilitated glu; 8.86
		409342; AJ077058; Hs.54089; BRCA1 associated RING domain 1; BRCA1 associated RING domain 1; 8.83
		420367; AA259090; Hs.257028; ESTs; ESTs; 8.82
		415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1); mutS (E. coli) homolog 2 (colon cancer; 8.73
		419613; AA744529; Hs.85575; mitogen-activated protein kinase kinase kinase kinase 1; mitogen-activated protein kinase kinase ; 8.71



- 417407; AA923278; Hs.290905; ESTs, Weakly similar to protease [H.sapiens]; ESTs, Weakly similar to protease [H.sapi]; 8.64  
 407239; AA076350; Hs.57846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor; ; 8.58  
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-conjugating enzyme; HSPC150 protein similar to ubiquitin-con; 8.55  
 412140; AA219891; Hs.73625; RAB6 interacting, kinesin-like (rabkinesin 6); RAB6 interacting, kinesin-like (rabkines); 8.52  
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group 1, member 3; nuclear receptor subfamily 1, group 1, m; 8.51  
 424800; AL035588; Hs.153203; MyoD family inhibitor; MyoD family inhibitor; 8.45  
 447198; H65423; Hs.17831; hypothetical protein DKFZp434E2135; hypothetical protein DKFZp434E2135; 8.45  
 430056; X97548; Hs.228059; KRAB-associated protein 1; KRAB-associated protein 1; 8.42  
 417389; BE260964; Hs.82045; midkine (neurotrophin growth-promoting factor 2); midkine (neurotrophin growth-promoting factor); 8.40  
 430676; AF084866; Hs.72585; gb:Homo sapiens envelope protein RIC-3 (env) gene, complete cd; gb:Homo sapiens envelope protein RIC-3 (c); 8.38  
 420758; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.38  
 406621; X57809; Hs.181125; immunoglobulin lambda locus; immunoglobulin lambda locus; 8.37  
 453914; NM\_000507; Hs.574; fructose-1,6-bisphosphatase 1; fructose-1,6-bisphosphatase 1; 8.25  
 423198; M81933; Hs.1634; cell division cycle 25A; cell division cycle 25A; 8.19  
 418299; AA279530; Hs.83568; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin, beta 2 (antigen CD18 (p95), ly; 8.17  
 453988; AA847843; Hs.62711; High mobility group (nonhistone chromosomal) protein 4; High mobility group (nonhistone chromoso; 8.16  
 453985; N44545; Hs.261865; ESTs; ESTs; 8.14  
 451106; BE382701; Hs.25960; N-MYC oncogene; N-MYC oncogene; 8.10  
 420347; AL033539; Hs.97124; Human DNA sequence from clone RP1-309H15 on chromosome 6p22.1-22.3 Contains a gene similar to HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)), ESTs, GSSs and a CpG Isl; Human DNA sequence from clone RP1-309H15; 8.03  
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.02  
 425601; AW629486; Hs.140720; GSK-3 binding protein FRAT2; GSK-3 binding protein FRAT2; 7.90  
 421016; AA504583; Hs.101047; transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47); transcription factor 3 (E2A immunoglobul); 7.89  
 432407; AA221036; ; gb:zr03f12.1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL\_BAEVM P10272 POL POLYPROTEIN ; mRNA sequence; gb:zr03f12.1 Stratagene NT2 neuronal pr; 7.83  
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); neutrophil cytosolic factor 1 (47kD, chr; 7.80  
 433228; F28212; Hs.14953; KIAA1491 protein; KIAA1491 protein; 7.73  
 446523; AJ076640; Hs.15243; nucleolar protein 1 (120kD); nucleolar protein 1 (120kD); 7.71  
 447350; AJ375572; Hs.172634; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HERA); v-erb-a avian erythroblastic leukemia vi; 7.71  
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; nudix (nucleoside diphosphate linked mo; 7.71  
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; hypothetical protein FLJ10652; 7.70  
 444784; D12485; Hs.11851; ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1); ectonucleotide pyrophosphatase/phosphodi; 7.62  
 443537; D13305; Hs.203; cholecystokinin B receptor; cholecystokinin B receptor; 7.57  
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; interferon, gamma-inducible protein 30; 7.55  
 410006; AW732308; Hs.57783; eukaryotic translation initiation factor 3, subunit 9 (ets, 116kD); eukaryotic translation initiation factor; 7.53  
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551 protein, partial cds; Homo sapiens mRNA for KIAA1551 protein; ; 7.52  
 411975; AB16058; Hs.144583; 3'UTR of: dead ringer (Drosophila)-like 1; 3'UTR of: dead ringer (Drosophila)-like ; 7.50  
 439864; A1720078; Hs.291997; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell pr; 7.47  
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4689, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 2700; 7.47  
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; hypothetical protein FLJ14541; 7.47  
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; protein tyrosine phosphatase, receptor t; 7.47  
 407710; AW022727; Hs.23616; ESTs; ESTs; 7.45  
 445093; AJ071197; Hs.374149; ESTs; ESTs; 7.41  
 418113; AJ272141; Hs.83484; SRY (sex determining region Y)-box 4; SRY (sex determining region Y)-box 4; 7.39  
 417900; BE260127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae, homolog); CDC20 (cell division cycle 20, S. cerevi; 7.37  
 429469; M64590; Hs.11801; glycine dehydrogenase (decarboxylating); glycine decarboxylase, glycine cleavage system protein P; glycine dehydrogenase (decarboxylating; ; 7.33  
 422726; U11680; Hs.1572; facioscapular dysplasia (Aarskog-Scott syndrome); facioscapular dysplasia (Aarskog-Scott sy; 7.33  
 430504; H52761; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 7.32  
 448981; AJ968719; Hs.195387; ESTs; ESTs; 7.28  
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); FK506-binding protein 4 (59kD); 7.26  
 435092; AL137310; Hs.47499; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; Homo sapiens mRNA; cDNA DKFZp761E13121 (c); 7.25  
 434414; A1798376; ; gb:tr34607.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone 3 similar to TRC015475 O15475 UNNAMED HERV-H PROTEIN ; mRNA sequence; gb:tr34607.x1 NCI\_CGAP\_Ov23 Homo sapiens; 7.24  
 428977; AK001404; Hs.194698; cyclin B2; cyclin B2; 7.19  
 434274; AA628538; Hs.57783; ESTs, Moderately similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Moderately similar to ALU1\_HUMAN A; 7.19  
 446700; AW205257; Hs.156328; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc f; Human DNA sequence from clone RP11-145L2; 7.18  
 420524; AB010575; Hs.98547; aniloride-sensitive cation channel 3, testis; aniloride-sensitive cation channel 3, te; 7.15  
 439053; BE244588; Hs.6456; chaperonin containing TCP1, subunit 2 (beta); chaperonin containing TCP1, subunit 2 (b; 7.14  
 445076; AJ208888; Hs.154131; ESTs; ESTs; 7.14  
 448583; AJ970276; Hs.155905; KIAA1676; KIAA1676; 7.13  
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; hypothetical protein FLJ10339; 7.10  
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E. coli RecA homolog); RAD51 (S. cerevisiae) homolog (E. coli Re; 7.04  
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds; Homo sapiens DNA helicase homolog (PIF1); 7.02  
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; interferon-stimulated protein, 15 kDa; 7.02  
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840937, mRNA, partial cds; Homo sapiens, clone IMAGE:3840937, mRNA; 6.96  
 418658; U03272; Hs.79432; fibrillin 2 (congenital contractural arachnodactyly); fibrillin 2 (congenital contractural ara; 6.92  
 438450; AJ050866; Hs.65853; nodal, mouse, homolog; nodal, mouse, homolog; 6.90  
 415323; BE269562; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); neutrophil cytosolic factor 2 (65kD, chr; 6.90  
 444381; BE387335; Hs.283713; hypothetical protein BC014245; hypothetical protein BC014245; 6.89  
 447582; BE293520; Hs.18910; prostate cancer overexpressed gene 1; prostate cancer overexpressed gene 1; 6.89  
 424779; AL046851; Hs.153063; CD37 antigen; CD37 antigen; 6.89  
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; TYRO protein tyrosine kinase binding pr; 6.84  
 427298; AA400495; ; ESTs; ESTs; 6.82  
 414732; AW410978; Hs.77152; minichromosome maintenance deficient (S. cerevisiae) 7; minichromosome maintenance deficient (S; 6.81  
 424959; NM\_005781; Hs.153937; activated p21cdc42Hs kinase; activated p21cdc42Hs kinase; 6.81  
 428866; U02330; Hs.172816; neuregulin 1; neuregulin 1; 6.80  
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CDC28 protein kinase 2; 6.80  
 427521; AW973362; ; ESTs; ESTs; 6.75  
 430397; A1924533; Hs.105607; bicarbonate transporter related protein 1; bicarbonate transporter related protein ; 6.75  
 427719; AJ393122; Hs.134726; ESTs; ESTs; 6.74



- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72  
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71  
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein; 6.70  
 445363; NM\_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70  
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69  
 418054; NM\_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63  
 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62  
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59  
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58  
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58  
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57  
 414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57  
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55  
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete; 6.55  
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:77279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55  
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51  
 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin); minichromosome maintenance deficient (S.; 6.50  
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell; 6.49  
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A; 6.44  
 427747; AW411426; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43  
 408142; AW176401; Hs.334612; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42  
 430280; AA361258; Hs.237868; Interleukin 7 receptor; interleukin 7 receptor; 6.42  
 432838; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42  
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40  
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3\_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3\_HUMAN TUBBY; 6.40  
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39  
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (C); 6.39  
 441384; AA447849; Hs.288660; retinoic acid induced 3; retinoic acid induced 3; 6.38  
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34  
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34  
 451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; 6.31  
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright; 6.31  
 425274; BE281191; Hs.155462; minichromosome maintenance deficient (mms1, S. pombe) 6; minichromosome maintenance deficient (m; 6.31  
 436449; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcrip; 6.30  
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30  
 415829; AW450188; Hs.163742; ESTs; ESTs; 6.28  
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26  
 446539; BE091826; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25  
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25  
 428918; ALD36957; Hs.2324; protamine 2; protamine 2; 6.24  
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19  
 424415; NM\_001875; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19  
 407246; X90568; Hs.172004; titin; titin; 6.18  
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18  
 421379; Y16221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (C); 6.16  
 435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13  
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12  
 430521; NM\_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10  
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10  
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino; 6.09  
 402260; ; NM\_001436; Homo sapiens fibrillin (FBL), mRNA, transcript (F8A), mRNA; NM\_001436; Homo sapiens fibrillin (FBL); 6.09  
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05  
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04  
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); Interferon, alpha-inducible protein (c; 6.04  
 402678; ; Target Exon; Target Exon; 6.03  
 453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01  
 439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 2168212; hypothetical protein from EUROIMAGE 2168; 6.01  
 420596; NM\_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01  
 420676; AI434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00  
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99  
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98  
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98  
 413313; NM\_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95  
 417777; AJ823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/th; 5.94  
 449569; AI656634; Hs.195389; ESTs; ESTs; 5.92  
 436576; AI458213; Hs.77542; ESTs; ESTs; 5.90  
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89  
 420009; AW271109; Hs.133294; ESTs; ESTs; 5.89  
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88  
 403171; ; C2001472:gi5809678[gb|AA841848.2] (U64675) sperm membrane protein BS-63 [Homo sapiens]; C2001472:gi5809678[gb|AA841848.2] (U64; 5.87  
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87  
 406137; ; NM\_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA, VERSION NM\_000178.1 GI; NM\_000179; Homo sapiens mutS (E. coli) h; 5.85  
 423787; AJ295745; Hs.238204; nuclear pore complex protein; nuclear pore complex protein; 5.85  
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84  
 452796; AB011100; Hs.30655; KIAA0528 gene product; KIAA0528 gene product; 5.84  
 416322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80  
 447359; NM\_012093; Hs.18268; adenylylase kinase 5; adenylylase kinase 5; 5.79  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78  
 420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1\_HUMAN ALU S; 5.75  
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5\_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5\_HUMAN LEUKE; 5.74  
436251; BE515055; Hs.295585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73  
421535; AB002359; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synthase; 5.71  
414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69  
425159; NM\_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspartate; 5.69  
401704; ; NM\_021195; Homo sapiens claudin 6 (CLDN6), mRNA. VERSION NM\_020982.1 GI; NM\_021195; Homo sapiens claudin 6 (CLDN6); 5.66  
425358; AL079558; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin assoc; 5.65  
402677; ; NM\_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM\_000478; Homo sapiens alkaline phosphatase; 5.64  
409264; NM\_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63  
432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63  
409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63  
430252; AL638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61  
419359; AL043202; Hs.30073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61  
452816; AA131789; Hs.61509; ESTs; ESTs; 5.60  
402679; ; NM\_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM\_000478; Homo sapiens alkaline phosphatase; 5.60  
414291; AJ288619; Hs.13040; G protein-coupled receptor 85; G protein-coupled receptor 85; 5.58  
453028; AB006532; Hs.31442; RacQ protein-like 4; RacQ protein-like 4; 5.58  
453905; NM\_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56  
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-assoc; 5.55  
419860; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino; 5.55  
446979; AL654443; Hs.197683; ESTs; ESTs; 5.54  
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kin; 5.53  
418962; AA174835; Hs.271863; ESTs; ESTs; 5.53  
447388; AW830534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 5.52  
427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); integrin, alpha L (antigen CD11A (p180); 5.52  
449322; AL638616; Hs.198586; ESTs; ESTs; 5.51  
428450; NM\_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51  
415141; AA189099; Hs.268171; ESTs, Weakly similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7\_HUMAN ALU S; 5.48  
454048; H05628; Hs.6921; ESTs; ESTs; 5.46  
417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; Interleukin 1 receptor antagonist; 5.45  
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11880 fls, clone HEMBB1001304; Homo sapiens cDNA FLJ11880 fls, clone HE; 5.44  
414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44  
452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisiae; 5.44  
438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class; 5.44  
427668; AA289760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43  
449437; AL702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fls, clone KAT05581; Homo sapiens cDNA: FLJ22902 fls, clone K; 5.41  
453653; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40  
450746; D82873; Hs.278589; general transcription factor II, I; general transcription factor II, I; 5.40  
425966; NM\_001781; Hs.1973; cyclin F; cyclin F; 5.39  
418134; AA397769; Hs.86617; ESTs; ESTs; 5.38  
432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37  
417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, m; 5.36  
428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.; 5.35  
406811; U82979; Hs.67848; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITM domains), member 4; leukocyte immunoglobulin-like receptor,; 5.34  
415818; ALU077330; Hs.380791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII); 5.33  
448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33  
424762; AL119442; Hs.183884; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor; 5.32  
421958; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 5.32  
429271; U839950; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32  
456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A; 5.30  
414807; X90725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30  
422897; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29  
440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosop; 5.28  
418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26  
416176; AL808627; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer anti; 5.21  
450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20  
409670; AL368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20  
429063; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20  
449523; NM\_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20  
408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19  
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 75kD); lymphocyte cytosolic protein 2 (SH2 doma; 5.19  
436088; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 5.18  
437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-assoc; 5.15  
448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15  
436540; BE397032; Hs.14468; hypothetical protein MGC14228; hypothetical protein MGC14228; 5.14  
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor t; 5.14  
426752; X69490; Hs.172004; ttn; ttn; 5.13  
415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2; 5.13  
400263; ; Hs.75309; Eos Control; Eos Control; 5.13  
437099; N77793; Hs.48669; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin alpha; 5.12  
427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10  
407347; AA829847; ; gbcd40d07.s1 NCL\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element, mRNA sequence.; gbcd40d07.s1 NCL\_CGAP\_GCB1 Homo sapiens; 5.10  
458933; AL638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10  
450431; AW136797; Hs.268041; ESTs; ESTs; 5.09  
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08  
410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-recept; 5.08  
417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05  
412723; AA648459; Hs.335851; hypothetical protein AF301222; hypothetical protein AF301222; 5.05

- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03  
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03  
 410082; AA081694; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02  
 433592; NM\_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog); 5.02  
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, Importin alpha 1); karyopherin alpha 2 (RAG cohort 1, impor; 5.00  
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00  
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99  
 402145; ; Target Exon; Target Exon; 4.99  
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99  
 408279; AF216955; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 4.98  
 419525; T79257; Hs.1269; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97  
 424439; AA578635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97  
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96  
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96  
 448589; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94  
 426427; M66699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91  
 440129; AA858118; Hs.368523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-like; 4.91  
 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1; 4.90  
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89  
 452698; NM\_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88  
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88  
 437182; ZB3844; Hs.5464; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87  
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIC61) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIC; 4.87  
 421350; AW301608; Hs.278188; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene; 4.87  
 409093; BE24834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86  
 424304; NM\_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86  
 437696; ZB3844; Hs.5790; hypothetical protein DJ37E16.5; hypothetical protein DJ37E16.5; 4.86  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleoside transporters), member 1; solute carrier family 23 (nucleoside tra; 4.84  
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83  
 448939; BE267796; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82  
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82  
 424081; NM\_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81  
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81  
 412278; BE262621; Hs.73793; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor; 4.81  
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80  
 409101; NM\_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79  
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79  
 447250; AI078909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79  
 429345; R11141; Hs.196695; hypothetical protein; hypothetical protein; 4.78  
 448950; AF288687; Hs.9275; CGI-162 protein; CGI-162 protein; 4.78  
 412926; AI078076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C; 4.78  
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76  
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 4.76  
 421905; AI650247; Hs.32689; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein; 4.75  
 413880; AI660842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75  
 424805; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74  
 418356; L42561; Hs.1166; ATPase, H<sup>+</sup> transporting, nongastric, alpha polypeptide; ATPase, H<sup>+</sup> transporting, nongastric, alp; 4.74  
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74  
 428024; Z29067; Hs.2236; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74  
 421846; AK017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72  
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72  
 437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70  
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (bemarcan); chondroitin sulfate proteoglycan 6 (bemar; 4.70  
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69  
 449475; AI348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69  
 420082; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69  
 429335; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIIIB (25-hy; 4.69  
 436856; AI469355; Hs.127310; ESTs; ESTs; 4.68  
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds.; gb:Human transketolase-like protein gene; 4.67  
 411296; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67  
 426726; AA488915; Hs.171955; trophoblast associated protein (tastin); trophoblast associated protein (tastin); 4.67  
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67  
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66  
 431681; AK000378; Hs.287568; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.66  
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent, ; 4.65  
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64  
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64  
 415724; NM\_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63  
 435045; BE297155; Hs.143698; ESTs; ESTs; 4.62  
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62  
 414972; BE263782; Hs.77895; KIAA0008 gene product; KIAA0008 gene product; 4.62  
 436885; W28681; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62  
 449515; AI653378; Hs.302012; ESTs; ESTs; 4.61  
 425998; AF076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61  
 420027; AU009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61  
 438469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61  
 413441; AI929374; Hs.75367; Src-like-adapter; Src-like-adapter; 4.60  
 456847; AI360456; Hs.08088; ESTs; ESTs; 4.58  
 421505; BE302798; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57  
 426935; NM\_000088; Hs.172928; collagen, type 1, alpha 1; collagen, type 1, alpha 1; 4.57  
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56  
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L OR; 4.55

- 443066; AI188710; Hs.374480; ESTs; ESTs; 4.55  
 441607; NM\_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54  
 453227; AW135852; Hs.243991; ESTs; ESTs; 4.52  
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51  
 422585; BE259035; Hs.118400; slinged (Drosophila)-like (sea urchin fascin homolog like); slinged (Drosophila)-like (sea urchin fas); 4.51  
 453613; F06638; Hs.374476; ESTs; ESTs; 4.50  
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70); 4.50  
 412507; L36545; Hs.73964; EphA4; EphA4; 4.50  
 419034; NM\_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49  
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo); 4.49  
 406547; ; Target Exon; Target Exon; 4.49  
 443216; WB0487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48  
 417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47  
 448695; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47  
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46  
 446238; NM\_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46  
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46  
 420340; NM\_000734; Hs.37087; CD32 antigen, zeta polypeptide (TIT3 complex); CD32 antigen, zeta polypeptide (TIT3 com); 4.46  
 413426; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt); 4.44  
 421819; NM\_013403; Hs.108665; zinedin; zinedin; 4.44  
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44  
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, D); 4.43  
 434551; BE397162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 (H.sapiens); ESTs, Highly similar to A35661 DNA excis; 4.43  
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42  
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42  
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42  
 413186; AJ077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic); 4.42  
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40  
 424078; AB006626; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39  
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi; 4.37  
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36  
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35  
 400440; X83957; Hs.83870; nabulin; nabulin; 4.35  
 437218; AL117497; Hs.68185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 proliera; 4.34  
 430473; NM\_014349; Hs.241535; apolipoprotein L, 3; apolipoprotein L, 3; 4.34  
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33  
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33  
 415995; NM\_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33  
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30  
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re; 4.30  
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfam; 4.29  
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Fc fragment of IgG, low affinity IIb, r; 4.29  
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29  
 412314; AA825247; Hs.358084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled receptor; 4.28  
 447827; U37227; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28  
 426108; AA622037; Hs.165468; programmed cell death 5; programmed cell death 5; 4.28  
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component; 4.27  
 437908; AJ082424; Hs.351043; ESTs; ESTs; 4.27  
 444664; N26362; Hs.11816; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27  
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26  
 439334; AJ148976; Hs.112062; ESTs; ESTs; 4.26  
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25  
 413869; NM\_000878; Hs.75588; interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25  
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24  
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA100358; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24  
 447528; AJ612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23  
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22  
 445810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22  
 447198; D51523; Hs.283435; ESTs; ESTs; 4.22  
 416714; AF283770; Hs.79530; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated; 4.22  
 425358; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 145kD; inositol polyphosphate-5-phosphatase, 14; 4.22  
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21  
 444535; AF011456; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21  
 417088; M54915; Hs.61170; pim-1 oncogene; pim-1 oncogene; 4.20  
 421707; NM\_014921; Hs.107054; leiomedin-2; leiomedin-2; 4.20  
 408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20  
 438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19  
 419452; U33835; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18  
 418755; Y14443; Hs.88218; zinc finger protein 200; zinc finger protein 200; 4.18  
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17  
 413686; AJ69213; Hs.71404; ESTs; ESTs; 4.17  
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus); chemokine (C-X-C motif), receptor 4 (fus; 4.16  
 408482; NM\_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16  
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15  
 409421; AA198883; Hs.67624; ESTs; ESTs; 4.15  
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14  
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14  
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to M; 4.13
- 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbonate; 4.13
- 433436; BE645277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitochondrial; 4.13
- 420253; A1656055; Hs.96200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 95; 4.12
- 5 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12
- 400205; Hs.81848; NM\_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA (APO-1/CD95 [Fas]-associated phosphatase) (PTPN13), mRNA; NM\_006265; Homo sapiens RAD21 (S. pombe); 4.12
- 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11
- 10 419607; RS2557; Hs.91578; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10
- 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - *Caenorhabditis elegans* [C.elegans]; ESTs, Weakly similar to T31611 hypothetical; 4.10
- 432512; NM\_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to ; 4.10
- 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09
- 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); Interferon-stimulated transcription factor 3, gamma (48kD); 4.09
- 15 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09
- 442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G protein) alpha 12; 4.09
- 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/apyrimidinic endonuclease(APEX); 4.08
- 421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08
- 432841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-receptor type 12; 4.08
- 20 452068; AB028849; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08
- 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker-related; 4.07
- 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic acid transporters), member 3; 4.07
- 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12168 fls, clone MAMMA1000643; Homo sapiens cDNA FLJ12168 fls, clone MA; 4.07
- 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe combined immunodeficiency); 4.06
- 25 446793; A1632276; Hs.195922; ESTs; ESTs; 4.06
- 432055; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), catalytic; 4.06
- 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta 3 subunit; 4.06
- 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); 4.06
- 30 425923; NM\_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, delta; 4.05
- 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04
- 448272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrate 1; 4.04
- 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; 4.04
- 417890; BE241595; Hs.62848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule 1); 4.04
- 35 410068; A1633888; Hs.58435; FYN-binding protein (FYN-120/130); FYN-binding protein (FYN-120/130); 4.03
- 410539; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03
- 427716; L38951; Hs.180448; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03
- 451050; AW937420; Hs.351868; ESTs; ESTs; 4.02
- 449687; AB023227; Hs.23880; KIAA1010 protein; KIAA1010 protein; 4.02
- 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01
- 40 437527; A1241019; Hs.145644; ESTs; ESTs; 4.01
- 425118; AU076611; Hs.154872; methylene tetrahydrofolate dehydrogenase (NAD dependent), methylenetetrahydrofolate cyclohydrolase; methylene tetrahydrofolate dehydrogenase (NAD dependent), methylenetetrahydrofolate cyclohydrolase; 4.00
- 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fls, clone COLF1240; Homo sapiens cDNA FLJ20201 fls, clone CO; 4.00
- 412939; AW411491; Hs.75089; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor 1 gamma; 4.00
- 408581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99
- 433577; AW007080; Hs.284102; ESTs; ESTs; 3.99
- 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); 3.99
- 418528; BE247550; Hs.86889; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99
- 448533; AA311426; Hs.21636; tubulin, gamma 1; tubulin, gamma 1; 3.98
- 50 402398; ; C19000283; g[3108023]g[3108023]AAC15755.1 (AC004659) BC62940\_2 [Homo sapiens]||66335; C19000263; g[3108023]g[3108023]AAC15755.1 (AC004659) BC62940\_2 [Homo sapiens]||66335; 3.97
- 408414; A1144888; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; 3.97
- 415012; NM\_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97
- 416084; L16891; Hs.79006; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kinase); 3.95
- 55 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; 3.95
- 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine protease; 3.95
- 430770; AA765894; Hs.123296; ESTs; ESTs; 3.94
- 442894; A1026718; Hs.18954; ESTs; ESTs; 3.94
- 420333; AJ001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46); lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46); 3.94
- 60 438458; AA913381; Hs.279763; ESTs; ESTs; 3.94
- 422598; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A) expressed in; 3.93
- 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93
- 424829; NM\_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR superfamily, member 16); 3.93
- 447574; AF162666; Hs.18895; tousel-like kinase 1; tousel-like kinase 1; 3.93
- 425797; AF002986; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93
- 65 421910; NM\_014586; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associated kinase; 3.92
- 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenase 1; 3.92
- 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fls, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fls, clone NT; 3.92
- 400262; ; Hs.75309; Eos Control; Eos Control; 3.90
- 424877; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fls, clone KAT05581; Homo sapiens cDNA: FLJ22902 fls, clone K; 3.90
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90
- 435206; A1432364; Hs.160594; ESTs; ESTs; 3.90
- 439853; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90
- 413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90
- 75 426266; AA421069; Hs.97896; ESTs; ESTs; 3.89
- 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89
- 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89
- 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88
- 400261; ; Hs.1802; Eos Control; Eos Control; 3.88
- 404047; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88
- 80 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); 3.87
- 414251; A1042306; Hs.97689; VASA protein; VASA protein; 3.87
- 417767; BE242241; Hs.82542; acylxyacyl hydrolase (neutrophil); acylxyacyl hydrolase (neutrophil); 3.87
- 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor, beta polypeptide; 3.87

- 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86  
 419593; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86  
 427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86  
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86  
 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86  
 410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 3.85  
 450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85  
 418978; T85295; Hs.268606; ESTs; ESTs; 3.84  
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84  
 442980; AA857025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84  
 447232; AW499834; Hs.327; Interleukin 10 receptor, alpha; Interleukin 10 receptor, alpha; 3.84  
 434688; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyme; 3.83  
 432539; AL138168; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83  
 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83  
 451598; N29102; Hs.79658; ESTs; ESTs; 3.82  
 449433; A1672098; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82  
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81  
 435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80  
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80  
 422753; A1928999; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79  
 421508; NM\_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79  
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79  
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79  
 421654; AW163267; Hs.106469; suppressor of var1 (Scerelvisae) 3-like 1; suppressor of var1 (Scerelvisae) 3-like; 3.79  
 439668; A1091277; Hs.302634; fozzled (Drosophila) homolog 8; fozzled (Drosophila) homolog 8; 3.78  
 411126; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78  
 425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78  
 423909; AL223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78  
 429667; A1675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77  
 414177; A1351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77  
 445817; NM\_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77  
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76  
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repair; 3.76  
 413011; AW068115; Hs.821; biglycan; biglycan; 3.76  
 428157; A1738718; Hs.198427; hexokinase 2; hexokinase 2; 3.76  
 400288; X08286; Hs.149609; Integrin, alpha 5 (fibronectin receptor, alpha polypeptide); integrin, alpha 5 (fibronectin receptor, ; 3.75  
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75  
 405484; ; C3002124\*gi12737280|refXP\_006682.2|keratin 18 [Homo sapiens]]6533; C3002124\*gi12737280|refXP\_006682.2|k; 3.75  
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75  
 432460; H12812; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75  
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74  
 431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8\_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar  
 to ALU8\_HUMAN ALU S; 3.74  
 463329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.74  
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74  
 438330; AW450572; Hs.257316; ESTs; ESTs; 3.74  
 419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74  
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73  
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypothet; 3.73  
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73  
 410772; BE275297; Hs.194685; Homo sapiens clone 24875 mRNA sequence; Homo sapiens clone 24875 mRNA sequence; 3.73  
 426251; A424283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72  
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpor; 3.71  
 423523; AW299828; Hs.193580; ESTs; ESTs; 3.71  
 413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71  
 448336; R53848; Hs.44976; ESTs; ESTs; 3.70  
 422083; NM\_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70  
 416087; AF046184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70  
 442200; AW590572; Hs.236766; ESTs; ESTs; 3.70  
 414280; BE410769; Hs.75873; zyxlin; zyxlin; 3.69  
 409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69  
 415276; U88666; Hs.76353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69  
 439659; AW970780; Hs.58483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69  
 446522; NM\_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.68  
 422785; A1824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68  
 401083; ; NM\_016582; Homo sapiens peptide transporter 3 (LOC51295), mRNA, VERSION NM\_016579.1 GI; NM\_016582; Homo sapiens peptide transpor; 3.68  
 413048; M93221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68  
 452690; A153607; Hs.16065; ESTs; ESTs; 3.68  
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2\_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar  
 to ALU2\_HUMAN ALU S; 3.68  
 415010; NM\_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68  
 428579; NM\_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68  
 446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.68  
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG Islands. Contains the NIFS gene for  
 cysteine desulfurase, two genes for novel proteins and the gene for the; Human DNA sequence from clone RP11-353C1; 3.66  
 416602; NM\_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65  
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0510012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0510;  
 3.65  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65  
 429303; AW137635; Hs.44238; ESTs, Weakly similar to G65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to G65657 alpha-1C; 3.65  
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN2), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

- 451558; NM\_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65
- 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65
- 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyrosine kinase; 3.64
- 437689; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA657999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64
- 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep); 3.64
- 444368; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64
- 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63
- 451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63
- 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63
- 447495; AW401884; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc); 3.62
- 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62
- 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62
- 411168; NM\_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62
- 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62
- 453020; AL162038; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61
- 438798; AA825792; Hs.377119; gb:od84b11.s1 NCL CGAP\_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:od84b11.s1 NCL CGAP\_Ov2 Homo sapiens; 3.61
- 445515; BE388865; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61
- 407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60
- 423217; NM\_000094; Hs.1840; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60
- 444985; AJ677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60
- 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM\_023929); zinc finger protein RINZF (NM\_023929); 3.59
- 427657; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59
- 415020; BE249315; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STGs, GSSs and CpG Islands. Contains the gene for a novel glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59
- 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57
- 458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57
- 423576; NM\_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57
- 404070; NM\_015988; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57
- 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57
- 404976; ; NM\_014323; Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM\_014323; Homo sapiens zinc finger prot; 3.57
- 449656; AA020008; Hs.188633; ESTs; ESTs; 3.56
- 413796; AL040178; Hs.142003; ESTs; ESTs; 3.56
- 408859; AI581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56
- 411030; BE387193; Hs.67898; 7-60 protein; 7-60 protein; 3.56
- 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.s]; 3.56
- 424263; M77640; Hs.1767; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55
- 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high aff; 3.55
- 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible IkappaB kinase; IKK-related kinase epsilon; Inducible Ik; 3.55
- 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55
- 450931; N25158; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55
- 425836; AW55696; Hs.90960; ESTs; ESTs; 3.54
- 441054; AA913691; Hs.126480; ESTs; ESTs; 3.54
- 440692; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54
- 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53
- 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53
- 421862; NM\_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53
- 422732; AA577455; Hs.24937; transformer-2 alpha (hra-2 alpha); transformer-2 alpha (hra-2 alpha); 3.53
- 424870; T16545; Hs.244624; ESTs; ESTs; 3.52
- 442794; AI744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52
- 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51
- 419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A.1 - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51
- 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51
- 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51
- 421921; H83363; Hs.355893; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50
- 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50
- 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil; 3.50
- 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50
- 429592; AB028041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49
- 430847; AC033682; Hs.127988; ESTs, Weakly similar to Z211\_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211\_HUMAN ZINC; 3.47
- 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44
- 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07
- 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77
- 430439; AL133661; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76
- 435897; AF269223; Hs.128322; t-complex 11 (a murine top homolog); t-complex 11 (a murine top homolog); 2.53
- 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosom; 2.46
- 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35
- 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33
- 425627; AF012369; Hs.185885; ESTs; ESTs; 2.12
- 438983; AF085884; Hs.20029; proscrocin binding protein sp32 precursor; proscrocin binding protein sp32 precursor; 2.07
- 426709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99
- 433724; AI827749; Hs.144924; serine/threonine protein kinase SSTK; serine/threonine protein kinase SSTK; 1.68
- 420710; NM\_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey:	Unique Eos probeset identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	
Pkey	CAT Number	Accession



417886 1031334\_1 AA210987 D57294 AA214564 AA207006 D56572  
 432407 MH1429\_12 BG036675 BF772005 BF771866 BG960386 BG960381 NM\_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104  
 5 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279  
 BE748870 BG319640 BE748864 BF739224 BG988155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849  
 AA584918 BG969570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AK075321 L13623 AA216700 BF771864 AW881859  
 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928  
 10 434414 35978\_1 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA065592  
 AF134164 BF809407 AA218557 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422  
 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298  
 AA223267 BG997695 BG997697 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175  
 BF854337  
 15 427298 115241\_1 AA933717 BF081897 AW628327 AA641788 AA400495  
 427521 513212\_1 AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165  
 407347 810943\_1 T23514 AK655785  
 430439 6750\_2 AL133561 AL117481 AL122069 AW436292 AI968826 AL041090

TABLE 57C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA  
 sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768,139702-139693,140475-14050
402260	3399665	Minus	113785-113910,115663-115765,116808-11694
402678	8113438	Plus	37395-37514,37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3087841	Plus	24712-25374
402677	8113438	Plus	22135-22309,23063-23238
402679	8113438	Plus	132079-132216
402145	8018280	Plus	113086-114800
406547	7711513	Minus	172780-174358
402398	4082817	Minus	24019-24973
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
401083	3242744	Plus	33192-33360
404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion\_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar accession number, GenBank accession number  
 UniGeneID: UniGene number  
 Pred.Protdomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).  
 UniGene Title: UniGene gene title  
 R1 90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Protdomains; R1

430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 35.25  
 422282; AF019225; Hs.114309; apolipoprotein L; MotA\_ExtB;TM=Y;SS=M; 33.25  
 414655; N98568; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip;TM=M;SS=Y; 31.68  
 415182; D17793; Hs.78183; aldo-keto reductase family 1, member C3; aldo\_ket\_red;TM=M; 31.04  
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarot; none,none; 28.50  
 439180; AI393742; Hs.199087; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep\_L\_domain,Furin-like,pkinase,Recep\_L\_domain,Peptidase\_M24; 27.43  
 417079; U66590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 25.98  
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM\_PNT,none; 25.38  
 418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT,none; 25.28  
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA\_gyrase3,DNA\_topoisolV,HATPase\_c;SS=M; 23.58  
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; lg,pkinase;TM=Y;SS=M; 21.24  
 424008; R02740; Hs.137556; putative chemokine receptor; GTP-binding; 7tm\_1;TM=Y;SS=M; 20.45  
 447343; AA256841; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 19.78  
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 18.90  
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M; 18.75  
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl\_oxidase;SS=M; 18.63  
 444381; BE387335; Hs.283713; ESTs, Weakly similar to 864054 hypohef; Collagen;TM=M;SS=M; 18.60  
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; Ig,Rhbd\_glycop;TM=Y;SS=M; 18.55  
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M; 18.25



- 413132; NM\_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic); PKD;SS=M; 17.73  
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; Ig;TM=Y;SS=M; 17.68  
 450746; D82673; Hs.278589; general transcription factor II, r; none;SH3,FX; 17.12  
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 16.88  
 420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone\_rec,zf-C4;TM=M; 16.78  
 439941; A1392640; Hs.18272; amino acid transporter system A1; Aa\_trans;TM=Y; 16.75  
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 16.56  
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,Ig,FAD\_Synth,kdh,kdh\_C,ptkinase;SS=M; 16.43  
 414883; AA926960; CDC28 protein kinase 1; CKS; 16.20  
 438091; AW373062; nuclear receptor subfamily 1, group 1, m; hormone\_rec,zf-C4;none; 15.80  
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH1b,LIpase\_GDSL;TM=M; 15.70  
 428450; NM\_014791; Hs.184339; KIAA0175 gene product; KA1,ptkinase;TM=M; 15.63  
 422278; AF072873; Hs.114216; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm\_2;TM=Y;SS=M; 15.45  
 434293; NM\_004445; Hs.3798; EphB6; EPH1bd,fn3,ptkinase,SAM;TM=Y;SS=M; 15.43  
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF,lectin\_c,sushi;TM=M;SS=M; 15.28  
 443991; NM\_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK\_channel,ion\_trans;TM=Y;SS=M; 15.10  
 416305; AU076628; Hs.78187; coxsackie virus and adenovirus receptor; Ig;TM=Y;SS=M; 14.90  
 432306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib); CBM\_21;TM=M; 14.80  
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; ptkinase;TM=M; 14.73  
 429345; R11141; Hs.199695; hypothetical protein; K,letra,SAM; 14.58  
 449230; BE613348; Hs.211679; melanoma cell adhesion molecule; ig,isochn,Ribosomal\_L6,F-box;TM=Y;SS=M; 14.55  
 421508; NM\_004533; Hs.105115; absent in melanoma 2; PAAD\_DAPIN,HIN;TM=M; 14.53  
 446008; NM\_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 14.35  
 429556; AW139399; Hs.98988; ESTs; none;TM=M; 14.18  
 416224; NM\_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; ehand;SS=M; 14.13  
 429573; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y\_phosphatase,Band\_41,PDZ;SS=M; 13.90  
 428657; NM\_015865; Hs.171731; solute carrier family 14 (urea transport); UT;TM=Y; 13.83  
 428157; AJ738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 13.80  
 400843; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_g,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 13.78  
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC\_tran,CoaE;TM=M; 13.38  
 432314; AA533447; Hs.312989; ESTs; Xlnk,none; 13.25  
 413109; AW389845; Hs.110865; ESTs; PHO4,none; 13.15  
 424490; AJ278016; Hs.55555; ankyrin repeat domain 3; ank,ptkinase;TM=M; 13.13  
 426490; NM\_001621; Hs.170067; aryl hydrocarbon receptor; PAC,PAS;TM=M; 12.93  
 426158; NM\_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,ptkinase,Recep\_L\_domain,Furin-like,ptkinase,Recep\_L\_domain,Peptidase\_M24; 12.43  
 440249; A1248590; Hs.249175; ESTs; TaD\_DNase,ptkinase,death,none; 12.38  
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 12.38  
 404942; U03825; ; splicing factor, arginine/serine-rich 9; CD38;TM=Y;SS=M; 12.03  
 439569; AW802166; Hs.222399; CEGP1 protein; EGF,TNFR\_p6,granulin,CUB,Keratin\_B2,TIL;TM=M;SS=M; 11.93  
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fls, clone NT; Aa\_trans,none; 11.88  
 408000; L11690; Hs.198689; bulbus pemphigoid antigen 1 (230240kD); ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose\_isom,FLID,bZIP,Tropomyosin,Myc-LZ,M,ldh\_C,CH,ALP3;TM=M; 11.88  
 412182; AA205588; Hs.155180; Splicing factor, arginine/serine-rich, 4; rrm,hormone\_rec,zf-C4,sugar\_tr; 11.85  
 433470; AW960584; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.80  
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb\_DNA-binding,THF\_DHG\_C,THF\_DHG\_C,THF\_DHG\_C,CAP\_GLY,AAA,LON,Peptidase\_C9,bZIP,Mxan\_ur permease,HCO3\_cotransp;TM=M; 11.69  
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus); 7tm\_1,7tm\_2;TM=Y;SS=M; 11.50  
 426761; A1015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586I2022 (f; none;TM=Y;SS=M; 11.48  
 439760; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH\_C,IMPDH\_N,CBS,Integrin\_B,Ricin\_B,lectin; 11.38  
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 11.23  
 436728; BE21807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.18  
 409960; BE261944; Hs.339673; hexokinase 1; none,none; 11.02  
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate\_kdn;TM=M; 10.78  
 417821; BE245149; Hs.82643; protea tyrosine kinase 9; cofilin\_ADF;SS=M; 10.63  
 427654; AA410183; Hs.137475; ESTs; lon\_trans,vwc,IgFBP,isp\_1; 10.58  
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member; aldedh;TM=M;SS=M; 10.53  
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (f; SH3,PH,RhoGEF;TM=M; 10.53  
 449437; A1702038; Hs.100057; Homo sapiens cDNA; FLJ22902 fls, clone K; none,none; 10.52  
 436858; A1469355; Hs.127310; ESTs; ptkinase,rrm;TM=M; 10.48  
 451035; AU076785; Hs.430; plasmin 1 (f isoform); ehand,CH,Adaptin\_N;SS=M; 10.38  
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; Integrin\_B,EGF,PSI;TM=Y;SS=M; 10.35  
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,Integrin\_A,FG-GAP;TM=Y;SS=M; 10.34  
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD\_DAPIN,NA;NA; 10.25  
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf\_5;TM=Y;SS=M; 10.18  
 437852; BE001838; Hs.256897; ESTs, Weekly similar to dJ365O12.1 (H.s); GPS,7tm\_2;TM=Y; 10.13  
 400752; ; NM\_003105; Homo sapiens sortilin-related; EGF,fn3,ldl\_recept\_a,ldl\_recept\_b,granulin,BNR;TM=Y;SS=M; 10.08  
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSF;TM=M; 10.05  
 426728; NM\_007118; Hs.171957; triple functional domain (PTPRF interact; SH3,Ig,ptkinase,PH,spectrin,RhoGEF;TM=M; 10.05  
 400496; ; ENSP00003224716; GTP-binding protein SAR; none;TM=Y; 10.01  
 413898; AF083692; Hs.75608; tight junction protein 2 (zone occludens; SH3,PDZ,Guanylate\_kdn;TM=M; 10.00  
 404568; ; NM\_022071; Homo sapiens hypothetical pro; SH2;TM=M; 10.00  
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 9.93  
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehand,kazal,arf,ras,7tm\_1;TM=M; 9.90  
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 9.90  
 424954; NM\_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,JRK;TM=M; 9.88  
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; ptkinase;TM=M; 9.85  
 439223; AW238299; Hs.250618; UL16 binding protein 2; ldl\_recept\_a,PKD,MHC\_J;TM=M;SS=Y; 9.83  
 429238; NM\_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y\_phosphatase;TM=Y;SS=M; 9.80  
 414135; NM\_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSF,Y\_phosphatase;TM=M; 9.73  
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none,none; 9.73  
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y\_phosphatase,DSF;TM=M; 9.72  
 403912; ; CS000394; gij12737280[refXP\_006682.2] k; none;TM=M; 9.70  
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 9.70

- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc; pkinase; TM=M; 9.68  
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3, Y\_phosphatase; TM=M; 9.63  
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; 9.63  
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3\_P14\_kinase, FAT, FATC; TM=M; 9.55  
 430259; BE5650182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3, RA, RasGEF; TM=M; SS=M; 9.50  
 428520; AA331961; Hs.184736; hypothetical protein FLJ10097; none; TM=M; 9.50  
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; 9.50  
 448913; AA194422; Hs.22564; myosin VI; mm, zif-RanBP, pkinase, GST\_C, Ets, SAM\_PNT, ABC2\_membrane, myosin\_head, IQ, Myosin\_N, bZIP, zif-C2H2, PHD, BTB, TFIIS, AT\_hook, SAM; TM=M; 9.50  
 414911; NM\_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40, homeobox, LIM; TM=M; 9.48  
 451295; A1557212; Hs.17132; ESTs, Moderately similar to 154374 gene; pkinase, DAG\_PE-bind, pkinase\_C, OPR, none; 9.45  
 402328; ; Target Exon; pkinase; TM=M; 9.44  
 443710; A1928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fls, clone C; G-alpha; none; 9.42  
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; 9.42  
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS\_kinase, ATP-sulfurylase, PRK, Thymidylate\_kin; SS=M; 9.40  
 418827; BE327311; Hs.47166; HT021; none; TM=M; 9.40  
 440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1\_HUMAN CALCI; pkinase, none; 9.35  
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE\_p10, ICE\_p20; SS=M; 9.28  
 410668; BE379794; Hs.65403; hypothetical protein; death, TNFR\_c6; TM=Y; SS=M; 9.25  
 430024; A1808780; Hs.227730; integrin, alpha 6; integrin\_A, FG-GAP; TM=Y; SS=M; 9.23  
 452696; A1826645; Hs.211534; ESTs; ArfGap, PH, ank, Guanylate\_kin, PDZ, SH3; 9.13  
 434263; N34895; Hs.44648; ESTs; ig, none; 9.13  
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell; Ribosomal\_S14, ank, pkinase, death, none; 9.10  
 429332; AF030403; Hs.189263; Sta-20 related kinase; pkinase, metalthio; TM=M; SS=M; 9.03  
 417426; NM\_002291; Hs.82124; laminin, beta 1; laminin\_EGF, laminin\_Nterm, integrin\_B; SS=M; 9.08  
 443951; F13272; Hs.111334; fibrin, light polypeptide; PMP22\_Claudin, none; 9.07  
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK, CoaE; 8.98  
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3; TM=M; 8.93  
 438000; A1825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none; TM=M; 8.90  
 446620; AA128808; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 8.90  
 436075; BE090176; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 8.88  
 437056; A147061; ; gbok33a11.1; Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S; none, spectrin, SH3, PH, CH; 8.78  
 445496; AB007880; Hs.12802; development and differentiation enhancer; SH3, ank, PH, ArfGap; TM=M; 8.78  
 418203; XS4942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75  
 434603; AA805443; Hs.179809; hypothetical protein FLJ22995; none; TM=M; 8.70  
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.68  
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none; TM=M; SS=M; 8.65  
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept\_Y\_phosphatase; SS=M; 8.65  
 430397; A1924533; Hs.105607; bicarbonate transporter related protein; HCO3\_cotransp; TM=Y; 8.64  
 448858; AW196563; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 8.60  
 442994; A1026718; Hs.16954; ESTs; ank, pkinase, death, Ribosomal\_S14; 8.60  
 429109; AL006637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3, OPR, PX; TM=M; 8.60  
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8\_HUMAN ALU S; none, 7m\_1; 8.55  
 437763; AA469369; Hs.5631; tissue inhibitor of metalloproteinase 1; TIMP, pkinase, DAG\_PE-bind, RBD; 8.43  
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE451939, mRNA seq; none, none; 8.40  
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 8.39  
 448209; AW160488; Hs.20709; tetraspan 5; transmembrane4; TM=Y; SS=M; 8.33  
 450139; AK001838; Hs.286323; serum/glucocorticoid regulated kinase; none, none; 8.33  
 446350; AF052112; Hs.12540; lysophospholipase I; atylhydrolase\_2; TM=M; 8.31  
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7m\_1; TM=Y; SS=M; 8.30  
 445633; A145396; Hs.17287; ESTs, Weakly similar to S26689 hypothetical; IRK, none; 8.28  
 446719; W33900; Hs.301872; hypothetical protein MGC4840; AAA, SKI; TM=M; 8.23  
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none, none; 8.20  
 427274; NM\_005211; Hs.174142; colony stimulating factor 1 receptor, for; ig, pkinase; TM=Y; SS=M; 8.18  
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none, none; 8.15  
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS, zif-C2H2, SET; 8.15  
 417386; AL037228; Hs.82043; D123 gene product; NUDIX, secY, E1\_dehydrog, transket\_pyr; TM=Y; SS=M; 8.13  
 431236; AV656840; Hs.285116; interleukin 13 receptor, alpha 1; fn3; TM=Y; SS=M; 8.10  
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none; TM=M; SS=M; 8.09  
 425424; NM\_004964; Hs.157199; ELKL motif kinase; pkinase, UBA, KA1; TM=M; 8.08  
 422573; AW297986; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP, integrin\_A, none; 8.05  
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo\_seg; TM=M; SS=M; 8.03  
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase; SS=M; 8.03  
 404891; ; Target Exon; none, none; 7.95  
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none, none; 7.93  
 452888; AW955464; Hs.30942; ephrin-B2; Ephrin, fn2; TM=Y; SS=M; 7.93  
 433211; H11850; Hs.12808; MARK; pkinase, UBA, KA1; SS=M; 7.91  
 436486; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase, ABC1, none; 7.90  
 413219; AA678200; Hs.118727; Homo sapiens cDNA FLJ13692 fls, clone PL; HLH, death, TNFR\_c6, Acyl-CoA\_hydro; 7.90  
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan\_ur\_permease, RA; 7.88  
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2; Furin-like, pkinase, Recept\_L\_domain, YLP; TM=Y; SS=M; 7.86  
 405036; ; NM\_021628; Homo sapiens arachidonate lip; lipoygenase, complex1\_49kd, PLAT; TM=M; 7.83  
 418529; AW005595; Hs.250897; TRK-fused gene; Band\_41, ERM, pkinase, LRR, LRRC, MAM, Nucleoplasm, Tropomyosin, OPR, filament, bZIP, G-gamma\_M, DUF164; TM=M; 7.83  
 431912; A1660552; Hs.76549; ESTs, Weakly similar to A56154 Abi subst; none, Acyl-CoA\_ch, Acyl-CoA\_ch\_M, Acyl-CoA\_ch\_N; 7.80  
 432981; NM\_002733; Hs.3136; protein kinase, AMP-activated, gamma 1 n; CBS, Aa\_trans; TM=M; 7.78  
 422940; BE077458; ; gb:RC1-BT0605-090500-015-b04 BT0606 Homo; Sec7, PH, ANF\_receptor, ig\_chan, WD40, IRK; 7.78  
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonin; CNH, DAG\_PE-bind, PH, Involucrin, M; TM=M; 7.78  
 431183; NM\_008855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER\_lumen\_recept; TM=M; SS=M; 7.78  
 400845; ; NM\_003105; Homo sapiens sortilin-related; EGF, fn3, kL\_recept, ald\_recept, bgranulin, BNR; TM=Y; SS=M; 7.73  
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosom; ABC\_tran, M, SMC\_N, SMC\_C, DUF164, none; 7.73  
 437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ\_con, Y\_phosphatase, SH2; 7.70  
 403212; ; NM\_018695; Homo sapiens Intersectin 2 (IT; SH3, effhand, C2, PH, RhoGEF; TM=M; 7.70  
 441190; H09073; Hs.25046; ESTs; E1-E2\_ATPase, Cation\_ATPase\_C, Cation\_ATPase\_N, Hydrolase, none; 7.68

- 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm\_1,zf-C3HC4,m3,SPRY,KRAB,zf-C2H2,rve,zf-B\_box;TM=Y;SS=M; 7.68
- 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,pkinase;SS=M; 7.65
- 447898; AW969638; Hs.112318; 6.2 kd protein; none;none; 7.65
- 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD\_DAPIN,HIN;SS=M; 7.63
- 401927; ; C17000914\*gi8394367ref|NP\_058549.1|s; none; 7.60
- 407347; AA829847; ; gb:cd40d07.s1 NCI\_CGAP\_GCB1 Homo sapiens; RhoGAP,SH2,pkinase,POLO\_box;none; 7.58
- 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3;none; 7.57
- 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin\_A,PHO4,pkinase,ubiquitin; 7.55
- 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase; ty; none;none; 7.55
- 421489; AF922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
- 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
- 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylylkinase,SRP54;TM=M; 7.50
- 430670; A1417881; Hs.292464; ESTs; 7tm\_2,Fz,Frizzled;none; 7.50
- 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48
- 420676; A1434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG\_PE-bind;none; 7.48
- 444252; R21135; Hs.54985; ESTs; none;none; 7.47
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3\_P14\_kinase;TM=M; 7.47
- 443428; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45
- 418546; AA224827; gb:nc32g04.s1 NCI\_CGAP\_Py2 Homo sapiens; vwa,Integrin\_A,FG-GAP;none; 7.45
- 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone I; none;NA;NA; 7.43
- 452007; AA428234; Hs.34906; ESTs, Weakly similar to T17210 hypothet; none,pkinase; 7.40
- 432407; AA221036; ; gb:z03f12.r1 Stratagene NT2 neuronal pr; DEAD,helicase\_C,rmr,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,QJ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPC,isp\_1,Ribosomal\_S21,rvp;TM=M; 7.40
- 424943; AJ077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal\_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 7.40
- 421429; NM\_014922; Hs.104305; death effector filament-forming Ced-4-l; LRR,PAAD\_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
- 417141; U22682; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone\_rec,zf-C4;SS=M; 7.38
- 430016; NM\_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38
- 422813; AV656571; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
- 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp781G18121 ( ; none,spectrin,SH3,PH,CH; 7.26
- 409213; U81412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M; 7.24
- 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23
- 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 7.19
- 407591; NM\_000910; Hs.37125; neuropeptide Y receptor Y2; 7tm\_1;TM=Y; 7.18
- 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
- 450285; AW383258; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18
- 403344; ; NM\_000341;Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15
- 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage\_CLC;TM=Y; 7.14
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar\_tr;TM=Y;SS=M; 7.14
- 404876; ; NM\_022819;Homo sapiens phospholipase A2; phospho;SS=M; 7.11
- 433618; AA802539; Hs.345494; ESTs; G-alpha\_A\_deaminase; 7.10
- 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate\_transp,STAS,HMG\_box; 7.08
- 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 7.05
- 426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M; 7.05
- 423387; AJ012074; ; vasocutic intestinal peptide receptor 1; 7tm\_2,HM,CSD;TM=Y;SS=M; 7.03
- 400211; ; NM\_003898;Homo sapiens PAK-Interacting ; SH3,PH,RhoGEF,Terpene\_synth;TM=M; 7.03
- 438150; AA037634; Hs.342874; transforming growth factor, beta recepto; zona\_pellucida;none; 6.93
- 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; ; proteasome;TM=M; 6.93
- 405275; AB028989; ; mitogen-activated protein kinase 8 inter; Cys\_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
- 415392; Z44057; Hs.10957; ESTs; PIP5K;none; 6.89
- 429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadillo\_seg;none; 6.88
- 426683; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; ; C2,PLA2\_B;TM=M; 6.85
- 427832; AF035362; Hs.180930; TBP-associated factor 172; SNF2\_N,helicase\_C,Armadillo\_seg,HEAT;TM=M; 6.83
- 447887; AA114050; Hs.19849; caspase 8, apoptosis-related cysteine pr; ICE\_p10,ICE\_p20,DED;TM=M; 6.80
- 400158; ; ENSP0000024302; cDNA FLJ11591 fis, clone Sm;SS=M; 6.78
- 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT\_bind,STAT\_prot,lon\_trans,PAC,PAS;none; 6.78
- 400844; ; NM\_003105;Homo sapiens sortilin-related; EGF,m3,lid\_recept\_a,lid\_recept\_b,granulin,BNR;TM=Y;SS=M; 6.73
- 457239; U07358; Hs.211601; mitogen-activated protein kinase kinase ; pkinase; 6.73
- 404440; ; NM\_021048;Homo sapiens melanoma antigen; ; MAGE;TM=M; 6.73
- 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kina; Els,SAM\_PNT;TM=M; 6.70
- 426746; J03626; Hs.2057; uridine monophosphate synthetase (cortia; Priboyltran,OMPdecase;TM=M; 6.70
- 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65
- 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate\_kin;SS=M; 6.64
- 408639; AW451353; Hs.173328; ESTs; B55;none; 6.63
- 408058; AA312328; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
- 401057; BE563196; ; eukaryotic translation elongation factor; lon\_trans,IQ;TM=Y; 6.60
- 446528; H99616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none;none; 6.60
- 400528; ; NM\_020975;Homo sapiens rel proto-oncoge; cadherin,pkinase;TM=Y;SS=M; 6.58
- 418562; R60869; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57
- 453826; AL138129; ; gb:DKFZp547F152\_r1 547 (synonym: htrb1) ; PK,PK\_C;none; 6.55
- 437412; BE089288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (tr; ABC\_tran,ABC\_membrana;none; 6.54
- 415088; AJ077288; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 6.50
- 453489; AA300067; Hs.33032; hypothetical protein DKFZp434N185; F5\_F8\_type\_C,pkinase,Els,F5\_F8\_type\_C,pkinase,Els; 6.47
- 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M; 6.46
- 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 6.46
- 441712; AW391927; Hs.7946; KIAA1288 protein; ALP3;TM=M; 6.44
- 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; pkinase,7tm\_1; 6.43
- 432211; BE274530; Hs.273333; hypothetical protein FLJ10886; FGGY\_C;TM=M; 6.43
- 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40
- 438941; AF075947; Hs.31864; ESTs; Ca\_channel\_B,SH3,anf;none; 6.40
- 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB;none; 6.33
- 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothet; lipoxygenase,PLAT;none; 6.33
- 433255; A1274270; Hs.96840; KIAA1527 protein; MHCK\_EF2\_kinase;TM=M;SS=M; 6.33
- 427801; AW979155; Hs.298275; amino acid transporter 2; Aa\_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubikullin,BAG,Tropomyosin;; 6.30  
 439464; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none:none; 6.30  
 453977; AA865006; Hs.250427; ESTs; pklnase,P2X\_receptor,E1-E2\_ATPase,Hydrolase; 6.30  
 412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras,arf,PP2C;TM=M; 6.30  
 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180kD); DNA\_gyraseB,DNA\_topoisolV,HATPase\_c,DNA\_gyraseB,DNA\_topoisolV,HATPase\_c; 6.29  
 404342;; C7002192; gll7299207[gb|AAAF54404.1] (AEQ); none;TM=M; 6.27  
 409274; NM\_003930; Hs.52644; SKAP55 homologue; SH3,PH;SS=M; 6.25  
 419593; AA133749; Hs.301350; FYXD domain-containing ion transport reg; ATP1G1\_PLM\_MAT8;TM=Y;SS=M; 6.23  
 405429;; Target Exon; Y\_phosphatase;none; 6.23  
 404975; AL042279;; uncharacterized hypothalamus protein HT0; kringler;TM=Y;SS=M; 6.20  
 452929; AW954938; Hs.172816; neuregulin 1; Neuregulin,EGF;ig,Neuregulin,EGF;ig; 6.18  
 446883; AW452756; Hs.16364; hypothetical protein FLJ10955; DEAD,helicase\_C,nm,Ndr,Cys\_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TFR,DSpc,isp\_1,Ribosomal\_S21,rvp;TM=M; 6.18  
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M; 6.15  
 456791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y; 6.15  
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none:none; 6.14  
 447727; AI421079;; tumor necrosis factor receptor superfamily; none,synapticbrevin; 6.13  
 401536;; NM\_002530; Homo sapiens neurotrophic tyr; ig, pklnase,LRP,LRNT,LRRT;TM=M;SS=M; 6.11  
 444317; AI140568; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H; PAN,kringle,trypsin,PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN; 6.10  
 427557; NM\_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR\_LY6,ET,PLA2\_inh;SS=M; 6.08  
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M; 6.08  
 450107; AI873287; Hs.257812; ESTs; ICE\_p20,DED;TM=M; 6.05  
 418175; AW967054; Hs.206312; ESTs, Weakly similar to I38022 hypothetical; zf-C2H2,BTB,K\_tetra,Synlaxn;none; 6.05  
 408933; NM\_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC\_tran,ABC\_membrane,PRK,Bac\_export\_3;TM=Y; 6.05  
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema,PSI,integrin\_B;TM=Y; 6.03  
 427625; AF008216; Hs.285013; putative human HLA class II associated p; none:none; 6.03  
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanase;none; 6.03  
 440650; AB016825; Hs.15813; solute carrier family 22 (organic cation; sugar\_tr;TM=Y;SS=M; 6.03  
 405102;; C15001220; gll4469558[gb|AAD21311.1] (AF; DAG,PE-blind,PH,RhoGEF,DC1;SS=M; 6.03  
 400121;; Eos Control; SH3,PH,RhoGEF,Terpene\_synth;TM=M; 6.03  
 415327; H22769;; gb|ym54c02.r1 Soares infant brain 1N1B H; SH3,PDZ,Guanlylate\_kin;SS=M; 6.03  
 404148;; NM\_002944; Homo sapiens v-ros avian UR2; fn3,phklnase,DUF139;TM=Y;SS=M; 6.03  
 405531;; Target Exon; PDZ,CARD,Guanlylate\_kin;TM=M; 6.00  
 433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B); NDK;none; 6.00  
 427270; H47921; Hs.174139; chloride channel 3; voltage\_CLC,CBS;none; 5.99  
 423774; L39064; Hs.1702; interleukin 9 receptor; none;TM=M;SS=M; 5.98  
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked; pklnase,TBC; 5.98  
 411040; AF007393; Hs.177674; protein-kinase, interferon-inducible dou; HLH;TM=M; 5.95  
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer,7tm\_1;none; 5.88  
 453902; BE502341; Hs.3402; ESTs; none:none; 5.88  
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa\_trans;TM=Y; 5.86  
 436154; AA764950; Hs.119898; ESTs; ehfand,DAG\_PE-bind,DAGKa,PHD,DAGKc,PSI;none; 5.85  
 455358; AW902641;; gb|CV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase,Somatostatin\_B,Phosphodiester;none; 5.83  
 414108; AI287592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol\_BP,phklnase;TM=M; 5.82  
 452547; AA335295; Hs.74120; adipose specific 2; LEA;TM=M; 5.82  
 415204; T27434;; gb|hbc2294 Human pancreatic islet Homo s; Na\_Ca\_Ex,Calx-beta;none; 5.80  
 435553; AF210317; Hs.95497; solute carrier family 2 (facilitated glr; sugar\_tr;TM=Y; 5.78  
 456097; C15702; Hs.288028; ESTs, Moderately similar to I54374 gene; dsrm,FKBP; 5.78  
 422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle; E1-E2\_ATPase,Cation\_ATPase\_C,Cation\_ATPase\_N,Hydrolase;TM=Y; 5.77  
 436246; AW450363; Hs.119991; ESTs; none,DNA\_gyraseB,DNA\_topoisolV,HATPase\_c; 5.75  
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC\_tran,PRK;TM=Y;SS=M; 5.75  
 425854; AA749190;; ESTs; RhoGAP,SH2,phklnase,PCLO\_box;none; 5.74  
 424160; T74062;; gb|yc81f01.r1 Soares Infant brain 1N1B H; ROK;none; 5.70  
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN\_MK;TM=M;SS=Y; 5.69  
 437613; R19892; Hs.10267; MLL1 protein; none:none; 5.68  
 410820; BE391493; Hs.16476; Human DNA sequence from clone RP5-852M4; TBC;SS=M; 5.68  
 423393; R37772; Hs.21420; p21-activated protein kinase 6; phklnase,PBD;TM=M; 5.66  
 426500; NM\_014638; Hs.170156; KIAA0450 gene product; C2,PI-PLC-Y;TM=M; 5.63  
 406930; U04891;; gb|Human olfactory receptor (OR17-219) g; none;TM=Y;SS=M; 5.60  
 401044;; Target Exon; none,ICE\_p20,ICE\_p10,CARD,Peptidase\_M1; 5.56  
 428479; Y00272; Hs.334582; cell division cycle 2, G1 to S and G2 to; phklnase,ICE\_p10,ICE\_p20;TM=M;SS=M; 5.55  
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RR; ea\_permases,pyridoxal\_deC,bromodomain,PHD,MBD,AT\_huok,DDT,PI3\_P14\_klnase,FAT,FATC,BoIA,RUN;TM=M; 5.53  
 426248; T18988; Hs.293668; ESTs; phklnase;none; 5.50  
 418426; NM\_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; phklnase,death;TM=M; 5.43  
 417086; AA194446;; ESTs, Weakly similar to S55024 nebulin; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.43  
 447437; U07225; Hs.339; putative receptor P2Y, G-protein coupl; 7tm\_1,SH2;TM=Y;SS=M; 5.40  
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF;SS=M; 5.40  
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA; cor; phklnase,TBC,Rhodanase;TM=M; 5.38  
 418355; AA428520; Hs.90061; progesterone binding protein; hema\_1;TM=Y;SS=M; 5.35  
 411188; BE161168;; gb|PMO-HTD425-170100-002-ct10 HTD425 Homo; adenylatekinase;none; 5.35  
 422461; NM\_003417; Hs.117077; zinc finger protein 284; zf-C2H2,KRAB,TFHS;TM=M; 5.28  
 426348; BE468586; Hs.17433; hypothetical protein FLJ20967; none:none; 5.25  
 429170; NM\_001394; Hs.2359; dual specificity phosphatase 4; Rhodanase,DSPc,Y\_phosphatase,Ribosomal\_S3\_N;TM=M; 5.23  
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin,Exo\_endo\_phos,IQ;TM=M; 5.22  
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER\_lumen\_recept,Ribosomal\_L11,Ribosomal\_L11\_N;TM=Y;SS=M; 5.21  
 434368; AW519020; Hs.73893; dopamine receptor D2; phklnase,SH3;none; 5.15  
 405586;; NM\_000299; Homo sapiens plakophilin 1 (ec; Armadillo\_seg;TM=M; 5.13  
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase;none; 5.12  
 407443; AF227138;; gb|Homo sapiens candidate taste receptor; none;TM=Y;SS=M; 5.11  
 415817; AA398045; Hs.104679; ESTs; Furin-like,phklnase,Recep\_L\_domain,fn3;none; 5.10  
 401886;; NM\_021783; Homo sapiens XEDAR (XEDAR), mR; TNFR\_c6;TM=M;SS=M; 5.08  
 410314; AW660708; Hs.18851; hypothetical protein FLJ10875; myb\_DNA-binding,PAR,BAH,bromodomain,PHD,SET;TM=M; 5.08

- 401579; AL031447; : Homo sapiens, clone IMAGE:4053044, mRNA; Neur\_chan\_LBD, Neur\_chan\_memb, none; 5.05  
 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-; PABP, mm, pkinase, 14-3-3; 5.05  
 417528; AA203634; : gb:zx58b09.r1 Soares\_fetal\_liver\_spleen.; pkinase, UBA, KA1, none; 5.03  
 417527; AA203624; : gb:zx58e10.r1 Soares\_fetal\_liver\_spleen.; SH3; SS=M; 4.98  
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; pK8; TM=M; 4.95  
 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid\_phosphat, none; 4.93  
 404298; : : C6001238\*gl|121715|sp|P26697|GTA3\_CHICK; none, GST\_C, GST\_N, pkinase; 4.85  
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; none; TM=M; 4.82  
 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC\_tran, ABC\_membrane; TM=Y; 4.73  
 422366; T83882; Hs.97927; ESTs; pkinase, none; 4.64  
 424905; NM\_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; 4.48  
 426925; NM\_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fls, clone H; Esterase, enolase, Peptidase\_S9; TM=M; 4.46  
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm\_1; TM=Y; SS=M; 4.40  
 400749; : : NM\_003105\* Homo sapiens sortilin-related; EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 4.38  
 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4; TM=Y; SS=M; 4.33  
 444008; BE395085; Hs.10086; type I transmembrane protein Fnt14; ldl\_recept\_a, PKD, MHC\_2; TM=M; SS=Y; 4.31  
 400751; : : NM\_003105\* Homo sapiens sortilin-related; EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 4.18  
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; SS=M; 3.90  
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none, none; 3.88  
 458760; A1498631; Hs.111334; ferritin, light polypeptide; cystatin, ferritin, histone, HCO3\_cotransp, SH3, RhoGAP, xan\_vr\_permease, FCH; SS=M; 3.85  
 441218; BE327561; Hs.202345; ESTs; none, WD40, E1-E2\_ATPase, Calton\_ATPase\_C, Calton\_ATPase\_N, Hydrolase; 3.78  
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fls, clone NT; death, ZU5; SS=M; 3.76  
 451385; AA017656; : gb:zx39h01.r1 Soares retina N2b4HR Homo; Atrophin-1, enolase, Atrophin-1\_Y, phosphatase, SH2, fibrinogen\_C, TIM; 3.60  
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase, DAG\_PE-bind, pkinase\_C, OPR; TM=M; 3.30  
 409582; AK001531; Hs.271565; ESTs; none, Neur\_chan\_LBD, Neur\_chan\_memb; 3.28  
 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1\_LC3; SS=M; 3.23  
 436740; AW975133; : gb:EST387239 IMAGE resequences, MAGN Homo; none, EPH\_1, fn3, pkinase, SAM; 3.20  
 418319; AW611703; Hs.150173; ESTs, Weakly similar to A46010 X-linked; none, IRK; 3.20  
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none; NA; NA; 3.13  
 418764; NM30531; Hs.42215; protein phosphatase 1, regulatory subunit; none, none; 3.10  
 400846; : : sortilin-related receptor, L(DLR class); EGF, fn3, ldl\_recept\_a, ldl\_recept\_b, granulin, BNR; TM=Y; SS=M; 3.09  
 422006; BE266558; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (fr; none, Na\_H\_Exchange; 3.03  
 426440; BE382755; Hs.169902; solute carrier family 2 (facilitated glt; sugar\_tr; TM=Y; SS=M; 3.02  
 424187; AA335551; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK, none; 2.98  
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death, TNFR\_c5; TM=Y; SS=M; 2.93  
 401279; : : C13000351\*gl|2494033|sp|Q54398|KDG\_D\_MES; none, none; 2.88  
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema, pkinase, TIG, PSI, none; 2.83  
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK; TM=Y; 2.80  
 453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase; TM=M; 2.75  
 441699; AW511128; Hs.127572; ESTs; none, Aa\_trans; 2.73  
 458781; A444821; Hs.63085; ESTs, Weakly similar to MPP3\_HUMAN MAGUK; SH3, PDZ, Guanylate\_kin, L27; TM=M; 2.73  
 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tet; transmembrane4; TM=Y; SS=M; 2.70  
 453487; R31770; Hs.56562; ESTs; 7tm\_1, none; 2.68  
 421279; AW664878; Hs.106645; ESTs; pkinase, none; 2.68  
 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none, none; 2.65  
 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPs; TM=M; 2.63  
 422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF; TM=Y; 2.62  
 425212; AW962253; Hs.171618; ESTs; pkinase, none; 2.60  
 427344; NM\_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur\_chan\_LBD, Neur\_chan\_memb; TM=Y; SS=M; 2.58  
 423629; AW021173; Hs.18812; Homo sapiens cDNA: FLJ21909 fls, clone H; voltage\_CLC, CBS, none; 2.55  
 456737; BE247203; Hs.124831; C61-67 protein; abhydrolase\_2; TM=M; SS=M; 2.53  
 421585; U95628; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm\_1; TM=Y; SS=M; 2.53  
 424028; AW05504; Hs.153692; Homo sapiens cDNA FLJ14354 fls, clone Y7; none, none; 2.50  
 448324; A1571356; Hs.34174; ESTs, Moderately similar to ALU8\_HUMAN A; ICE\_p20, CARD, ICE\_p10, none; 2.50  
 402256; : : Target Exon; pkinase, UBA, none; 2.43  
 452258; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fls, clone HE; GDI, 7tm\_1, none; 2.40  
 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothet; none, spectrin, SH3, PH, CH; 2.40  
 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP\_binding, lon\_trans; TM=Y; 2.35  
 419630; W57756; : gb:zd20g10.r1 Soares\_fetal\_heart\_NbHH19W; zf-C3HC4, none; 2.35  
 426227; U87058; Hs.154295; Human proteinase activated receptor-2 mR; 7tm\_1; TM=Y; SS=M; 2.35  
 400704; : : Target Exon; lig\_chan, SBP\_bac\_3, ANF\_receptor; TM=Y; SS=M; 2.33  
 400149; : : Eos Control; acid\_phosphat; TM=Y; SS=M; 2.30  
 459327; AW149706; Hs.7859; gb:zx41d02.x1 NCL\_CGAP\_Bm50 Homo sapiens; PHD, PWWP, SET, pkinase; lg; 2.30  
 452220; BE158008; Hs.212296; ESTs; Integrin\_A, FG-GAP, none; 2.25  
 416690; H84078; Hs.108551; ESTs; pkinase, none; 2.23  
 408354; A1382803; Hs.159235; ESTs; none, none; 2.23  
 452203; X57522; : transporter 1, ATP-binding cassette, sub; ABC\_tran, ABC\_membrane, SRP54, Thymidylate\_kin; TM=Y; SS=M; 2.21  
 405093; : : C12001101\*gl|7522643|pi|T32733 AMPA g; none, none; 2.20  
 412723; AA648458; Hs.335951; hypothetical protein AF301222; none; TM=M; 2.20  
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 2.18  
 417185; NM\_002484; Hs.81469; nucleotide binding protein 1 (E.coli Min; ParaA, fer4\_NiH, ArsA\_ATPase; TM=M; 2.18  
 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 2.18  
 413627; BE182082; Hs.246973; ESTs; Armadillo\_seg, IBB; TM=M; 2.18  
 407415; AF073328; : gb: Homo sapiens tetracycline transporter; none, none; 2.15  
 450592; A1701555; Hs.202562; ESTs; pkinase, none; 2.15  
 428767; A1421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1; none, pkinase; lg; 2.15  
 429012; AW829596; Hs.194726; BCL2-associated atlanogene 4; Sm, BAG; SS=M; 2.15  
 419122; A1401360; Hs.44410; ESTs; ABC\_tran, ABC\_membrane, none; 2.10  
 446420; AW015693; Hs.135614; ESTs; lon\_trans, none; 2.05  
 420078; AA827850; Hs.293717; ESTs; DUF59, pkinase; 2.05  
 409416; AW388359; Hs.10667; ESTs; transmembrane4; TM=Y; SS=M; 2.03  
 428768; AA477989; Hs.98800; ESTs; TPR, 7tm\_1; 2.03  
 427001; NM\_005482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase; TM=M; 2.03

453709; AL119133; ; protein kinase C substrate 80K-H; none,histone; 2.03  
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00  
 466772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.88  
 427786; BE407863; Hs.258871; ESTs; none,FG-GAP,7m,1; 1.65  
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.00  
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 588

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey CAT Number Accession

414883 8371\_2 AF274943 BG494894 A1719075 AA908783 A1935150 A1422691 AA910644 AA583187 BM272167 A1828996 AA527373 AW972459 A1831360 AA772418  
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 AA987230 BE467708 AW896628 AW898644 A1146984 AW043642 A1286245 A1186932 A1635262 A1139455 A1298739 A1813854 A1024768 BE699445  
 BE699444 A1707807 D52654 A1214518 A1004723 A1698085 AW087420 A1565133 AA845571 AW888622 BF110144 AW513280 A1081128 BF362770  
 A1268839 A1435818 BF476318 A1024767 BE174213 AA757598 AA513019 AA902859 A1860794 A1334784 BF108411 BM310532 AW513771 A1951391  
 A1337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 A1922204 AW898625 BE699466  
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 BF939091 BF434180 AW579001 T55662 H01811 T52622 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 RB3430 Z28822 T85791  
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 X75684 AL573167 A1445461 A153743 A1903655 A1564644 AA977180 A1694111 A1591358 AW071625 A1678712 A1720939 A1927769 BE439796  
 A1963432 AA292856 AW192593 A1865838 A1865805 A1424384 A1161312 A1911921 A1597801 B1494959 A1240988 A1492554 AW262737 BE044033  
 AW008570 AW629505 B1494958 AA088439 AA708057 BF222820 BF583608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186  
 AA043217 BE219784 A1799814 AA129575 A1671727 A1700033 BE646195 AW779725 AA903050 AA147228 AA404570 A1075878 W38161 A1972739  
 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827  
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 A1344943 A1348877 A1334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW805183 AA043216 BG482886 AA182734 AA877242  
 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA036067 AA837326 T10930 BF906587 B1755027 BG506731 BC008442  
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 B1552770 B1259210 B1256520 B1255569 BG485098 B1258228 BG498501 BM044512 AU133984 AL566586 BE745111 B1222633 AU133917 BG288151  
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			AW651691 BM048974 BM043805 BG142185 AA315188 AM46615 C06300 BG497644 AA086544 AB15987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D66120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI070221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA218013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AD011222 T97525 AW976388 AI147061 AA765223 AA743380 AI803927 BC012771 BG397153 BF366195 AA337277 AA319285 AWB43252 BI030997 AA921874 AW188622 BI027862 AI347618 AI361453 AI088754 AW207491 AD077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI023884 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BC015789 BI033807 AA341445 T23514 AI655785 T59708 AA224827 T59843 BE156903 BG036675 BF772005 BF771886 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AAD99426 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BI910138 NM_003899 C63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AI535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044634 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802964 AA902292 AA468752 AI380374 AA722690 AI667708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306666 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369654 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22456 T15901 AA825298 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5	437056 422940 409745	428504_3 58443_1 MH1944_5	
10	407347 418546 432407	810943_1 242836_1 MH1429_12	
15			
20	423387	2812_2	
25	400211	3532_1	
30			
35	400158	2165_1	
40			
45	453826 447727 400121	366136_1 10123_14 3532_1	
50			
55			
60	415327	9792_2	
65	456358 415204 425954	1160035_1 1865508_1 2638_3	
70	424160	5320_3	
75	417086	1154_2	
80	411188 417529 417527 451385 436740 419530 400149	1072487_1 3302462_1 2431831_1 85022_1 1239008_1 37310_5 16458_1	



5 452203 2630\_1 BF093671 AA053070 T28548 AL570460 B1006862 B1007207 AA373620 W95069 AA629136 AA708164 A1014886 AW168697 D51623 AA577168  
 10 A1094208 AA028946 AA975078 R16815 BG151132 A1276297 D51676  
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 15 453709 59915\_1 AA676742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 B1560216 B1753586  
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 20 R85153 BE380058 AA082637 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851  
 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 A1073587 AA004957 A1539585 N95093 H98798 H95072 H96853 AA215712  
 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 A1693577 BE181027  
 AA709461 BE181002 W60239 BF967598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734  
 R58508

TABLE 58C

Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA  
 30 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5963-5970,7653-7784,8892-9023,9573-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36461
400496	9743564	Plus	41515-41695
404568	9866985	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84874-85125
405036	7543748	Minus	121857-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

50 Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03  
 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 5.2. The "average" prostate cancer level was set to the  
 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific  
 55 background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the  
 ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number  
 ExAcct: Exemplar Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAcct	Unigene ID	Unigene Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420823	AF097021	Hs.273321	differentially expressed in hematopoietic	90.5
416854	H40164	Hs.80296	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	A1093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microsomal protein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nal (chicken)-like 2	54.6
428398	A1249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7



	437145	AF007216	Hs.5482	solute carrier family 4, sodium bicarbon	49.6
	446057	AJ420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222866	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
5	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	416314	N88802	Hs.5422	glycoprotein M6B	43.2
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000531	Hs.52256	hypothetical protein FLJ20624	41.1
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AJ46444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
15	416585	X54162	Hs.79386	kelomodulin 1 (smooth muscle)	39.0
	447726	AL137638	Hs.19368	matrilin 2	38.6
	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.6
20	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23185 fis, clone L	37.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	36.5
	400302	N48056	Hs.11915	folate hydrolase (prostate-specific memb	36.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
25	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
	415639	AJ733881	Hs.72472	BMP-R18	34.9
	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0675 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
30	452114	N22687	Hs.8236	ESTs	34.0
	426990	AL044315	Hs.173694	Homo sapiens mRNA for KIAA1750 protein,	33.8
	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AJ918950	Hs.123642	EphA3	32.7
35	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sera domain, immunoglobulin domain (Ig),	32.4
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AJ888490	Hs.55802	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
40	406380	AF123050	Hs.44532	dubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytostatin)	31.4
	453370	AJ70523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H???) transport	31.2
	408001	AA046458	Hs.96296	ESTs	30.8
45	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
	442983	BE018662	Hs.186195	ATPase, Class I, type 8B, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg	29.2
	418827	BE327311	Hs.47166	HTO21	29.0
	410330	AW023630	Hs.46786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
55	424012	AW368377	Hs.137569	tumor protein 83 kDa with strong homology	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1396	early growth response 2 (Krox-20 (Drosop	27.6
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
	446100	AW967189	Hs.13804	hypothetical protein dJ462023.2	27.4
	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
65	403047			NM_005656*:Homo sapiens transmembrane pr	27.2
	407709	AA456135	Hs.23023	ESTs	27.0
	433444	AW975324	Hs.129816	ESTs	26.8
	415889	AJ267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
70	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	26.4
	437179	AA393508	Hs.300642	serologically defined colon cancer anti	26.4
	426457	AW894667	Hs.189965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
75	400292	AA250737	Hs.72472	BMP-R18	26.0
	433647	AA603367	Hs.222294	ESTs	26.0
	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.58622	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448105	AJ800470	Hs.171941	ESTs	25.5
80	415992	C05837	Hs.145807	hypothetical protein FLJ13593	25.5
	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin laucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	416951	AW957646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothe	24.5
	409731	AA125985	Hs.55145	thymosin, beta, identified in neuroblast	24.4
5	418396	A1765805	Hs.26691	ESTs	24.1
	412088	A1689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	24.0
	409619	AK001015	Hs.55220	BCL2-associated atlanogene 2	23.9
10	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431667	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypothe	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
15	424720	M89907	Hs.152292	SW/SNF related, matrix associated, acti	22.9
	440260	AI972857	Hs.7130	copline IV	22.5
	443622	AI911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
	425363	D63407	Hs.156007	Down syndrome critical region gene 1-lik	21.9
20	450642	R39773	Hs.7130	copline IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AI970672	Hs.46538	chromosome 11 open reading frame B	21.6
	408000	L11890	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936: Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AI821895	Hs.193481	ESTs	21.5
	442799	AI564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190642	ESTs	21.2
	430887	N66801	Hs.260287	KIAA1841 protein	21.1
40	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
	408812	AE011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
	445133	AW157648	Hs.153505	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413745	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AI797713	Hs.156471	ESTs	20.7
45	440774	AI420611	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049176	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
50	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
	411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogeni	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409768	AW474960	Hs.182258	ESTs, Weakly similar to I78895 serine/th	20.5
	424897	D53216	Hs.153684	fizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263: HSPC213.	20.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14629	20.3
	429918	AW873986	Hs.118383	ESTs	20.2
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	20.2
60	453469	AB014533	Hs.33010	KIAA0533 protein	20.2
	444822	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.90419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
65	441890	R81733	Hs.33106	ESTs	19.9
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PNO099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410829	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
70	431556	AF016028	Hs.183428	sarcospan (Kras oncogene-associated gene	19.6
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	19.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AI799909	Hs.158989	ESTs	19.3
	420120	AL049810	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_006769	Hs.3844	LIM domain only 4	19.2
80	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
	409062	AL157468	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.108276	latexin protein	18.9
	431548	AI834273	Hs.9711	novel protein	18.9
	418565	AK001629	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

5	445829	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_0151310	Hs.6763	KIAA0942 protein	18.8
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (vadulin)	18.8
	434987	AW975114	Hs.293273	ESTs	18.7
	407890	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteolectin (osteoclast-inductive factor, mime	18.7
	418619	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
15	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443968	Hs.31595	ESTs	18.4
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
20	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439569	AW602165	Hs.222399	CEGP1 protein	18.1
25	417061	AI675944	Hs.186601	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
	424582	AW604804	Hs.161717	KIAA0437 protein	18.0
	432435	BE216886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12866	17.8
30	431121	AW971167		gb:EST383245 MAGE resequences, MAGL Homo	17.8
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	17.6
35	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
	429943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
40	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277852	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447609	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.15244	ESTs	17.1
45	421823	NA0850	Hs.28625	ESTs	17.1
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp554B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.169983	ESTs	16.9
	432966	AA650114	Hs.325188	ESTs	16.9
55	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF086833	Hs.135624	ESTs	16.8
	418555	AI417215	Hs.87169	hypothetical protein FLJ12577	16.8
60	442054	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zm51g01.r1 Stratzene fibroblast (937	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	16.4
	443601	AW206942	Hs.253594	ESTs	16.3
	437536	X91221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12a02.s1 Soares_testis_NHT Homo sap	16.2
70	408050	AI815667	Hs.50130	necdin (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239823	Hs.30098	ESTs	16.0
75	429653	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	1-box and leucine-rich repeat protein 4	16.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0860 protein	15.9
	430299	W28873	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	428501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AJ093577	Hs.255416	hypothetical protein FLJ21986	15.6
	434988	AJ418055	Hs.161160	ESTs	15.6
15	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AJ433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.6
20	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	15.5
	415672	N53097	Hs.193579	ESTs	15.5
	450325	AJ935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278696	Homo sapiens protein mRNA, complete cds	15.4
	443574	AJ081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445467	AJ239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418593	AJ750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	448091	AW022192	Hs.200197	ESTs	15.2
	409341	AJ963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase	15.1
	427707	NM_005678	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AJ557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	lumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432305	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
55	453510	AJ699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440629	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	428044	AA502490	Hs.336895	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simi	14.7
	433226	AW503733	Hs.9414	KIAA148B protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	14.6
70	453861	AJ028839	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.62463	KIAA0968 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proti	14.5
75	410339	AJ916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.146858	protocadherin 10	14.5
	431933	AJ187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.78334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413788	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
5	416836	D54745	Hs.80247	cholecystokinin	14.4
	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
10	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule)	14.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	AI927288	Hs.196779	ESTs	14.2
	412828	AL133395	Hs.74821	prion protein (p27-30) (Creutzfeldt-Jakob)	14.2
	432712	AG016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA463278	Hs.288906	WW Domain-Containing Gene	14.1
	466508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
20	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170066	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-Interacting protein ERBIN	13.9
	418648	AI020951	Hs.193465	ESTs	13.9
25	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153028	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
30	447384	AI377221	Hs.40528	ESTs	13.9
	444880	AW118683	Hs.154150	ESTs	13.9
	433409	AI278802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
35	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430588	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
40	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	13.8
	407839	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452261	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96867	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
50	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
	428966	AF069214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
55	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
60	410001	AB041035	Hs.57771	kallikrein 11	13.6
	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021965: Homo sapiens phosphoglucomuta	13.6
65	428648	AF052728	Hs.186021	potassium voltage-gated channel, subfam	13.6
	414279	AW021691	Hs.101067	GCNs (general control of amino-acid synt	13.6
	411573	AB029000	Hs.70623	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431487	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
70	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN IIII	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
75	447082	T85314	Hs.42644	thioredoxin-like	13.5
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.56279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypoteti	13.3
80	433517	AW022133	Hs.189838	ESTs	13.3
	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (	13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371146	Hs.226527	leptin receptor	13.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
10	407538	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.166800	ESTs	13.2
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68785	Hs.237731	ESTs	13.1
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428639	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI352575	Hs.167133	ESTs	13.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
25	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
30	447866	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
	446779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
35	417315	AK080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW286451	Hs.24605	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	FS2795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
40	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA592480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
	459513	AI032946		gbxx06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
45	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
50	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AG040928	Hs.65306	KIAA1495 protein	12.6
	453830	AA534286	Hs.20953	ESTs	12.6
	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI588801	Hs.71721	ESTs	12.6
55	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
	450253	AL133047	Hs.24716	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
60	427078	AI676062	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
65	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
70	432205	AI805583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1624	12.4
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965: Homo sapiens phosphoglucoma	12.4
75	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25686	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI59306	Hs.24908	ESTs	12.4
	441269	AW015206	Hs.178784	ESTs	12.3
80	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AI048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
	408920	AL120071	Hs.48598	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165580	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-prote	12.2
	400880			NM_000611: Homo sapiens CD69 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449525	NM_014253	Hs.23796	odc (odd Oz/ten-m, Drosophila) homolog 1	12.1
15	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AI085198	Hs.164226	ESTs	12.0
	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984525	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730046	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206086	ESTs, Moderately similar to ALUR_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42663	ESTs	11.8
35	431645	AF078849	Hs.266483	dynein light chain-A	11.8
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	428981	AL044675	Hs.173081	KIAA0530 protein	11.8
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE587335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
45	438032	BE045624	Hs.152992	ESTs	11.7
	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
50	423782	AI472209	Hs.323117	ESTs	11.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453957	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
55	411096	U80034	Hs.68583	mitochondrial intermembrane peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	11.5
	412677	AW029608	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.108541	ESTs	11.5
	443161	AI039316		gb:cx48c08.x1 Soares_t0tal_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428529	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687638	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118881	Hs.128051	Homo sapiens thymic stromal lymphopoietin	11.4
75	458804	AI421645	Hs.139851	caveolin 2	11.4
	422546	AS007969	Hs.301478	KIAA0500 protein	11.4
	417350	U60928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
80	433577	AW007080	Hs.8817	ESTs	11.4
	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEF8_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AI473827	Hs.31793	ESTs	11.3

5	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
10	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476:g 12737279:ref XP_012163.1	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
15	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.118410	ESTs	11.2
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
20	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
	429163	AA894766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T06534	Hs.14372	ESTs	11.1
25	414341	D80004	Hs.75809	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
30	425289	AW139342	Hs.155630	Interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270268	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
35	412622	AW864708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
40	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
45	417189	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104695	KIAA1324 protein	10.9
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
50	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.158110	Immunoglobulin kappa constant	10.9
	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
	441540	C01367	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	10.9
55	418777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI823752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcomagen (Kras oncogene-associated gene	10.8
	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
	447982	I22853	Hs.137551	ESTs	10.8
60	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phospholipase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
	448019	AW847164	Hs.195841	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
65	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
	450205	AI786460	Hs.201600	ESTs	10.8
	428413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
70	421977	W94187	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	msl transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 3	10.8
	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.75400	KIAA0280 protein	10.8
75	438962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW976944	Hs.237396	ESTs	10.7
80	419693	AA133749	Hs.301350	FXFD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430689	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7



5	433923	A1823453	Hs.146625	ESTs	10.7
	418186	A1746649	Hs.26549	KIAA1708 protein	10.7
	416155	A1807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheli	10.7
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
	429350	A1754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	calmagin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	A1801098	Hs.151500	ESTs	10.6
	449685	AW296659	Hs.66095	ESTs	10.6
	441111	A1806867	Hs.126594	ESTs	10.6
	436671	AW137159	Hs.146151	ESTs	10.6
15	447974	R76886		gbcy64b03.s1 Soares placenta NbZHP Homo	10.6
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.6
	424562	A1420859	Hs.150657	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965059	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	A1694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284186	forkhead box C1	10.6
	419441	AW023731	Hs.274368	MSTP032 protein	10.6
30	426011	AW998096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	461900	AB023199	Hs.27207	KIAA0882 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
	424368	AB037786	Hs.146085	KIAA1345 protein	10.5
35	402078			C5002020:gil108287[pir]S55467 tropomy	10.5
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64183	Hs.282982	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	A1377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	A1380429	Hs.172445	ESTs	10.5
	443684	A1891307	Hs.55098	ESTs	10.5
45	429281	AA630858	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cyolin T2	10.5
	418564	AA631143	Hs.278895	Homo sapiens protein mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182982	golgin-87	10.5
	416182	NM_004354	Hs.79089	cyclin G2	10.4
	418365	AW014345	Hs.161690	ESTs	10.4
	452286	A1368570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	A1033985	Hs.239926	sterol-C4-methyl oxidase-like	10.4
	446716	AA436575	Hs.16602	ESTs	10.4
	419544	A1908154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	408151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293788	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW579960	Hs.135160	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB038063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26405	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homeo box A13	10.3
	426581	AB040956	Hs.135890	KIAA1523 protein	10.3
75	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AL204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
	440426	A1158800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE061916	Hs.125849	chromosome B open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13855 fis, clone PL	10.3
	451593	AF151879	Hs.26708	CGI-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174800 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

5	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gb:U3-CT0214-291299-052-A12 CT0214 Homo	10.2
	446553	AB021179	Hs.15299	HMBA-Inducible	10.2
	418278	AI088489	Hs.83937	hypothetical protein	10.2
	419791	AI679909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	10.2
10	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922192	Hs.54709	ESTs	10.2
	457498	AI732230	Hs.191737	ESTs	10.2
	425828	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
15	414523	AJ076633	Hs.76353	serine (or cysteine) proteinase inhibitor	10.2
	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.846	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
20	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N76276	Hs.135904	ESTs	10.1
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444518	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
25	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
	444100	AA383343	Hs.22115	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016878	Hs.20509	HBV pX associated protein-8	10.1
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
30	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423581	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
	448035	NM_008558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
35	432589	AL135725	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419972	AA466113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
40	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	10.0
	451424	AI662026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
45	425833	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA063564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
50	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (scfo	9.9
55	408832	AW086690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
	452357	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
60	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI658308	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	9.9
	441054	AA913591	Hs.125480	ESTs	9.9
	416875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
65	453078	AF053551	Hs.31504	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI858732	Hs.30443	senf/in/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
70	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
75	434579	T55958		gb:yc35f05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
	427528	AJ077143	Hs.179585	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
80	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397988	Hs.179962	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
	404571			NM_015902: Homo sapiens progesterone induce	9.7
5	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278526	Arg/Abi-interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A48010 X-link	9.7
15	417171	BE613486	Hs.81412	tipin 1	9.7
	421709	AA159394	Hs.107056	CED-5 protein	9.7
	415156	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016609	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW445893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409190	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523938	Hs.185258	ESTs	9.6
	409752	AW953990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.6641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW982712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
35	412766	BE544475	Hs.54347	ESTs	9.6
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AJ280341	Hs.166571	ESTs	9.6
	424534	DB7682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447889	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AJ933808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411830	U42349	Hs.71119	Putative prostate cancer tumor suppressor	9.5
	408915	NM_016651	Hs.48950	hepaticellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AJ376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H48008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002965	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23698	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AJ636310	Hs.28310	ESTs	9.4
	449645	AW971183	Hs.96883	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	telomeron 1	9.4
	415083	AJ632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430987	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428260	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10563	ESTs	9.4
65	412446	AJ768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	intermediate filament protein syncollin	9.4
	421689	N87820	Hs.108826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44368	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
	441499	AW298235	Hs.101689	ESTs	9.4
	429184	AA188408	Hs.95565	hypothetical protein	9.4
	420051	AW024837	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA923276	Hs.280905	ESTs, Weakly similar to protease [Hsap]	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419826	AW900992	Hs.93796	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
80	429786	AL000232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

5	448807	A1571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
	445704	A1493742	Hs.166210	ESTs, Moderately similar to E38022 hypot	9.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
10	428465	AW970976	Hs.293553	ESTs	9.3
	422664	A1148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
15	433862	D86980	Hs.3610	KIAA0205 gene product	9.2
	429227	A1961456	Hs.21275	hypothetical protein FLJ111011	9.2
	401558			ENSP00000220478*:SECRETORANIN III.	9.2
	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
	437678	AA829860	Hs.122834	ESTs	9.2
20	416853	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450606	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102505	eukaryotic translation initiation factor	9.1
25	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
	448822	BE149845	Hs.289038	hypothetical protein MGC4126	9.1
	468161	BE254845	Hs.282093	hypothetical protein FLJ21918	9.1
30	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (	9.1
	432189	AA527941		gbcnh30c04.s1 NCLCGAP_Pr3 Homo sapiens	9.1
	434361	AF129755	Hs.117772	ESTs	9.1
	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
35	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-catalytic	9.1
	448704	AW090932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	A1500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
40	427213	AW007211	Hs.18131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.95423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
	434194	AF119847	Hs.283940	Homo sapiens PRD150 mRNA, partial cds	9.1
	447033	A1357412	Hs.157601	ESTs	9.0
45	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
50	430294	A1538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope H1scpi	9.0
	405523			C8001409*:glj7441226 pir S31212 collage	9.0
55	416652	T25853	Hs.7538	ESTs	9.0
	422763	AA033639	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
	448183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09783	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
60	448523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.76426	secretogranin II (chromogranin C)	8.9
	414917	C04863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
65	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA768268	Hs.265273	hypothetical protein FLJ13348	8.9
	424683	N87519	Hs.27196	ESTs	8.9
	426168	NM_001982	Hs.189067	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalytic	8.9
70	425490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	445896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502683	Hs.145037	ESTs	8.9
75	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	A1821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
	463344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostosin (multiple)-like 2	8.9
80	417173	U61397	Hs.81424	ubiquitin-like 1 (senilin)	8.9
	408161	AW852912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	A1338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny9711.s1 NCLCGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417365	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	AI940676	Hs.20914	hypothetical protein FLJ23056	8.8
5	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428847	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61795	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
15	424113	AJ743880	Hs.12876	ESTs	8.8
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW008798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypotheti	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	445686	AW072813	Hs.270868	ESTs, Moderately similar to ALUA_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AI929802	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA584489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32980	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606518, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251594	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gb:cl27e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypotheti	8.7
40		X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein [S. c	8.7
	425704	U79293	Hs.158264	Human clone 23948 mRNA sequence	8.7
	427723	AI355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
45		447335	BE617695	hypothetical protein FLJ20940	8.7
	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	Motho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50		452335	AW188944	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55		433759	AA680063	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002276: Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
60		425907	AA365752	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79138	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
65		413992	W26276	RNA, U2 small nuclear	8.6
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119553	ESTs	8.6
70		438160	AA779332	ESTs	8.6
	433254	D85782	Hs.122671	ESTs	8.6
	434851	AA808164	Hs.116502	cysteine dioxygenase, type I	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AI077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75		411667	BE160198	gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	AI273419	Hs.135148	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446585	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80		447894	AW204253	ESTs	8.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lk	8.5
	416208	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

5	434747	AA837085	Hs.220685	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PKA) anchor protein 1	8.5
	450813	AI739625	Hs.203376	ESTs	8.5
	413966	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypothetical	8.5
	407891	AA486620	Hs.41135	endomucin-2	8.5
10	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
	432620	AA777749	Hs.5978	LIM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	462670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 Interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE268026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
20	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pc3 Homo sapiens	8.4
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
	421622	AB037748	Hs.106204	KIAA1327 protein	8.4
25	431160	AW971174	Hs.324330	ESTs	8.4
	449567	AI990790	Hs.188614	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	8.3
30	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
	425692	D90041	Hs.155966	N-acetyltransferase 1 (arylamine N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431952	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
35	422295	AF051151	Hs.114408	tol-like receptor 5	8.3
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433515	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	AI799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149			NM_001450:Homo sapiens four and a half L	8.3
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA510150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	8.3
	453121	AI968284	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434C0821 (f	8.3
50	426101	AL049987	Hs.186381	Homo sapiens mRNA; cDNA DKFZp564F112 (f	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (els domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	8.2
	432695	D83480	Hs.278634	KIAA0146 protein	8.2
	407300	AA102616		gb:zn43e07.s1 Stralagene HeLa cell s3 5S	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN IIII	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.283690	ESTs, Weakly similar to I38022 hypotheti	8.2
	430468	NM_004673	Hs.241519	angiotensin-like 1	8.2
65	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone c	8.2
70	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypotheti	8.2
	408108	AI580492	Hs.42743	hypothetical protein	8.2
	408418	AW563897	Hs.44743	KIAA1435 protein	8.2
	430334	AI824719	Hs.328700	ESTs	8.2
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 59B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

	409752	115301_1	AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
5	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW858073 AW861034
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	418866	179788_1	T66754 AA229857 AA229658
	418876	179960_1	AA740616 AA654854 AA229923
	419536	185688_1	AA603305 AA244095 AA244183
10	419544	185760_2	A1909154 AA526337 AA244153 A1909153
	423800	232161_1	AA331166 AA331157 AA331155
	426413	266650_1	AA377823 AW954494 A1022688
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	430848	324821_1	AW021726 AA487752 AA488085
	431121	328275_1	AW971157 AA492575 AA492520
15	432189	342819_1	AA527941 A1810608 A1620190 AA635266
	432600	350959_1	A1821085 AW973464 AA554802 A1821831 AA657438 AA640756 AA650339
	434415	385931_1	BE177494 AW276909 AA632849
	434579	38916_1	T55958 T57205 AF147348
	439518	47334_1	W76326 AF086341 W72300
20	443161	581305_1	A1038316 A1344631 A1261653
	447974	745643_1	R76886 AA63674 R77049

TABLE 59C

	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
30	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	400860	9757499	Minus	151830-162104,152649-152744
35	400880	9831121	Plus	29235-29336,36353-36580
	401197	9719705	Plus	176341-176452
	401424	8176894	Plus	24223-24428
	401519	6649315	Plus	157315-157950
	401558	7139678	Plus	103510-104090
40	401747	9789672	Minus	118586-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	402076	8117410	Plus	128316-128627
	402812	6010110	Plus	25026-25091,25844-25920
	402855	9662953	Minus	59763-59908
45	403047	3540153	Minus	59793-59968
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403149	9799833	Plus	25034-25185
	403362	8571772	Plus	64099-64260
	404210	5006246	Plus	168926-170121
50	404571	7249169	Minus	112450-112648
	404641	9788810	Minus	32247-32362
	404642	9796810	Plus	102999-103145
55	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

65	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of prostate tumor to normal adult body tissue			
70					
	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	426747	AA635210	Hs.171995	kalikrein 3, (prostate specific antigen	56.6
	419526	A1821895	Hs.193481	ESTs	56.2
75	420154	A1093155	Hs.95420	JM27 protein	44.0
	432441	AW292425	Hs.163484	ESTs	41.9
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
	431616	AA508552	Hs.195839	ESTs, Weakly similar to 138022 hypothesis	37.9
	400299	X07730	Hs.171995	kalikrein 3, (prostate specific antigen	36.0
80	446057	A1420227	Hs.149358	ESTs, Weakly similar to A45010 X-linked	32.9
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	30.0
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	A1918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H7?? transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
10	401424			NM_001172:Homo sapiens arginase, type II	24.5
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AI267700		ESTs	20.2
15	407708	AA456135	Hs.23023	ESTs	20.0
	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
20	410629	H47293	Hs.30643	ESTs	18.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418661	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656*:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	AI765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
30	440260	AI972867	Hs.7130	copine IV	16.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	425220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
35	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AI202703	Hs.152414	ESTs	14.4
	450693	AW460461	Hs.203965	ESTs	14.4
40	431548	AI834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	14.3
	430187	AI799909	Hs.158969	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AI970672	Hs.48638	chromosome 11 open reading frame 8	14.2
45	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450642	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432886	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.158425	ESTs	13.4
50	434666	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	AI127076	Hs.308201	hypothetical protein DKFZp56401278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55899	NK homeobox (Drosophila), family 3, A	12.5
55	453961	AK026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	12.3
	428398	AI249388	Hs.98558	ESTs	12.2
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone D11P1B6 mRNA, CAG rep	12.2
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	438032	AA150797	Hs.109276	relaxin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA648253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW176665	Hs.278695	Homo sapiens protein mRNA, complete cds	11.9
70	418339	AA699902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	AI821085		glns95a12y5 NCL_CGAP_P13 Homo sapiens	11.8
	413697	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp56401278	11.6
75	424701	NM_003923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218866	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.83931	dactshund (Drosophila) homolog	11.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	11.5
80	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb.Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8



	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA503305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	10.5
5	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN IIII	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	435518	W76326		gb:zd80d04.r1 Soares_fetal_heart_AbHH19W	10.3
10	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
	415263	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
15	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone T47H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
	415079	R43179	Hs.22896	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65386	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
25	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odc (odd Oz/en-m, Drosophila) homolog 1	9.4
30	450325	AI935962	Hs.26289	ESTs	9.4
	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416785	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
35	418848	AI820961	Hs.193465	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW528686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021955: Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	426342	AI739168		Homo sapiens cDNA FLJ13456 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.267924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
50	420120	ALD49610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW958543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI086198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016825	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005605	Hs.5464	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453005	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	8.2
65	440749	W22336	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (SBK1)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	428330	L22624	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
	424592	AA429834	Hs.151781	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA525279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
	453180	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6

	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
5	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AI750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040956	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RF-XANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AWB21182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
20	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI086489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to ZZZ3_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AL077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
	439492	AF086310	Hs.103169	ESTs	6.8
50	449919	AI674685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.280024	Cdc42 effector protein 3	6.7
	441111	AI806867	Hs.126594	ESTs	6.7
	457498	AI792230	Hs.191737	ESTs	6.7
55	415293	R49462	Hs.106541	ESTs	6.7
	429163	AA894766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.7
60	418575	AA226313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB038570	Hs.9728	ALEX1 protein	6.6
	427858	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627932	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250619	phorbol-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AA851687	Hs.120691	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D54745	Hs.80247	cholecystokinin	6.6
70	447033	AI367412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10502	6.4
75	411630	UA2349	Hs.71119	Potative prostate cancer tumor suppresso	6.4
	432682	AI376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
	421077	AK000061	Hs.101590	hypothetical protein	6.4
80	452784	BE463857	Hs.151258	hypothetical protein FLJ21052	6.4
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76655	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	6.3
	453350	AA862496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone Z3948 mRNA sequence	6.3
	433510	AA806822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	AB22183	Hs.213246	ESTs	6.3
	443812	R37257	Hs.184780	ESTs	6.3
	429281	AA830855	Hs.29808	Homo sapiens cDNA: FLJ21122 fs, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
15	426466	L18964	Hs.1904	protein kinase C, iota	6.2
	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AB000470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
20	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
	427078	AB76062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KEX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282908	ESTs	6.1
25	437323	AA371145	Hs.194397	leptin receptor	6.1
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	AB076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.280024	ESTs	6.0
30	421863	AB52677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AB62236	Hs.49376	hypothetical protein FLJ20844	6.0
	408047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmagin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AB766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AB62028	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
45	431359	AW993522	Hs.292934	ESTs	5.9
	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AB149048	Hs.30211	hypothetical protein FLJ22313	5.9
	448118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9
	405523			C8001409*gi 7441226 pir J531212 collagen	5.9
50	448807	AB151940	Hs.7549	ESTs	5.8
	404642			NM_021965~Homo sapiens phosphoglucomuta	5.8
	452598	AB131594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fs, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031289-011-e11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414628	AA148950	Hs.188836	ESTs	5.7
	432712	AB018247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408828	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AB79560	Hs.98613	Homo sapiens cDNA FLJ12292 fs, clone MA	5.7
65	420184	AA188408	Hs.95665	hypothetical protein	5.7
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AB041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N76276	Hs.135904	ESTs	5.7
	433332	AB367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JCI087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fs, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AB739625	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fs, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermembrane peptidase	5.6
	451684	AF216751	Hs.26813	CDA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AB364186		gb:qw34h07.x1 NCI_CGAP_U04 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AB044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970876	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gbns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	5.5
5	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA766553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2970	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	A1241733	Hs.43871	ESTs	5.4
	424084	A1940675	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	A459306	Hs.24908	ESTs	5.4
15	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW008986	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gbv11c07.s1 Stratagene lung (937210) H	5.4
20	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
	436679	A1127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972585	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
25	412677	AW029608	Hs.17384	ESTs	5.3
	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	A1829192	Hs.22380	ESTs	5.3
	435672	AW975339	Hs.238828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
30	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 fami	5.3
	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
	433409	A1278802	Hs.25561	ESTs	5.3
	441102	AA973905		intermediate filament protein syncollin	5.3
35	453367	A1990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	A1823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD	5.2
40	447574	AF162666	Hs.18895	taused-like kinase 1	5.2
	421896	N62293	Hs.45107	ESTs	5.2
	410870	U61599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	ET4-like factor 1 (ets domain transcript	5.2
	429467	NM_004477	Hs.203772	F5HD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	tol1-like receptor 5	5.2
	453942	AW190820	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452588	AA899120	Hs.110537	homeo box A10	5.2
55	448944	AB014505	Hs.22559	abrophin-1 interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	446795	A1797713	Hs.156471	ESTs	5.1
	407300	AA102816	Hs.120769	gbzn43e07.s1 Stratagene HeLa cell s3 93	5.1
60	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	5.1
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogeni	5.1
	453293	AA362267	Hs.10653	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409543	AW450856	Hs.257359	ESTs	5.1
65	427723	A1365260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
	432261	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425843	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068558	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
	450671	A1356957	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
	433023	AW884793	Hs.87409	thrombospondin 1	5.0
80	433862	D86960	Hs.3610	KIAA0205 gene product	5.0
	451244	AW008796	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	A1734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW381569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
15	417407	AA923278	Hs.290805	ESTs, Weakly similar to protease [Hsap]	4.9
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.9
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
20	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100283	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
25	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
	418618	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225705	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.444811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
45	408990	AL022395	Hs.49526	T-box and leucine-rich repeat protein 4	4.8
	416030	HI5261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	428749	U05848	Hs.132390	zinc finger protein 36 (KOX 18)	4.8
	410268	AA318181	Hs.81635	six transmembrane epithelial antigen of	4.7
50	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphatase cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA463208		RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RPS-978E18 from 7	4.7
	418836	AI855499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*:SECRETOGRANIN III.	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22098 fis, clone H	4.7
	443881	R84512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	4.7
70	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALU8_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	418005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403045			NM_005656*:Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF128533		gb:Homo sapiens F-box protein FB3b (FBL	4.6
	426011	AW966096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
80	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861898	Hs.304505	ESTs	4.6

5	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA364891	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
	432093	H28383		gb:yl52c03.r1 Soares breast 3NbHBst Homo	4.6
10	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW186687	Hs.44748	ESTs	4.6
	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
	434423	NM_006769	Hs.3844	LM domain only 4	4.5
15	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
	437330	AL363944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
	446720	AI439136	Hs.140646	ESTs	4.5
20	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
	433507	AI817336	Hs.191791	ESTs	4.5
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.5
25	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.175909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.266720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
	428715	AW293716	Hs.53126	ESTs	4.5
30	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459661	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
	414272	AI651603	Hs.46988	ESTs	4.5
	424890	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
35	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174047	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	4.5
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C15000476*:g[12737279]ref[XP_012163.1]	4.5
40	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
	418958	AW961805	Hs.21145	hypothetical protein RG083M05.2	4.4
	433617	AW022133	Hs.189838	ESTs	4.4
45	429569	AI865345	Hs.26425	ESTs	4.4
	452338	AW068920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.4
50	430320	BE245290	Hs.238218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
	434384	AA631910	Hs.162849	ESTs	4.4
	444564	AI107677	Hs.143716	ESTs	4.4
55	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL048280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	ubiquitin	4.4
	448768	AI473827	Hs.31793	ESTs	4.4
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
60	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	4.4
	447247	AW369351	Hs.287965	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
	434022	R18374	Hs.117956	ESTs	4.4
	422365	AF035537	Hs.116521	REV3 (yeast homolog)-like, catalytic sub	4.4
65	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	4.4
	426810	AI823627	Hs.31803	ESTs	4.4
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
	448650	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
70	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82749	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
	429718	R25685	Hs.211933	collagen, type XII, alpha 1	4.3
	450316	WB4446	Hs.226434	hypothetical protein MGC4643	4.3
75	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
	435023	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	4.3
80	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
	420405	AA743396	Hs.189023	ESTs	4.3
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26536	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

5	431583	AL042513	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155594	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
	414680	AA743331		hemoglobin, alpha 2	4.3
10	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629686		ESTs, Weakly similar to S64054 hypotheti	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
	434574	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulation 3	4.2
15	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
	441623	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!	4.2
	450546	AA010200	Hs.175551	ESTs	4.2
20	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.60785	SEC22, vesicle trafficking protein (S. c	4.2
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fls, clone C	4.2
	442891	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
25	447439	AA313565	Hs.146020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449885	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	450377	AB033091	Hs.74313	KIAA1285 protein	4.2
	419847	AA348847	Hs.91816	hypothetical protein	4.2
30	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW989657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fls, clone HE	4.1
35	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D28954	Hs.13421	KIAA0056 protein	4.1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
	407198	H91679		gbyyv04s07.s1 Soares fetal liver spleen	4.1
	447762	M73700	Hs.105938	lactoferrin	4.1
40	402855			NM_001839*:Homo sapiens calponin 3, acid	4.1
	443161	AI038316		gbox48c08.x1 Soares fetal liver spleen	4.1
	415827	H17462	Hs.23079	ESTs	4.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418365	AW014345	Hs.161690	ESTs	4.1
45	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AI335191	Hs.280702	ESTs, Weakly similar to 2109260A B cell	4.1
	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239409	KIAA0185 protein	4.1
50	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
55	423698	AA328798	Hs.1098	DKFZp434J1813 protein	4.1
	426534	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236944	hypothetical protein FLJ10652	4.1
	426211	M18667	Hs.1887	progastricsin (pepsinogen C)	4.0
	443273	AI042063	Hs.132156	ESTs	4.0
60	428055	AA420584	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AI457338	Hs.29894	ESTs	4.0
	430519	AF128534	Hs.49210	F-box only protein 4	4.0
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
65	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
	446354	AW449850	Hs.346336	ESTs	4.0
	451468	AW503388	Hs.293663	ESTs, Moderately similar to 138022 hypot	4.0
	409706	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
70	418594	AI732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
	418288	H51299		gbyyv07c06.s1 Soares breast 3Nb13st Homo	4.0
	419885	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
75	425920	AL049977	Hs.162209	claudin 8	4.0
	416858	U03272	Hs.79432	fibrillin 2 (congenital contractural era	4.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW227121	Hs.254881	ESTs	4.0
80	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
	400895			C11002514*gi11280151 pit  E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [Hsa	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fls, clone L	3.9

	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
5	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445796	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	AI767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
10	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0882 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	425083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2G5	3.9
	442320	AI287617	Hs.129636	ESTs	3.9
15	447541	AK000268	Hs.18800	hypothetical protein FLJ20261	3.9
	444636	T96667	Hs.17877	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412676	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
20	437916	BE566249	Hs.20899	hypothetical protein FLJ23142	3.9
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	NA0087		ESTs	3.8
25	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
30	426226	AA769045		gb:aa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
	437816	AI823445	Hs.280698	ESTs	3.8
	444534	AW271628	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
35	443484	AI091458	Hs.134559	ESTs	3.8
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004716	Hs.105940	jerky (mouse) homolog-like	3.8
40	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283531	hypothetical protein DKFZp547G183	3.8
	432278	AL137508	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
45	427636	BE397988	Hs.179962	tumor protein p53-binding protein	3.8
	430968	AW872830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B188 protein	3.8
50	431197	AL036596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R96299	Hs.177602	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
55	435655	AW106863	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
60	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	AI800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
65	448207	AI75490	Hs.170577	ESTs	3.7
	450628	AW382884	Hs.204715	ESTs	3.7
	432506	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
70	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20657 fis, clone KA	3.7
	408312	AF263813	Hs.44198	intracellular membrane-associated calci	3.7
	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.7
	424882	AI379481	Hs.153636	far upstream element (FUSE) binding prot	3.7
75	425898	AA366649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE580821	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
80	425988	BE045897	Hs.274454	ESTs, Weakly similar to I36022 hypotheti	3.7
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7



	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AJ831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	femochelataase (protoporphyrin)	3.7
	445941	AJ267371	Hs.172635	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochond	3.6
10	412533	AA679863	Hs.69606	ESTs	3.6
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721.67	3.6
	442710	AJ015631	Hs.23210	ESTs	3.6
	448212	AI475858		gb:tc87d07.x1 NCL CGAP CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.6
15	453038	AW292415	Hs.20509	HBV pX associated protein-B	3.6
	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoietic	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	3.6
20	406815	AA833930	Hs.288036	IRNA isopentenylpyrophosphate transferase	3.6
	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN IIII	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
25	433887	AW204232	Hs.279522	ESTs	3.6
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
30	435703	AW630133	Hs.83313	GK003 protein	3.6
	445674	BE410347	Hs.13083	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
	415111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	3.6
	432840	AK001403	Hs.279621	hypothetical protein FLJ20530	3.6
35	439726	AW448893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944.1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55858		gbyb35f05.r1 Stratagene fetal spleen (9	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70696	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:cc44f08.s1 NCL CGAP_GCB1 Homo sapiens	3.6
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.5
	419440	AB020889	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
50	419241	AA523939	Hs.165258	ESTs	3.5
	410782	AF228053	Hs.56170	HSKM-B protein	3.5
	413364	NM_000401	Hs.75334	exostoses (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449583	Hs.161393	glutamate-cysteine ligase, catalytic sub	3.5
55	420360	AA330047	Hs.191187	ESTs	3.5
	418862	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014518	Hs.110488	KIAA0980 protein	3.5
60	413950	AA240086	Hs.32783	ESTs	3.5
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A48010 X-fin	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411148	N68715	Hs.289128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410606	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
70	419438	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF088431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
75	432589	AL135725	Hs.131708	ESTs	3.5
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI824707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE438899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AI391470	Hs.158818	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositide 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

	456497	AW967966	Hs.123648	ESTs, Weakly similar to AF108460.1 ubl1n	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
5	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419584	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK64_YEAST HYPOT	3.5
10	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BEG13337	Hs.234896	geminin	3.4
	437187	AL080209	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
15	423645	AI215632	Hs.147487	ESTs	3.4
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate synthase	3.4
	434866	AA657494		gb:nt6604.s1 NCI_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902*:Homo sapiens progesterone induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
20	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheli	3.4
	452721	AJ269629	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*:Plasma membrane calcium	3.4
25	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AJ655882	Hs.197698	ESTs	3.4
	425692	D90041	Hs.155856	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437357	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
30	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AJ732722	Hs.187894	ERGL protein; ERGLC-53-like protein	3.4
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331158		gb:EST35034 Embryo, 6 week, subtracted (	3.4
	439375	AA689528	Hs.344249	steroid dehydrogenase homolog	3.4
35	429084	AJ001443	Hs.185614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	408267	AW380526	Hs.343564	tubulin-specific chaperone e	3.4
	408632	AW085680	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
40	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
45	442910	AJ365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheli	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
	445469	AW288370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.156936	complement component 3a receptor 1	3.4
50	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320828	Hs.97266	protocadherin 18	3.4
	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
55	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA408283	Hs.41167	ESTs	3.4
60	423178	AI033140	Hs.124883	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102570	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapl	3.3
65	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
70	427083	NM_005363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
	436654	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
75	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1461	histidine decarboxylase	3.3
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*:HSPC213.	3.3
80	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443894	N20517	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450682	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143638	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD58 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H66196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (tr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410860	AI061118	Hs.66328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/thr	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AI080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (tr	3.3
	432363	AA534489		gb:nf76g11.s1 NCLCGAP_Co3 Homo sapiens	3.3
	435102	AW889053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288884	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134767		gb:DKFZp547G1050_r1 547 (synonym: hfor1)	3.3
	422017	NM_003877	Hs.110778	STAT induced STAT inhibitor-2	3.3
30	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279908	cydin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200588	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20389	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-prote	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chal	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44655	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	408401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001863	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.76574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein veszelin; hypotheti	3.2
80	452295	BE379836	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214283	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415591	AW963979	Hs.24723	ESTs	3.2
5	433852	AI378329	Hs.126629	ESTs	3.2
	439735	AI636386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.105200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30364	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
15	408784	AW971350	Hs.63386	ESTs	3.2
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	same domain, immunoglobulin domain (Ig),	3.2
	405658			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
20	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
	426991	AK001535		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
25	412530	AA766268	Hs.266273	hypothetical protein FLJ13345	3.2
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AFD30933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08266	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220650	ESTs	3.1
	406827	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419905	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp5648083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137838	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AI052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gb2065a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	HB0696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197098	ESTs	3.1
70	438979	AW976218	Hs.32565	ESTs	3.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
75	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440093	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29689	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412086	A1699496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.B8474	ESTs	3.1
5	400684			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	A1879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc28a07.s1 NCL CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152875	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPC034 protein	3.0
15	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
	445819	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294908	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4290026, mRNA,	3.0
20	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876810	3.0
	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	A1805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431862	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	A1929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA298264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW619403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H08323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428895	A1356647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443667	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128367	ESTs	3.0
	441889	A1090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	A499220	Hs.71573	hypothetical protein FLJ10074	3.0
	419564	AA171850	Hs.42251	ESTs	3.0
50	419544	A1909154		gb:CV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	A1066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330206	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299668	Hs.24183	ESTs	3.0
	448264	A1478933	Hs.184260	ESTs	3.0
	428573	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	heat domain and RLD 3	3.0
60	403030	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	A1791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.0
	447968	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:zr97g10.r1 NCL CGAP_GCB1 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIIE protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	436986	AF086888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	A1932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

80

TABLE 60B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number  
Accession: Genbank accession numbers

	Pkey	CAT Number	Accessions
5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
10	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	414680	147525_1	AA743331 AA837388 AW884540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
15	415989	156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416268	1585983_1	H51299 H44619 H46391 RB6024 H51892 T72744
	416982	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068956 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40835 H05100 R40597
20	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	417379	167238_1	AA196390 AA507837 AA196468
	418304	173658_2	AA215702 AA368006 AA215703 BE068555 BE068576
	418647	177521_1	AA226198 AA226513 AA383773
	418866	179788_1	T65754 AA229857 AA229658
	419536	185688_1	AA803305 AA244095 AA244183
	419544	185780_2	AI909154 AA526337 AA244183 AI909153
	423412	228001_1	AF109300 AI299378 AF202654
25	423800	232161_1	AA331156 AA331157 AA331155
	426226	262918_1	AA769045 AA372590 AW963633
	426413	266850_1	AA377823 AW954494 AI022688
	426503	268283_1	AA380153 AA380233 AW963529
	426775	271683_1	AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
30	426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL363968 AA134266
	428342	290035_2	AI739168 AA426249 AI199536 AW505195 AW977291 AA824583 AA863419 AA724079 AI015524 AI377728 AW293682 AI928140 AW731438 AI092404 AI085630 AA731340
35	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	429220	301384_1	AW207206 AW341473 AA448195 AI951341
	429258	301917_1	AA48765 C04967 C03045 AA658293
	430935	325772_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60837
	430968	326269_1	AW072830 AA527647 AA489620 AA570382
	431429	33313_1	AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA058148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T35956 BE18035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308
40	432093	341283_1	AI187581 AA311680
	432125	341776_1	H28383 AW972670 H28359 AA525808
	432189	342819_1	AW972667 AA526539 AI057032 AW167842
	432340	345248_1	AA527941 AI810608 AI620190 AA635266
45	432363	345469_1	AA534222 AA632632 T81234
	432600	350959_1	AA534489 AW970240 AW970323
	432810	354376_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
50	434579	38916_1	AA863400 AI991439 AW018017 AW014704 AI367512 H17550 AA744752 R46187 AW471324 AI126670 AA828033 AI276287 AI094253 AI286003
	434966	396504_1	AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI539156 AA565542
	435023	398093_1	T65958 T57205 AF147346
	437668	44433_2	AA657494 AI582663 AI581639
55	438147	45074_1	AI692552 AI393343 AI800510 AI377711 F24263 AA681876
	439092	468554_1	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
	439518	47334_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866886 AI572124 AA043777 AA040926 D20160 AI536733
	439904	479942_1	AA812489 AW874142 AI47188
	440840	50357_2	AW250553 L07876 Z36843 R30593 AI190097 AW966317
60	441102	509804_1	AA830149 AW978407 M85983 AW503637
	442562	54500_2	W76328 AF086341 W72300
65	443161	561305_1	AW892676 AA853877 D44747
	445808	65133_1	AW629666 AW969831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038546 AA534486 AI797207
	447082	707248_1	AA921877
	448212	755099_1	AA973905 AI299888 AA917019 H63235 T90771
70	449625	8113_1	BE379584 R34211 BE544788 AW973709 AI653056 AI653173 AI286043 AI686750 H74180 AI492830 AI376080 AI472184 D58940 AW170056
	450580	83929_1	AI082443 AW021142 AI167921 AI348677 AI278577 AW130865 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA554902 D52102 AI0007
75	450582	83933_1	AI088316 AI344831 AI281653
	452280	9074_1	AV655234 AW966332 AA340239
80	452598	92338_2	T85314 AI380684 T85528 T91254
	452815	93255_1	AI475858 AW966013
	453802	981589_1	NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760
	455100	1253334_1	N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45528 T61415 AA331486
			N40087 H12925 AA460779 AA086372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816888 AW816889 AW816940
			AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
			AA164518 AA730973 W00417 W65303
			AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
			AA453208 NM_004421 U44103 AI671547 N57463 AW007621 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
			BE326331 AI934576 AI922378 AW276431 AI718468 N36566 AA904753 BE464245 AI338752 AI659875 AW272338 AI423136 AI089270 AI160804
			AA664354 BE1
			AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AI138076 BE180510 AI926721 AI399955 AA749139
			AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI816834 N25206 AA828301 AI084565 AI020816 AA026905
			AA77255
			AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
			AL134757 AW079131
			BE160198 AW935898 T11520 AW935930 AW856073 AW861034

457728 393853\_1 AW974811 AA651634 AA650072

5 TABLE 60C

10 Pkey: Unique number corresponding to an Eos probeset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham 1. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 NL\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400664	8118495	Plus	13558-13721,13842-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	8834068	Minus	119928-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103610-104090
402031	7856761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59938
403790	8084957	Minus	67826-67947,60835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796610	Minus	32247-32362
404642	9796610	Plus	102959-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6063

35 Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

45 Pkey: Unique Eos probeset identifier number  
 ExAccn: Exempt Accession number, Genbank accession number  
 UnigenelD: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of prostate tumor to normal adult body tissue  
 R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000390	Hs.1395	early growth response 2 (Krox-20) (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*HSPC213.	3.0	12.6
450095	AI682068	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79089	cyclin G2	8.4	8.4
421913	AI934355	Hs.109439	osteoglycin (osteoblast-inductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U68468	Hs.159625	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429584	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
445048	Z45051	Hs.22920	similar to 668401 (cattle) glucose induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4	7.3
425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.286057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1	6.1
437147	AL049964	Hs.8358	hypothetical protein FLJ20366	2.6	6.0

5	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bett1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-1	3.3	5.9
	431548	AI834273	Hs.9711	novel protein	15.7	5.8
10	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72756	Hs.77367	monokine induced by gamma interferon	2.5	5.6
15	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A {	5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
	451684	AF216751	Hs.26813	CDA14	3.9	5.4
20	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 [E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D81594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
25	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA826509	Hs.122329	ESTs	5.1	5.0
	432697	AF155099	Hs.279760	NY-REN-18 antigen	3.3	5.0
	433660	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
30	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
	439024	R96696	Hs.36598	ESTs	5.4	4.8
35	407235	D20569	Hs.168407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA: cDNA DKFZp434P228 (tr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464	Hs.159993	gbit88f04.x1 NCL_CGAP_Pt28 Homo sapiens	9.1	4.7
40	452242	RS0956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			G16000476*gl 12737279 ref XP_012163.1	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.1	4.6
45	406380	AF123050	Hs.44532	ubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AI676062	Hs.111902	ESTs	4.8	4.5
	419455	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
50	431685	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N84742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
55	428826	AL048842	Hs.194019	aktactin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	416701	AA814948	Hs.98343	ESTs, Weakly similar to ALUC_HUMAN IIII	4.2	4.2
	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
60	409151	AA305105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
	443622	AI911627	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
65	421129	BE438899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433867	AW204232	Hs.279522	ESTs	4.1	4.1
70	436556	AI354997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443846	AI085198	Hs.164226	ESTs	4.1	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
75	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW359351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KIX 18)	3.9	3.9
	444765	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
80	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	460203	AF097994	Hs.301528	L-tyrosine/alpha-aminoacipale aminotra	3.9	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422601	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8



	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transpos	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
5	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ121901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	R49390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13575 fis, clone P1	5.4
	125186	AA610520	Hs.181165	major histocompatibility complex, class	5.4
15	131185	BE280074	Hs.23960	cyclin B1	5.4
	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
20	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW296587	Hs.61884	Homo sapiens, clone IMAGE4298026, mRNA,	5.3
	119040	R02394	Hs.269438	ESTs, Moderately similar to PCA259 ferri	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109894	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypothet	5.2
30	120830	AI568170	Hs.96886	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	5.2
	103318	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49183	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
40	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
	110799	AK089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW976998	Hs.58595	ESTs, Weakly similar to I38022 hypothet	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102827	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104448	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	118814	H50834	Hs.77899	gb:yp08a10.s1 Soares fetal liver spleen	5.0
50	130622	AI682291	Hs.16848	ESTs, Weakly similar to O44HUD1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127785	AA871146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.98473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 sarine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	125904	AA948033	Hs.130853	ESTs	4.9
60	134526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356784	Hs.17109	Integral membrane protein 2A	4.8
	125769	AA063456		gb:zn09g06.r1 Stratagene hNT neuron (937	4.8
	128098	H75881		gb:yl77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	hizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0963 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AW806510	Hs.87056	hypothetical protein FLJ21834	4.8
	105846	AW954064	Hs.24851	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129708	AA443241		ribosomal protein L44	4.7
	128598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126529	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9565	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	128521	AI475110	Hs.209933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptida, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

	420297	AI626272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (hls	2.9	2.9
	437812	AS82291	Hs.16846	ESTs, Weakly similar to C4HUD1 debrisou	2.9	2.9
5	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	2.9	2.9
	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451786	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (f	2.9	2.9
	407783	AW996872	Hs.172026	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
15	463628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calcardin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
20	433865	N29862	Hs.44104	ESTs	2.8	2.8
	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654850	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300676	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE522585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
35	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
40	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated atlanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269629	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	448238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014736	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
55	447509	AF107454	Hs.107637	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191080	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31576	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163700	ESTs	6.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [Hs	2.4	2.6
	425815	R94023	Hs.94580	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
70	431474	AL133990	Hs.190642	ESTs	9.3	2.5
	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO08	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656-Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.57594	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA446765		gb:zx10e09.r1 Soares fetal_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
15	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone a	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0885 gene product	2.2	2.4
20	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptoosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:CV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW460461	Hs.203965	ESTs	2.3	2.3
	462387	AI680772	Hs.308094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
	419438	AA406400	Hs.12482	glycerophosphate O-acyltransferase	2.7	2.3
	443184	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43a07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134767		gb:DKFZp547G1080_r1 547 (synonym: hibr1)	4.1	2.3
	421059	AI854133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST190805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AK027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405685			C2002829:gl 4507689 ref NP_003296.1  tra	2.3	2.3
	407917	U63139	Hs.41687	RAD50 [S. cerevisiae] homolog	2.3	2.3
	450378	AW240181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452018	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPUC	2.6	2.2
	431655	AI815470	Hs.260024	Odc42 effector protein 3	4.5	2.2
	440098	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478*:SECRETORANIN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	tol-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 fami	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452984	AW962587	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935952	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF066534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66062	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288456	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9	2.2
5	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
	424036	AA770888		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404541			NM_021965*-Homo sapiens phosphoglucomuta	2.2	2.2
10	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008.gij7303957[gb]AAFS9000.1  (AE00	3.1	2.1
	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	6.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
15	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447633	NM_004780	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
20	448956	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819542	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
	452959	AI933416	Hs.189574	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
25	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
30	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
35	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29843	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AJ077315	Hs.154970	transcription factor CP2	2.6	2.0
45	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XII, alpha 1	3.6	2.0
50	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
	413627	BE182082	Hs.246873	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.69583	mitochondrial intermediate peptidase	14.7	2.0
55	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
	408219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
60	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T36231	Hs.17762	ESTs	2.0	2.0
	443292	AK000213	Hs.9195	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
65	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
	449625	NM_014253		odx (odd Oz/tan-in, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	461369	AA017321	Hs.269691	ESTs	2.1	2.0
70	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408808	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
	433388	AI432672	Hs.258539	hypothetical protein FLJ22191	2.7	2.0
	432653	N52096	Hs.293185	ESTs, Weakly similar to JC7328 amino ac	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
75	437323	AA371145	Hs.194397	leptin receptor	2.6	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
80	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 61B

Pkey: Unique Eos probe/identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150955 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW165606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909164 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59486 AI040666 W60958 W94209 H27231 T84625 H75715 W04957 W63576 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW563548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
15	424036	23460_1	AA770588 H15373 AW161070 BE304523 BE378517 AA969300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268561 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290558 C15404
	426413	286650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA448765 C04957 CD3045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
20	432689	35275_1	AB018320 H55457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AI193203 N5581
	438569	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF066341 W72300
	442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173295 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV666234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AI022718 BE161779 AW863569 BE161640 AI039060 BE168542 AW295554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI489402 T613
	450580	83929_1	NA0087 H12925 AA460779 AA096372 BE180847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816869 AW816940 AW816892 AW816891 AW816878 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35

Pkey: Unique number corresponding to an Eos probe/

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt position: Indicates nucleotide positions of predicted exons.

40

Pkey	Ref	Strand	Nt_position
401197	9719706	Plus	175341-176452
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402802	3287166	Minus	53242-53432
403047	3540153	Minus	59793-59958
404641	9796810	Minus	32247-32362
405685	4508129	Minus	37956-38097
406068	9114084	Plus	382-543

45

50

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95<sup>th</sup> percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60	Pkey:	Unique Eos probe/identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
65	R1:	Ratio of prostate tumor to normal prostate tissue			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_006211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	16.8
75	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
	416188	BE157280	Hs.79070	v-myo avian myelocytomatosis viral oncog	13.6
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activat	13.1
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	12.6
80	401197			ENSP00000229263-HSPC213.	12.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
	449156	AF103907	Hs.171363	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE568568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419563	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	silt (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
10	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
15	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
	425174	D87450	Hs.154978	KIAA0261 protein	8.6
20	445701	AF055681	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protel	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoblastic factor, mime	8.4
	434217	AW014795	Hs.23349	ESTs	8.3
25	417363	AW129357	Hs.328700	ESTs	8.3
	425782	U86468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI954625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
35	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049510	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05669	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	451900	AB023199	Hs.27207	KIAA0882 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-link	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154186	E4F transcription factor 1	7.2
	447737	AK000543	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3518	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426769	AI580401	Hs.21213	ESTs	6.8
	416292	AA178233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AI786320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA822037	Hs.165468	programmed cell death 5	6.6
65	429490	AI971131	Hs.23689	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415762	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.196641	ESTs, Moderately similar to I38022 hypot	6.3
	408799	D11828	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	mitochondria maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AJ745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120859	Hs.6111	aryl-hydrocarbon receptor nuclear transi	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447985	AW292577	Hs.94446	ESTs	5.9

5	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	5.9
	431548	A1834273	Hs.9711	novel protein	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
10	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
	435080	A1831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
15	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157845	Hs.48783	sialyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA050597	Hs.85050	phospholamban	5.7
20	445467	A1239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
	408672	M26041	Hs.198253	major histocompatibility complex, class	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	5.6
25	453642	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90865	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
	414516	A1307802	Hs.135660	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
30	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fls, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
	458079	A1798870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
35	418758	AW859311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449807	AA004825	Hs.103281	ESTs	5.4
	419159	AW874945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
40	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	AU086991	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
	403851			C5002154*.gij7289016[gb]AA54217.1 (AEO	5.3
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fls, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
45	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.163023	ESTs	5.2
50	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61584	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fls, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
55	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6265	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
	414212	AA136589	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
60	417318	AW953837	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
	434170	AA826509	Hs.122329	ESTs	5.0
	424090	X99698	Hs.139262	XIAP associated factor-1	5.0
65	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GLQ4 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
	432897	AF155089	Hs.279780	NY-REN-18 antigen	5.0
	433560	A1925195	Hs.130891	hypothetical protein MGC4400	5.0
70	410762	AF228053	Hs.86170	HSKM-B protein	5.0
	421823	N40850	Hs.28626	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
75	453370	A1705523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10814	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
	452323	W44358	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
80	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
	445800	AA128419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.168407	SAC2 (suppressor of actin mutations 2, y	4.8
	430835	AW072916		zinc finger protein 131 (clone pIZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	4.7
	421863	A952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE568249	Hs.20899	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AJ807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	A1692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	A1685464		gb:U8804.x1 NCL_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C150004767.gij 12737279[ref XP_012163.1	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	O80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425807	AA365752	Hs.155966	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	A1676082	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 (is, clone L	4.5
	408705	AA512135	Hs.46967	HSPCO34 protein	4.5
30	429250	H56586	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW801325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp586M063 (fr	4.5
	456874	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443966	Hs.31595	ESTs	4.4
40	443250	A1041630	Hs.132107	ESTs	4.4
	411952	AA099050		gb:zk85d12.r1 Soares_pregnan_Uterus_NbH	4.4
	423645	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA328796	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
45	430259	BE560182	Hs.127826	RaKGEF-like protein 3, mouse homolog	4.4
	453787	AB011792	Hs.36094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170066	Homo sapiens cDNA FLJ13492 (is, clone PL	4.4
	436446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014403	Hs.128727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428626	AL046842	Hs.194019	atractin	4.3
	444212	AW503976	Hs.10849	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW087805	Hs.172665	methyltetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 (is, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408086	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	4.2
	406654	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814848	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN IIII	4.2
70	419083	AM79560	Hs.98613	Homo sapiens cDNA FLJ12292 (is, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b57	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA305105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430868	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	A1421645	Hs.139851	caveolin 2	4.2
	414291	A1289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA877577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	A1500642	Hs.289067	Homo sapiens cDNA FLJ11404 (is, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443522	A1911527	Hs.11805	ESTs	4.1



	436576	AM58213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430363	AI851854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567669	Hs.40342	putative nuclear protein	4.1
	448468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
15	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmh	4.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.236039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.278522	ESTs	4.1
20	436566	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.25146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223295	ESTs, Weakly similar to I38022 hypotheti	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 2453B mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA688282	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H87220	Hs.169881	death effector domain-containing	4.0
	438905	AW997484	Hs.5003	KIAA0458 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40587	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	406934			Target Exon	3.9
50	438231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444765	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9
	447276	AL048785	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abi subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine:alpha-aminoacidipate aminotra	3.9
60	450699	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axl)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0885 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	416156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422976	AA347720	Hs.122569	KIAA0264 protein	3.8
	403100			C2001027*gi 7296271 gb AAFS1562.1  (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382623	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432363	AA534489		gbcn776g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.02195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432906	AI861895	Hs.304506	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmab33 protein, 3'	3.7
	446554	AA151730	Hs.301769	nucleoside diphosphate linked moi	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59789	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087593	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-like	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439606	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443057	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452551	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.885	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350g1[6578126]b[AAF17706.1]AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030680	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoiet	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426831	NM_003416	Hs.2078	zinc finger protein 7 (KIX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	418594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446416	AV658289	Hs.163959	ESTs	3.5
	449008	AW678003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453555	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450065	H58499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gbcy912c04.r1 Soares infant brain 1NIB H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440843	M78878	Hs.7314	KIAA0614 protein	3.5
70	409065	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb:yy59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
	401744			Target Exon	3.4
75	432723	D29577	Hs.3085	KIAA0054 gene product, Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450528	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

5	432741	AI732358	Hs.185118	ESTs, Moderately similar to A37413 calbl	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
	428486	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
10	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AI046851	Hs.153053	CD37 antigen	3.4
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	426900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
15	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
	431689	AA306688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
20	403389			C3001393*gi3327090 dbj BAA31613.1  (AB	3.3
	440749	W22336	Hs.7392	hypothetical protein MGC3198	3.3
	408374	AW026430	Hs.155591	forkhead box F1	3.3
	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidyl/prolyl isomerase F (cyclophilin	3.3
25	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
	417295	AW893524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
30	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW855696	Hs.90960	ESTs	3.3
35	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	415700	AI963908	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
40	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.8631	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295769	Homo sapiens mRNA; cDNA DKFp564D1164 (f	3.3
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
45	430280	AA361258	Hs.237868	Interleukin 7 receptor	3.3
	408968	AI852236	Hs.49376	hypothetical protein FLJ20644	3.3
	463648	AL079983	Hs.116774	Integrin, alpha 1	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
50	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400668			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CD22-related protein kinase 7	3.2
	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFp434G0522	3.2
55	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
60	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	408973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
65	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
70	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
	417386	AL037228	Hs.82043	D123 gene product	3.2
	427288	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
75	442355	AA466539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
80	449944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	HB3520	Hs.153678	reproduction 8	3.2
	416959	D28459	Hs.80512	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	Immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QVO-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CCG14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0260 protein	3.1
15	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177664	KIAA0814 gene product	3.1
	434804	AA649530	Hs.348148	gb:ms44R05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
20	445840	AI277811	Hs.146291	ESTs	3.1
	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
25	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
30	403423			Target Exon	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
35	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
	422481	AL050163	Hs.117339	DNA-X-activation protein 10	3.1
	430467	D87742	Hs.241552	KIAA0268 protein	3.1
40	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2651	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fls, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fls, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293486	Hs.20680	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AF188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE618160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003860	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X83692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R06064		gb:ye85g07.r1 Soares fetal liver spleen	3.0
80	445921	AW016211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochondrion	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Play:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Play	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA090950 AA090956 T47733
414279	143227_1	AW021691 AI537404 R45431 AI333439 AI741845 AI874468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA818148
		AI983837 AA399623 AI676204 AI420077 N24944 D51042 AA282766 AA137264 AW238107 AW769
		AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA866905 AI141054 AW194991 AA252147 AA319500 AI184288
		AA708749 AA644620 AA652769 AA242975 AA151074 T19880
		R17235 R52580 F11642
415528	1539409_1	AA173632 AI174958 AA581361 AI700024 AA173988 BE165417 AI366964
416128	157163_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
416882	162718_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
		N59027 AA314694 N53937 R08100
		R06054 AA378789 AW956453
		AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
		BE167283 BE157287 AA502438
		AI685464 AW971336 AA513587 AA525142
		AW972667 AA526539 AI057032 AW167842
		AA534489 AW970240 AW970323
		AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
		AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
		AA156781 AW233639 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
		AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
		AW979177 AA846994 AA829672
		W76328 AF086341 W72300
		NM_004480 U09278 U76833 AW630065 AW471133 C02434 W45237 AW793518 BE070112 AI587478 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680295
		N40087 H12925 AA480779 AA096372 BE160847 AW816890 AW816893 AW816877 AW816891 AW816882 AW816868 AW816869 AW816840
		AW816892 AW816841 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AI571547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718465 N36586 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839048 AW903372 AW846755 AW846767 AW803368 AW846766 BE146826 AW839055 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984785 AW984793
		AW984789 AW984823 AW984802 AW984802 AW984800 AW984799 AW984825 AW984782 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632555 AW004030 BE502530 Z25032 AA805324 AA49241 AI651825 AI264883
		AW196918 AA948267 AI853735 AI263703 AA319159 AW964436 AI803440 AW594171 AI867447 AW2

TABLE 62C

Play:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Play	Ref	Strand	Nt_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8118067	Plus	198991-199188, 199316-199548
401197	9719706	Plus	178341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-68031
401744	2576349	Plus	14595-14751
401807	7331538	Plus	152325-152912
402474	7547175	Minus	53528-53628, 55765-55920, 57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671, 86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	68340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39524-40072
405141	8980911	Plus	99851-100054
405934	6758795	Plus	159913-160605
406038	8388537	Plus	37764-37877
406247	7417725	Minus	46234-46461

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75<sup>th</sup> percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75<sup>th</sup> percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of normal prostate tissue to prostate tumor tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M91650	Hs.1968	semonogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X63957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73960	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
416337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	A1738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	A1791314		gb:aa46g12.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	A1459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
406001	U58196		Interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404806			Target Exon	5.6
432326	A1280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434362	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11009336.g 3746443 gb AAC63969.1  (AFO	4.8
416935	AA190712		gb:zp87709.r1 Stratagene HeLa cell s3 B3	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440865	A1523846	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1N18 H	4.6
441040	AW449782	Hs.178903	ESTs	4.6
442764	A1762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
465895	A1536663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	A1801500	Hs.128457	ESTs	4.4
436781	A1914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004346*:Homo sapiens runt-related tra	4.3
442931	A1024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
438404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
456840	A1590296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331806		gb:EST35805 Embryo, 8 week I Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AJ216950	Hs.125461	hypothetical protein FLJ11539	4.1
5	425094	AJ955956	Hs.21417	ESTs	4.1
	415926	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AK028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24186		hypothetical protein	4.0
15	449233	BE048401	Hs.196511	ESTs	3.9
	435457	AA662421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-a05 LT0032 Homo	3.8
20	409679	BE250521		ras homolog gene family, member A	3.8
	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL035568	Hs.291	glutamyl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:np86b01.s1 NCL_CGAP_Thy1 Homo sapiens	3.8
	406917	X85964		gb:H.sapiens nestin gene.	3.8
25	455887	BE154173		gb:PM1-HT0340-201259-004-f12 HT0340 Homo	3.8
	443313	AI796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:z85d01.r1 Soares_fetal_heart_NbH119W	3.8
	400489			C10001858:gil[6679124]ref[NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
30	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
	427318	AF186081	Hs.175783	zinc transporter	3.7
	417820	R02530	Hs.191198	ESTs	3.7
	404660			C800841*:gil[12654691]gb[AAH01185.1]AAH0	3.7
35	409144	AW341187	Hs.279714	ESTs	3.7
	438524	AA922236	Hs.221037	ESTs	3.7
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418633	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
40	454649	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
	426736	AA431615	Hs.130722	ESTs	3.7
	434562	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
45	442097	AW015789	Hs.128474	ESTs	3.6
	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.285212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
50	400749			NM_003105*:Homo sapiens sortilin-related	3.6
	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:z85308.r1 NCL_CGAP_GCB1 Homo sapiens	3.5
55	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
	428043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AI371978	Hs.128326	ESTs	3.4
60	445045	AI652676	Hs.147256	ESTs	3.4
	408177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000262164*:KIAA1578 protein (Fragm	3.4
65	445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
	444286	AI625304	Hs.190312	ESTs	3.4
	442027	AI652928	Hs.126395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
70	402460			C1001261*:gil[2696979]emb[CAA70854.1] (Y0	3.4
	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
75	417959	AW977642	Hs.291742	ESTs	3.3
	418672	L44284	Hs.12915	ESTs	3.3
	446593	W79572	Hs.13277	hypothetical protein FLJ22064	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
80	410140	AL134435	Hs.247837	neurexin 3	3.3
	458539	AI733837	Hs.145661	ESTs	3.3
	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

5	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10964	3.2
10	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
	418092	R46154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
15	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	ttn-cap (telitronin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
	451686	AA059246	Hs.410293	ESTs	3.1
20	423637	AW937053	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
25	418087	AA961813	Hs.127838	ESTs	3.1
	421813	BE048255		gb:z49b05.y1 NCL_CGAP_Brn52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW283237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.186767	ESTs	3.1
30	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	ABD40919	Hs.210958	KIAA1486 protein	3.1
	421894	AJ418464	Hs.190836	ESTs	3.1
35	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658*HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
40	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AJ308855	Hs.301497	arginyltransferase 1	3.0
45	444576	AI400974	Hs.182045	ESTs	3.0
	430681	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459547	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
50	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_UI4 Homo sapiens	3.0
	456103	Z38430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI638539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NaHMPu_S1 Homo sapi	3.0
55	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-180400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
60	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp761071 (fr	2.9
	453126	AA032155	Hs.61822	ESTs	2.9
	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
65	442252	AI733395	Hs.129124	ESTs	2.9
	418254	AI469463	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ98362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	2.9
70	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
75	442640	AI205646	Hs.147220	ESTs	2.9
	436814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
	422482	AI439905	Hs.344476	gb:tl57g08.x1 NCL_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:z199b10.s1 Soares_testis_NHT Homo sap	2.8
80	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AJ023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.45039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALLU6_HUMAN A	2.8
	461632	BE005934	Hs.310625	EST	2.8



	426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656			Target Exon	2.8
	407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	Hs.117341	ESTs	2.8
	433585	AA599763	Hs.112520	ESTs	2.8
	451004	AA044967		gb:z53d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770			NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	Hs.189788	ESTs	2.8
	454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060	Hs.34382	ESTs	2.8
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	Hs.208919	ESTs	2.7
15	406337			C14000021:gil7242973[jbj]BAA92547.1  (AB	2.7
	401884			Target Exon	2.7
	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442864	Hs.201201	ESTs	2.7
	450044	R66444	Hs.51891	ESTs	2.7
20	403630			C3001708*:gil4758028[re]NP_004360.1  co	2.7
	445514	AI241280	Hs.148906	ESTs	2.7
	446362	AW612481	Hs.104105	ESTs	2.7
	432492	AW275110	Hs.271106	ESTs	2.7
	430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330	Hs.118796	annexin A6	2.7
	413155	BE067852		gb:CM0-BT0366-061299-122-g09 BT0366 Homo	2.7
	433329	AF015041	Hs.199291	nimb (Drosophila) homolog-like	2.7
	446523	NM_003063	Hs.334629	sarcosin	2.7
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hbr1)	2.7
	405678			CX001454:gil8393794[re]NP_058681.1  myo	2.7
	432789	D26361	Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	Hs.284284	zinc finger 1111	2.7
	415984	R19046	Hs.5010	gb:yg21111.r1 Soares infant brain 1N1B H	2.7
	402844			C1000118*:gil3951913[re]NP_052832.1  pr	2.7
	458666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	Hs.244621	ribosomal protein S14	2.7
40	404979			Target Exon	2.7
	412318	AW936911	Hs.326729	hypothetical protein MGC11082	2.7
	424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516	Hs.95097	ESTs	2.7
	441975	AW173248	Hs.344285	EST	2.7
45	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457851	AW450205	Hs.305890	BCL2-like 1	2.7
	439204	AF087987	Hs.42695	EST	2.7
	415642	U19878	Hs.338224	transmembrane protein with EGF-like and	2.7
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
50	443359	AI792583	Hs.135354	ESTs	2.7
	447336	AW139383	Hs.245437	ESTs	2.7
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
	436030	R02287	Hs.121052	ESTs	2.7
55	449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	438092	AI345985	Hs.127383	ESTs	2.6
	415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	Hs.293886	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	Hs.256879	ESTs	2.6
60	410483	BE163557		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083		weef1 (S. pombe) homolog	2.6
	426629	AI203933	Hs.97142	ESTs	2.6
	415831	H15145	Hs.30609	ESTs	2.6
	412281	AI810054	Hs.14119	ESTs	2.6
65	434898	AW500458	Hs.28956	KIAA0460 protein	2.6
	422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061		gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AI215687	Hs.175044	ESTs	2.6
	438648	AA813125	Hs.146335	ESTs	2.6
70	450399	AW511049	Hs.202007	ESTs	2.6
	420833	R47948	Hs.188732	ESTs	2.6
	453903	AW298606	Hs.232777	ESTs	2.6
	443650	AI698330	Hs.151444	ESTs	2.6
	427419	NM_000200	Hs.177888	histatin 3	2.6
75	423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	Hs.40730	ESTs	2.6
	441358	AW173212	Hs.129041	ESTs	2.6
	402706			Target Exon	2.6
	436054	AI076282	Hs.119813	ESTs	2.6
80	402749			Target Exon	2.6
	442472	AW806859		gb:MRO-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872		gb:oo57d07.s1 NCL_CGAP_Lu5 Homo sapiens	2.6
	405564			Target Exon	2.6

	408003		Target Exon	2.6	
	459584	A1910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.6
	445050	AAB30811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902.gi403440[gb]AAA73168.1  (MB17	2.6
	416628	W03955		gb:z62d04.r1 Soares fetal liver splean	2.6
	443864	N37059	Hs.38250	ESTs, Weakly similar to I38022 hypothe	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA226522		gb:nc25c06.r1 NCL_CGAP_Pr1 Homo sapiens	2.6
15	451256	AA020857	Hs.90744	ESTs	2.6
	456737	BE072246		gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	A1220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb:cn67b05.x1 NCL_CGAP_CML1 Homo sapiens	2.6
	446874	BE326671	Hs.170058	ESTs	2.6
20	441053	AA913819	Hs.188025	ESTs	2.6
	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	A1125263	Hs.170410	ESTs	2.5
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase klna	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW866599		gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AW693930	Hs.148816	ESTs	2.5
	413489	BE144228		gb:MRO-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	Hs.6658	ESTs	2.5
	419354	M52839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	2.5
	414623	AU076633	Hs.76353	serine (or cysteine) proteinase inhibitor	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb:EST388963 IMAGE resequences, MAGO Homo	2.5
	456401	W28146		gb:43111 Human retina cDNA randomly prim	2.5
45	404878			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	2.5
	429908	AL080137	Hs.193743	ESTs	2.5
50	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
	438353	BE538951	Hs.306995	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408229	1048482_1	AW176091 H24234
	408432	1056567_1	AW195262 R27868 AW811252
	409579	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 A1221491 AA194239 D63046 AA193426 AA773243 AA193293
65	410483	1204995_1	BE163567 BE073688 BE073747 BE073780 BE073739 BE073748 BE163495 AW760178 BE163491 BE073763 BE073671
	411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411356	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845993 AW845989
70	411829	1260308_1	AW865749 BE179419 BE179492
	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067953 BE067956 BE067946
	413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
75	415054	151827_1	A1733807 AA159708 A1732614
	415098	1522174_1	D59657 D59694 D59656 D59589
	415131	1523680_1	D81119 D81508 D81734
	415366	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35694 H12035 R53312
80	416628	1604848_1	W03955 H82332 H69247 H72486
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236857 AA237066 AA354236 AW957759 H08961
	419896	1888662_1	Z99362 Z99363
	420778	195389_1	AW970512 AA280251 A1652287 BE466438 A1650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 HB7796
	423772	23188_1	AA306637 NM_007241 AF156102 BE386339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW458227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009699
			C02215 AI6625
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421766 AA458078 AI290275 AA455679
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
15	436190	41555_1	AK001069 AA633055
	436535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
20	447518	724787_1	T80061 AI382804
	447600	728288_1	AI420990 AI399725 AI401757
	448516	756241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI526093
	449923	81926_1	BE256051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
25	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW748432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866811 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072256 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	455887	1380835_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844549_2	W28146 W28187

TABLE 63C

45	Key:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
50	Key	Ref	Strand	NL_position
	400461	9929654	Plus	32727-32846,32929-33051
	400489	9798071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	779797	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	69182-90053
	401898	8568194	Plus	115129-115294
	401917	9502466	Plus	25064-25229
	402422	9796344	Minus	32843-33008
65	402480	9796884	Minus	108901-109254,110246-110581,113613-113960
	402490	9797848	Plus	149982-150929
	402706	8854426	Minus	148540-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-16930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8489060	Minus	94723-94859
	403630	8568999	Minus	13909-14486,15251-15760,16898-17431,41742-42440
75	403649	8705159	Minus	27141-27247
	404250	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212935	Minus	22310-23269
	404660	9797068	Plus	168215-168916
80	404678	9797204	Plus	115196-115448
	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9829758	Plus	128475-128773

5	405152	9965561	Minus	137662-137969
	405258	7329310	Plus	129930-130076
	405422	7243869	Minus	101938-102079, 102261-102443, 102896-103202
	405564	2114222	Minus	16766-17344
	406678	4079670	Plus	151821-152027
	405736	9931101	Minus	29854-29976
	405770	2735037	Plus	61057-62075
	406003	8247800	Plus	42079-42516
10	406085	9123888	Plus	18665-18843
	406177	7279760	Minus	18930-19148
	406337	9213455	Plus	90117-90337
	406398	9256276	Minus	118691-118959
	406600	8248616	Minus	36296-36610

15

Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85<sup>th</sup> percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

25	Pkey:	Unique Eos probeset identifier number		
	ExAccon:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of BPH tissue to normal adult body tissue		
30	Pkey	ExAccon	Unigene ID	Unigene Title
	420154	AI093155	Hs.95420	JM27 protein
	425747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen
	419526	AI821895	Hs.193481	ESTs
	432441	AW292426	Hs.163484	ESTs
35	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti
	407202	N58172	Hs.109370	ESTs
	432101	AI918950	Hs.123642	EphA3
	400289	X07730	Hs.171995	kallikrein 3, (prostate specific antigen
	425075	AA506324	Hs.1852	acid phosphatase, prostate
40	414569	AF109298	Hs.118258	prostate cancer associated protein 1
	410929	H47233	Hs.30643	ESTs
	400287	S39329	Hs.181350	kallikrein 2, prostatic
	445057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr
45	415889	AI267700		ESTs
	428336	AA503115	Hs.183752	microseminoprotein, beta-
	450693	AW450461	Hs.203965	ESTs
	400286	AA032279	Hs.61635	six transmembrane epithelial antigen of
	407168	R45175	Hs.117183	ESTs
50	408369	R38438	Hs.182575	solute carrier family 15 (H7??) transport
	454119	BE549773	Hs.40610	uncoupling protein 4
	428819	AL136623	Hs.193914	KIAA0575 gene product
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278
55	416432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti
	433444	AW975324	Hs.128816	ESTs
	432240	AK694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL
	428342	AI739188		Homo sapiens cDNA FLJ13458 fis, clone PL
60	401424			NM_001172:Homo sapiens arginase, type II
	432435	BE218886	Hs.282070	ESTs
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1
65	407275	AI364186		gbxw34h07.x1 NCLCGAP_U4 Homo sapiens
	452340	NM_002202	Hs.506	ISL1 transcription factor, LIM/homeodoma
	432473	AI202703	Hs.152414	ESTs
	410330	AW023630	Hs.159425	ESTs
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH
70	452782	AB037785	Hs.30652	KIAA1344 protein
	418848	AI820861	Hs.193465	ESTs
	400292	AA250737	Hs.72472	BMP-R1B
	433647	AA033367	Hs.222294	ESTs
	453160	AI263307	Hs.239884	H2B histone family, member L
75	409262	AK000631	Hs.52256	hypothetical protein FLJ20624
	431474	AL133890	Hs.190642	CEGP1 protein
	429220	AW207208		ESTs
	428134	AA421773	Hs.161008	ESTs
80	408622	AA056080	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA
	456497	AW987956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu
	434792	AA648263	Hs.132458	ESTs
	433466	AA508353	Hs.105314	relaxin 1 (H1)
	439176	AI445444	Hs.190394	ESTs, Weakly similar to B28098 linc-1 pr
	428398	AI249368	Hs.98558	ESTs

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
5	429918	AW873986	Hs.119383	ESTs	9.1
	440260	AI972867	Hs.7130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450542	R39773	Hs.7130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.56989	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
20	446336	AW815036	Hs.151251	ESTs	8.4
	419743	AW408782	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417189	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA787382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.146825	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441890	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
	431446	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739: Homo sapiens E3 ubiquitin lig	7.3
	408557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:501117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.165689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fls, clone C	7.1
	449300	AI668959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288482	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	TS2285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799809	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 8	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
	415785	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA158790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-411 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fls, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA364940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCL_GGAP_Pr3 Homo sapiens	6.3
	436375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403657			Target Exon	6.1
	424846	AI077324	Hs.1832	neuropeptide Y	6.1
	439589	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCLE_HUMAN NUCLE	6.0
	415621	AI048602	Hs.55468	ESTs	6.0

5	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N98928		gb:za32:c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
	404003			Target Exon	5.9
10	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AJ359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
	438138	R98299	Hs.177502	ESTs	5.9
	440129	AA865818	Hs.174836	ESTs, Weakly similar to S71886 Ste20-lik	5.8
15	434973	AW449285	Hs.313636	EST	5.8
	406627	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606518, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
	434465	AJ623511	Hs.118567	ESTs	5.8
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
20	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
25	420848	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155684	Hs.191060	ESTs	5.6
	404571			NM_015802*:Homo sapiens progesteron induce	5.6
	424880	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
30	435092	AA830149		gb:acc4408.s1 NCL_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
	417511	AL049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	5.6
35	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
	432882	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
40	454171	AW854832		gb:QV2-CT0261-201099-011-005 CT0261 Homo	5.5
	426681	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF086937	Hs.38348	ESTs	5.5
	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
45	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp565J1922 (f	5.4
	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
50	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope (H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
	441111	AI806667	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
55	450244	AA007534	Hs.125052	ESTs	5.3
	400294	N95798	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
60	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	448715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I35022 hypothet	5.3
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	423101	M83941	Hs.123842	EphA3	5.3
65	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82085	Interleukin 6 signal transducer (gp130,	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:LL3-CT0214-150300-085-H06 CT0214 Homo	5.2
70	441054	AA913591	Hs.126480	ESTs	5.2
	408386	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437762	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	448072	AI458306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:mp12d11.s1 NCL_CGAP_Py3 Homo sapiens	5.2
75	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	438338	W92147	Hs.118394	ESTs	5.2
80	445238	AA863971	Hs.187506	ESTs	5.1
	450362	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

5	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
	418564	AA631143	Hs.278595	Homo sapiens prostein mRNA, complete cds	5.0
	407198	H91679		gb:Y0407.s1 Soares fetal liver spleen	5.0
10	403696			C4001100*cg 5852342 gb AAD54015.1  (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CLIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
15	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
20	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	436937	AA830893	Hs.119769	ESTs	4.8
	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
25	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29682		ESTs	4.8
	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
30	453843	D25215	Hs.35804	lect domain and RLD 3	4.8
	430172	AA488591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.106448	ESTs, Weakly similar to B34087 hypotheti	4.7
	452843	AI796769	Hs.208320	ESTs	4.7
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
35	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AI792628	Hs.133273	ESTs	4.6
40	409731	AA125085	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
	415788	AW628686	Hs.78861	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sestrin)	4.6
45	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	447805	AW627832	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
50	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AI655499	Hs.161712	ESTs	4.5
55	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
60	420133	AA428117	Hs.165543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 87	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
65	445372	N36417	Hs.144928	ESTs	4.5
	452056	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
	418019	R69911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
70	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412843	AW971239	Hs.138433	ESTs	4.4
	417412	X16986	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
75	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647808	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.139055	ESTs	4.4
80	435656	AW106653	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376*-PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST80805 Synovial sarcoma Homo sapien	4.3
	430535	AW968486		gb:EST380561 MAGE resequences, MAGE Homo	4.3

5	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW988065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41295	fibronectin leucine rich transmembrane p	4.3
10	420111	AA255652		gb:zs21h11.r1 NC1_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001654:gl 12688061 dbj BAB21849.1  (AB	4.3
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
15	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
	420905	AA521307	Hs.186651	ESTs	4.2
20	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
	450597	AJ701835	Hs.207077	ESTs	4.2
25	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	ABD40907	Hs.278436	KIAA1474 protein	4.2
	413525	9E145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
30	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
	458912	AI911066		ESTs	4.2
35	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
40	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AI350199	Hs.268890	ESTs	4.1
45	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.299116	ESTs	4.1
	448907	AA004825	Hs.103281	ESTs	4.1
	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
50	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL038402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58KD)	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
55	446416	AV658299	Hs.163959	ESTs	4.1
	451840	AA195601	Hs.25771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
	442338	AI781976	Hs.158080	ESTs	4.0
60	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415881	Z43123	Hs.144513	ESTs	4.0
	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
65	432229	AW290976	Hs.143687	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419063	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fls, clone MA	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
70	448131	AI575054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partial	4.0
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF167116	Hs.22350	hypothetical protein LOC56757	4.0
75	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346336	ESTs	4.0
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
80	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9



	416288	Hs1299	gbhyp07c06.s1 Soares breast 3N6H8st Homo	3.9
	420301	AA767525	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	ESTs	3.9
5	435878	R08330	ESTs	3.9
	446862	AV660697	ESTs	3.9
	447530	AW192063	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Homo sapiens, clone IMAGE:4298025, mRNA,	3.9
	401403		Target Exon	3.9
10	448779	BE042877	ESTs	3.9
	420533	AJ809510	ESTs	3.9
	411084	T18987	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020595	KIAA0888 protein	3.9
	423453	AW450737	CGI-09 protein	3.9
15	434833	AF156548	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420	gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AW848047	gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	Hs.190325	3.9
	421129	BE438899	ESTs	3.9
20	424332	AA338919	ESTs	3.9
	441766	R53790	hypothetical protein FLJ14393	3.9
	447033	AI357412	ESTs	3.9
	439306	BE220199	WD40 protein Clao1	3.8
	410352	AW969725	KIAA0373 gene product	3.8
25	407861	AW672939	origin recognition complex, subunit 2 (y	3.8
	410262	AW821182	microfibrillar-associated protein 1	3.8
	439560	BE565647	hypothetical protein FLJ12820	3.8
	440450	AJ333129	ESTs	3.8
	458611	AJ268407	DC-specific transmembrane protein	3.8
30	419589	AW973708	Homo sapiens cDNA FLJ13446 fls, clone PL	3.8
	431576	M75655	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE517907	ESTs	3.8
	438379	N23018	C-terminal binding protein 2	3.8
	416009	Z43062	gb:HSC12E041 normalized infant brain cDN	3.8
35	416534	H69043	Homo sapiens cDNA FLJ14366 fls, clone HE	3.8
	423044	AA320829	protocadherin 18	3.8
	424701	NM_005923	mitogen-activated protein kinase kinase	3.8
	433507	AJ817336	ESTs	3.8
	437718	AJ927288	ESTs	3.8
40	418831	AW448930	ESTs	3.8
	424830	AW270580	ESTs, Weakly similar to putative p150 (H	3.8
	426981	AL044675	KIAA0530 protein	3.8
	431447	AA505138	ESTs	3.8
	435932	W03928	ESTs	3.8
45	442447	AA999723	ESTs	3.8
	403242		Target Exon	3.8
	433908	AW298141	ESTs	3.8
	452323	W44356	ESTs, Weakly similar to T33468 hypotheti	3.7
	412095	AJ624707	Homo sapiens cDNA: FLJ21592 fls, clone C	3.7
50	418759	AA227879	ESTs	3.7
	422299	AK000181	hypothetical protein FLJ20174	3.7
	452452	BE173515	gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	423096	AA732684	progesterone induced protein	3.7
	454037	AW998716	gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420584	ESTs	3.7
	447785	AL041765	ESTs	3.7
	451746	M86178	ESTs	3.7
	453293	AA382267	ESTs	3.7
	436671	AW137159	ESTs	3.7
60	407437	AF220264	gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963697	KIAA1435 protein	3.7
	420092	AA814043	ESTs	3.7
	446947	AF148747	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384728	hypothetical protein FLJ23316	3.7
65	419875	AA853410	proenkephalin	3.7
	431231	AA853552	ESTs	3.7
	418348	AI537187	hypothetical protein FLJ23560	3.7
	419261	X07876	wingless-type MMTV integration site fami	3.7
	422899	D16471	Human mRNA, 3' terminal portion	3.7
70	429163	AA884766	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	ESTs	3.7
	440947	AA910403	ESTs	3.7
	404581		trichorhinopharyngeal syndrome 1 gene (T	3.6
	430096	U91935	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	uncharacterized hypothalamus protein HCD	3.6
	444794	AJ419991	ESTs	3.6
	426991	AK001535	Homo sapiens cDNA FLJ10674 fls, clone NT	3.6
	431316	AA502663	ESTs	3.6
	414178	AW957372	ESTs, Weakly similar to I38022 hypotheti	3.6
80	450630	AA010429	ESTs	3.6
	411057	AJ881006	ESTs	3.6
	436326	BE085236	aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	six transmembrane epithelial antigen of	3.6
	423590	AW952412	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29860	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.165335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
10	425465	L18964	Hs.1904	protein kinase C, $\iota$ ola	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517*:gij4758712[ref]NP_004659.1[ a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
15	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
	427304	AA761526	Hs.163853	ESTs	3.5
20	434763	AA648618		gbms07a11.1 NCLCGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
25	438880	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA684192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9883	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.180555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
40	432806	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.205768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
50	449517	AW500106	Hs.23543	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	418964	AA811857	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19528	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
65	436703	AW860814	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
70	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV853771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
75	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
80	434520	AA206273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
5	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AI215632	Hs.147487	ESTs	3.3
	429227	AI951456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
10	418719	AW975580	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f05 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
15	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	426657	NM_015965	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	438962	AW377314	Hs.5364	DKFZP584052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fs, clone PL	3.3
20	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA068767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
25	407385	AA610160	Hs.272072	ESTs, Weakly similar to t38022 hypotheti	3.2
	423595	R82825	Hs.220702	ESTs	3.2
	407021	U62077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	450687	AA495800		gb:zw05b07.s1 Soares_NhlHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
35	408480	AI360337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338:g[7459502]pir[574665] outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
40	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049510	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X01895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
45	432625	AI243596	Hs.94930	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437886	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.66731	homeo box B13	3.2
	436899	AF085833	Hs.135624	ESTs	3.2
	415862	RS1034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R80891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	410088	AI538323	Hs.52620	Integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378055	Hs.8687	ESTs	3.2
	405546			Target Exon	3.1
	439584	AA838114	Hs.221812	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fs, clone L	3.1
	429568	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262886	Hs.143817	ESTs	3.1
	417208	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
75	423855	AA331761	Hs.254859	ESTs	3.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456880	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
80	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	A1990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21158	ESTs	3.1
	433610	AA806822	Hs.112547	ESTs	3.1
	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
10	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogenit	3.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	Homo sapiens cDNA: FLJ22437 fs, clone H	3.1
15	410869	AW808351		gb:MR1-ST0111-111099-003-R04 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	425480	AB023198	Hs.158135	KIAA0581 protein	3.1
	441492	A1149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
20	459324	AW080953		gb:xc28c12.x1 NCL_CGAP_Co18 Homo sapiens	3.1
	433852	A1376329	Hs.126829	ESTs	3.0
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50956	Hs.158993	glycosyltransferase	3.0
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	3.0
25	405254			NM_030813*:Homo sapiens suppressor of po	3.0
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothes	3.0
	434497	A1821803	Hs.136580	ESTs	3.0
	420355	AW988283	Hs.123125	ESTs	3.0
30	403481			Target Exon	3.0
	412988	BE046680		gb:hmr42h03.x1 NCL_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416542	T96118	Hs.226313	ESTs	3.0
	418948	A1217097		gb:xd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547959	Hs.115838	ESTs	3.0
	430459	BE178539	Hs.278634	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	A1283476	Hs.263478	ESTs	3.0
	448898	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
40	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	Hs.132950	ESTs	3.0
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11564 fs, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450963	A1864668	Hs.48832	ESTs	3.0
45	432336	NM_002759	Hs.274382	protein kinase, Interferon-inducible dou	3.0
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp554H1916 f	3.0
	451458	AW503398	Hs.293863	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
50	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004896	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CTD103 Homo	3.0
55	437323	AA371145	Hs.194397	leptin receptor	3.0
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
60	423784	AK000039	Hs.132828	Homo sapiens cDNA FLJ14913 fs, clone PL	3.0
	435877	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	428634	AA811845	Hs.106290	Kelch motif containing protein	3.0
65	431869	AA521136	Hs.190176	ESTs	3.0
	435008	AF150262	Hs.182898	ESTs	3.0
	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retroviri	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	452959	A1933416	Hs.188674	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probeset Identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808613 AW808551 AW808676 AW808350 AW808408 AW808694 AW808934
80			AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
			AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245860_1	AW846433 AW846159 AW846377 AW846528

411479	1247077_1	AW848047 AW848202 AW848531 AW8486142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
412988	1342150_1	AW848905 AW848214
413081	1348563_1	BE046680 BE046738 BE044958
413525	1374635_1	BE064415 BE064430 BE064448
415989	156454_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
416009	1566379_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
416288	1585983_1	Z43062 R13213 H14422
416882	162718_1	H51299 H44619 H46391 R86024 H51892 T72744
418259	173388_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
418866	179788_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
418948	180808_1	AA215404 AI980908 BE464132 AW271459 N74332 AI262061
419536	185688_1	T86754 AA229857 AA229668
420111	190755_1	AI217097 AW886090 W38035 W38792 AA232835 AW935043
420352	192979_1	AA603305 AA244095 AA244183
423412	228001_1	AA255652 AA280911 AW967920 AA262684
424200	236595_1	BE258835 AW966316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
426413	266650_1	AF109300 AI299378 AI202654
426503	268283_1	AA337221 AA336756 AW966196
426991	27415_1	AA377823 AW954494 AI022688
428002	285602_1	AA380153 AA380233 AW963529
428342	290035_2	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
429163	300543_1	AA418703 AA418711 BE071915 BE071920 BE071912
429220	301384_1	AI739188 AA428249 AI199636 AW505198 AW977291 AA824583 AA863419 AA724079 AI015524 AI377728 AW293582 AI928140 AA731438
430535	319543_1	AI092404 AI085630 AA731340
432600	350959_1	AA884766 AW974271 AA592975 AA447312
432765	353907_1	AW207206 AW341473 AA448195 AI951341
433523	368873_1	AW958485 AW968670 AA480922 BE350425
434763	392847_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
436296	41733_1	AJ003429 AJ003367 AA564825
436326	41795_2	H28882 AW655533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
437866	44433_2	AA648818 AW974389 H51771
439092	468554_1	N73895 AJ001872
439306	47088_1	BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281
440640	50357_2	AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706
440947	505904_1	AW270601 AW873282
442481	543588_1	AA155781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW802574 BE164040 BE164012 BE163972 BE163974 BE163982
445432	63943_1	AA837481 AW68444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733
448044	747196_1	AA812489 AW874142 AI47188
449343	80517_2	AA830149 AW978407 M85983 AW503637
449570	81018_1	BE220199 W01813 AF086118 N70760 BE221405
449525	8113_1	AW629666 AW959831 AW205739 BE620243 AA412367 AW300026 AW061920 AI288591 AW238114 AI302852 AI038548 AA534496 AI797207
450317	831956_1	AA921877
450580	83929_1	AA910403 AI615593 W58361 AW162520 AI616550
450582	83933_1	N99828 BE079873 AI110738 AF074645
450687	84327_1	AV653771 BE089370
452462	918580_1	AI458682 H24240 R14537 R18426 AW867082
453682	977454_1	AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053
454037	998287_1	AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024805 C01747 AW173095 W61229 W92685 AA742467
454096	1007449_1	H00789 R76925 AW1828
454171	1049240_1	AA001793 AA001871
454457	1207274_1	NH_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AI039060 BE168542 AW296554 AA323193 AA235370 AW779760
454860	1237732_1	IA48574 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
454968	1247029_1	AI892689 R14223 R18395
455276	1272541_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816888 AW816889 AW816940
455646	1348557_1	AW818892 AW818941 AW818578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150683 AW687764 AW023806 AW022095
455710	1352388_1	AA164518 AA730973 W00417 W65303
457374	328758_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
458912	823104_1	AA495800 AA495737 AA010736 AA654716 AA840726
		BE173615 BE173560 AI902860
		T79703 T96307 AI079725
		AW998716 AW022148 N68020
		AW062757 AW176890 AW062758 AW176895 AW176899 AW176900 AW176897 AW176928 AW176865 AW176892
		AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
		AW753456 AW753036 AW854868 AW854862
		AW835767 AW835537 BE160187
		AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
		BE176479 BE176678 BE176357 BE176550 AW866079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
		BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
		BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
		AA493582 AW897396 BE154814
		AI911066 AI933734 AI680888 AJ003599

TABLE 64C

Pkey: Unlque number corresponding to an Eos probe set  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
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5	400533	6881826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85785
	401403	7710986	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9665004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943985	Minus	39067-39225
	404648	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

35	Key:	Unique Eos probeset Identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
35	R1:	Ratio of BPH tissue to prostate tumor tissue			
	Key:	ExAccn	Unigene ID	Unigene Title	R1
40	428134	AA421773	Hs.161008	ESTs	9.4
	446336	AW815036	Hs.151251	ESTs	9.3
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	8.9
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	8.8
	400533			ENSP00000208376*-FRED65 protein (Fragmen	8.7
	418310	AA814100	Hs.86693	ESTs	8.7
45	404592			NM_022739*Homo sapiens E3 ubiquitin lig	8.1
	464457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
	400080			Eos Control	7.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	7.4
	420362	BE258635		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
50	438231	AW594539	Hs.156689	ESTs	7.3
	418387	R18085		gb:yg16b12.r1 Soares infant brain 1N18 H	7.2
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	6.9
	404967			Target Exon	6.9
55	430535	AW969486		gb:EST380561 MAGE resequences, MAGJ Homo	6.9
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	6.9
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	6.8
	412988	BE946680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	6.8
60	400440	X83957	Hs.83870	nebulin	6.6
	454171	AW854832		gb:QV2-CT0261-201099-011-405 CT0261 Homo	6.6
	400086			Eos Control	6.4
	440911	AA909536	Hs.143562	ESTs	6.4
	425312	AA364940	Hs.145958	ESTs	6.4
65	426140	AF131788	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
	419015	T79262	Hs.14463	ESTs	6.3
	453789	AA628517	Hs.118502	ESTs	6.2
	424940	AA985308	Hs.283902	ESTs	6.1
	403667			Target Exon	6.1
70	429014	AI800518	Hs.118156	ESTs	6.0
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte	6.0
	419999	AI760942	Hs.191754	ESTs	6.0
	405348			C7801664.g[1]12698061[db]BAB21849.1] (AB	6.0
	404003			Target Exon	5.9
75	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zy98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
	432319	AW510770	Hs.126386	ESTs	5.7
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled-coil	5.6
	443361	AI792628	Hs.133273	ESTs	5.6
80	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	5.6
	439079	AF885937	Hs.38348	ESTs	5.5
	422081	AW136820	Hs.196011	ESTs	5.5
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	5.5
	423529	T87318	Hs.120411	ESTs	5.5

5	436578	AI091435	Hs.134869	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271546	ESTs, Weakly similar to I78885 serine/th	5.4
10	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
	454968	AW849046	gb:TL3-CT0214-150300-085-H06 CT0214 Homo	5.2	
15	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	435375	AI733610	Hs.187632	ESTs	5.2
20	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525	gb:EST366595 MAGE resequences, MAGEC Homo	5.2	
	405321		Target Exon	5.1	
	416706	AA314676	Hs.288946	hypothetical protein FLJ13448	5.1
	438206	AA780385	Hs.187685	ESTs	5.1
25	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910	gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1	
	420533	AI809510	Hs.118971	ESTs	5.1
	457374	AA493662	gb:cnh05d12.s1 NCL_CGAP_Thy1 Homo sapiens	5.0	
	440354	AA889386	Hs.125468	ESTs	5.0
30	440388	AI693520	Hs.223000	ESTs	4.9
	421168	AA284658	Hs.281493	ESTs	4.9
	403481		Target Exon	4.8	
	438132	AA907076	Hs.122060	ESTs	4.8
	403333		NM_002518*:Homo sapiens neuronal PAS dom	4.8	
35	450317	AI692689	gb:wd86g05.x1 NCL_CGAP_Lu24 Homo sapiens	4.8	
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
40	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
45	442255	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363	gb:Homo sapiens full length insert cDNA	4.6	
	404995		ENSP00000251890*:Monocytic leukemia zinc	4.6	
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549		C7001976*:g[4758712]ref NP_004659.1  al	4.5	
50	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643	gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5	
	444800	AW119071	Hs.163287	ESTs	4.5
	403371		Target Exon	4.5	
55	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591	gb:EST13437 Testis tumor Homo sapiens cD	4.5	
	439752	T78968	Hs.14411	ESTs	4.5
	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866	gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5	
60	454585	BE069128	gb:CV3-BT0379-310100-071-g06 BT0379 Homo	4.4	
	452978	AA029994	Hs.61623	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	418059	AA211586	gb:zn66d05.s1 Stratagene muscle 937209 H	4.4	
	451469	NM_014809	KIAA0319 gene product	4.4	
65	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345604	gb:EST51529 Gall bladder II Homo sapiens	4.3	
	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
70	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	ALD43362	Hs.7984	pleckstrin homology, Sec7 and collared/coi	4.3
	441620	R69595	Hs.26676	ESTs	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
75	432765	AJ003429	gb:AJ003429 Selected chromosome 21 cDNA	4.2	
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
	413525	BE145899	gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2	
80	403305	NM_006825	transmembrane protein (63kD), endoplasmic	4.2	
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	430124	AW204994	Hs.253450	ESTs	4.2
	410790	AW803357	gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1	
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
5	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-105-g05 DT0020 Homo	4.0
10	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotysin, moto	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
15	455646	BE064420		gb:RC4-BT0311-241199-012-c06 BT0311 Homo	3.9
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453367	AI990741	Hs.252809	ESTs	3.9
	434222	AF119868	Hs.263941	Homo sapiens PRO2591 mRNA, complete cds	3.9
20	454806	AW872430	Hs.273743	ESTs	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	436878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9558, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JCS238 galac	3.9
25	407834	AW084991	Hs.26100	ESTs	3.9
	400398	AF137395	Hs.283879	ubiquitin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482*:g 9790241 ref NP_062626.1  S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthine dehydrogenase	3.9
	436350	AA713861	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.180412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized Infant brain cDN	3.8
40	434381	AA631834		gb:np77h05.s1 NCL CGAP_Py2 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29582		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AK37649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-003 HT0560 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041785	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AI470874	Hs.343799	ESTs	3.7
	405510			EN6P00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU 6	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-a04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h05.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.7
70	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF086933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AT034005	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AAA46167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450530	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-436B2	3.6



	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	A1571141	Hs.211122	ESTs	3.6
5	451193	N28850	Hs.44098	ESTs	3.6
	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	A1732837	Hs.277901	ESTs	3.6
	427235	A126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517*:gij4758712[ref NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	A1808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:as07a11.1 r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	A1821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA538300	Hs.206768	ESTs	3.4
	455895	T89832	Hs.170278	ESTs	3.4
	456304	A1820973		gb:nc21c02.y6 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	A1457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prol	3.4
	410551	R38730	Hs.21816	ESTs	3.4
	423357	A1285124	Hs.157505	ESTs	3.4
	450582	A1339732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW863442	Hs.129485	ESTs	3.4
	445004	A1204616	Hs.148701	ESTs	3.4
	450597	A1701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191895	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047690	Hs.188785	ESTs	3.4
	407344	A1038025	Hs.271418	gb:ox29f07.x1 Soares_tetal_tetus_Nb2HFB_	3.3
50	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	A1989963	Hs.197505	ESTs	3.3
55	453328	AW282636	Hs.346145	ESTs	3.3
	418985	A1042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449258	AA059050	Hs.59847	ESTs	3.3
	432550	AW287206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	3.3
	410700	AA352335	Hs.55641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	A1291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW958263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I98022 hypothesi	3.2
	418986	A1123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh88c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05356	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*:gij129082[sp P23270 OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41164	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447597	A1886036	Hs.213575	ESTs	3.2
	432625	A1243598	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV854907		gb:AV854907 GLC Homo sapiens cDNA clone	3.2
80	447183	A1554733	Hs.173182	ESTs	3.2
	426529	A1203933	Hs.97142	ESTs	3.2
	447892	AA35848	Hs.172978	ESTs	3.2
	457138	AA428240	Hs.126083	ESTs	3.2
	443565	AW466983	Hs.283949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139832	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429669	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AJ754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
15	441817	AW969706	Hs.293332	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	416901	H08396	Hs.78118	ubiquitin carboxyl-terminal esterase L1	3.1
	445753	R80715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AJ990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269661	ESTs	3.1
	418423	H54375	Hs.268921	ESTs	3.1
25	448766	R16337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.158471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
30	441492	AJ149998	Hs.146346	ESTs	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-004 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	436628	W88732	Hs.36107	ESTs	3.0
	444326	AJ939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H80467		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21821	hypothetical protein DKFZp762C078	3.0
	418948	AJ217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140: Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CMD-CT0103-120899-037-g07 CT0103 Homo	3.0
	440128	AA865818	Hs.174936	ESTs, Weakly similar to S71885 S1e20-Ik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	AJ381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

## 55 TABLE 65B

Pkey:		Unique Eos probeset identifier number	
CAT number:		Gene cluster number	
Accession:		Genbank accession numbers	
Pkey	CAT Number	Accession	
408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810535 AW810288 AW810263 AW810325 AW810443 AW8	
65	409189	AA125984 AA127189 AA066075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084762 AA076512 AA085119 AA085208 AA085045	
	410559	AW754192 W00554 AW857797 AW754203 AW754197 AW754193	
	410790	AW803357 AW803423 AW812233 R06814	
70	410869	AW808361 AW808404 AW808386 AW808594 AW808654 AW808613 AW808661 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808621 AW808539 AW808609 AW808472 AW808673	
	411436	1245660_1	
	411518	1248692_1	
	411552	1249255_1	
75	412701	1322288_1	
	412988	1342150_1	
	413081	1348563_1	
	413525	1374635_1	
80	416009	1566379_1	
	416422	1593811_1	
	418059	171879_1	
	418387	174731_1	
	418948	180808_1	
		R18085 AA219028 R17712 Z44345	
		AJ217097 AW886090 W38035 W38792 AA232835 AW936043	

5	149386	184356_1	AA236867 AA237066 AA354236 AW957759 H08981
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 A1580388 BE071923 R36280
	421926	209246_1	AA300691 AW953893 AA300493
	424200	236595_1	AA337221 AA336756 AW966195
	424686	242486_1	AA345504 AA345251 AW953243
	424994	245786_1	AW954525 A1372685 AA349501 A1372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003357 AA564825
	433523	368873_1	H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 A1792312 A1792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
15	436295	41733_1	N73895 AJ001872
	440947	505904_1	AA910403 A1815593 W58361 AW162520 A1816550
	442481	543588_1	N99828 BE079873 A1110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	A1692689 R14223 R18395
	450582	83933_1	A1339732 AAD10300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	916580_1	BE173515 BE173560 A1902860
	453682	977454_1	T79703 T96307 A1079725
25	454086	1007449_1	AW062757 AW176880 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854796 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812748 AW812747 AW812864 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW851677 AW861689 AW861681 AW858056
	455276	1272541_1	BE176479 BE176578 BE176357 BE176550 AW886079 BE176876 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW963477 Z41970 F12435 T73989 T09387
	455646	1348657_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	A1820973 A1734077 A1820984 AA225796 AA225080 AA225101
	457374	328758_1	AA493662 AW897398 BE154814

45

TABLE 65C

50

Pkey: Unique number corresponding to an Eos probaset  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277596
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
401459	9212270	Minus	182001-183323
402145	8018280	Plus	113086-114800
402454	7534025	Minus	14826-15803
402703	8705069	Minus	15335-15500
403242	7637817	Minus	11297-12511
403291	7230870	Plus	95177-95435
403306	8099946	Plus	114632-114805
403333	8568833	Minus	124794-124941
403371	9087278	Plus	105655-106050
403433	9719611	Minus	72225-72437
403481	9965004	Plus	93498-93633
403510	7652047	Plus	61868-62027
403667	8850483	Minus	1344-1442,1545-1697
403805	8140491	Minus	51483-51742,53429-53511
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	9943955	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6008247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
405510	7630909	Minus	101028-101174
405549	1552494	Plus	10878-11048
405733	9884689	Plus	124832-125051

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Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75<sup>th</sup> percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85<sup>th</sup> percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10<sup>th</sup> percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigeneID:	Unigene number				
Unigene Title:	Unigene gene title				
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue				
Pkey	ExAccn	Unigene ID	Unigene Title	R1	
410929	H47233	Hs.30643	ESTs	21.1	
450693	AW450461	Hs.203965	ESTs	16.7	
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2	
432473	AI202703	Hs.152414	ESTs	11.3	
446336	AW815036	Hs.151251	ESTs	10.9	
407275	AI364188		gb:qv34h07.x1 NCL_CGAP_Ut4 Homo sapiens	10.7	
428134	AA421773	Hs.161008	ESTs	10.2	
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8	
433466	AA508363	Hs.105314	relaxin 1 (H1)	9.5	
415293	R49462	Hs.106541	ESTs	9.1	
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	8.8	
428927	AA441837	Hs.90250	ESTs	8.6	
420345	AW295230	Hs.25231	ESTs	8.5	
453367	AI90741	Hs.252809	ESTs	8.2	
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7	
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopole	7.5	
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4	
400080			Eos Control	7.4	
431448	AL137517	Hs.308201	hypothetical protein DKFZp564O1278	7.4	
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3	
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3	
438231	AW594539	Hs.155689	ESTs	7.3	
410330	AW023630	Hs.169425	ESTs	7.2	
449300	AI656959	Hs.346514	ESTs	7.1	
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0	
426384	AI472078	Hs.303682	hypothetical protein FLJ13189 (FLJ13189)	6.8	
454171	AW854832		gb:QV2-CT0261-201099-011-05 CT0261 Homo	6.6	
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6	
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6	
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fls, clone PL	6.5	
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5	
424433	H04607	Hs.9218	ESTs	6.5	
442461	N99928		gb:zs32c04.r1 Soares fetal liver spleen	6.4	
425312	AA354940	Hs.145958	ESTs	6.4	
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4	
440911	AA909538	Hs.143562	ESTs	6.4	
400533			ENSP00000209376*:PRED65 protein (Fragmen	6.2	
418310	AA814100	Hs.86693	ESTs	6.2	
403667			Target Exon	6.1	
436395	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1	
404003			Target Exon	5.9	
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9	
436138	R98299	Hs.177502	ESTs	5.9	
424940	AA985308	Hs.283902	ESTs	5.8	
434485	AI623511	Hs.118567	ESTs	5.8	
453200	AA033832	Hs.212433	ESTs	5.7	
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7	
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6	
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6	
443351	AI792628	Hs.133273	ESTs	5.6	
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5	
439079	AF083937	Hs.38348	ESTs	5.5	
430535	AW958485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5	
436578	AI091435	Hs.134859	ESTs	5.5	
424051	AL110208	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4	
421863	AI852677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4	
435072	AW592176	Hs.116932	ESTs	5.4	
435375	AI733610	Hs.187832	ESTs	5.4	
444609	AW571659	Hs.278081	ESTs	5.4	
416602	NM_006159	Hs.79389	nei (chicken)-like 2	5.4	
433087	AI720686	Hs.152520	ESTs	5.3	
439052	AA830149		gb:oc44R08.s1 NCL_CGAP_GCB1 Homo sapiens	5.3	
437267	AW511443	Hs.258110	ESTs	5.3	
441916	AA993571	Hs.129075	ESTs	5.3	
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3	
452531	AA429462	Hs.293946	ESTs, Weakly similar to 138022 hypotheti	5.3	

	423101	M83941	Hs.123642	EphA3	5.3
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
5	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W82147	Hs.118394	ESTs	5.2
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA855818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-Hk	5.1
	445238	AA863971	Hs.187506	ESTs	5.1
15	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
20	457374	AA433662		gb:nh05d12.a1 NCL_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_005042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AB207119	Hs.154662	DnaI (Hsp40) homolog, subfamily A, membe	4.9
	450497	H64159	Hs.15328	ESTs	4.8
25	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
	450317	AI892689		gb:wd86g05.x1 NCL_CGAP_Lu24 Homo sapiens	4.8
30	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
35	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	405348			C7001654.g[12698061]dbj[BAB21849.1] (AB	4.6
40	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939458	Hs.180870	ESTs	4.6
	428218	AA424268	Hs.123642	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	AI871141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
50	430188	AL048242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
	423352	AA324808	Hs.183576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI083155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647808	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255652		gb:cs21h11.r1 NCL_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	4.2
65	427808	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442785	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	AI701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438675	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241188-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE178479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	4.0
5	436136	R27299	Hs.10172	ESTs	4.0
	416780	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
10	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specifi	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
15	447530	AW192063	Hs.248665	ESTs, Moderately similar to JC5238 galac	3.9
	412988	BE046680		gb:hn42h03.x1 NCL CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10608	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419529	AB020695	Hs.91652	KIAA0885 protein	3.9
20	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	408111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW846047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
25	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW989118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12ED41 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
30	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
35	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433808	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0087-250300-002-f11 BN0067 Homo	3.7
40	432101	AI918950	Hs.123642	EphA3	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	452482	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	448568	AA149121	Hs.71847	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	438345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660687	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
50	450687	AA495800		gb:zw05b07.s1 Soares NhlHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
55	422899	O16471	Hs.121571	Human mRNA, 3' terminal portion	3.7
	439075	AF085933	Hs.282620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
60	404561			trichorhinophthalangeal syndrome 1 gene (T	3.6
	417665	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021887	Hs.59970	ESTs	3.6
65	450630	AA010428	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CY0255-200100-024-b02 CT0255 Homo	3.6
	423666	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
70	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
75	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
	401132			C120005177:gi4758712 ref NP_004659.1  a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ne07a11.r1 NCL CGAP_Ew1 Homo sapiens	3.5
80	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU77_HUMAN A	3.5
	450216	AA573345	Hs.50226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
5	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA465869	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
	436714	AA728964	Hs.293399	ESTs	3.4
10	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
20	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11295	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP9 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880814	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126289	Hs.192232	ESTs	3.4
	459646	AW863968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
40	448108	AW300021	Hs.170885	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI999963	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.67128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	465710	BE072049		gb:PM4-BT0532-170100-004-r06 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53128	ESTs	3.3
55	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H83281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1a01	3.2
60	420608	BE548277	Hs.103104	ESTs	3.2
	418966	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c05.r1 Soares_fetal_liver_spleen_	3.2
65	424994	AW954525		gb:EST386595 MAGE resequences, MAGC Homo	3.2
	417676	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA786296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI888036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X58411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
	453789	AA628617	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	416319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI538323	Hs.52620	Integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AA458682		gb:k13a01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1	
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	433444	AW975324	Hs.129816	ESTs	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
	415861	Z43123	Hs.144513	ESTs	3.1
	422289	AK000181	Hs.114556	hypothetical protein FLJ20174	3.1
10	432527	AW975028	Hs.102754	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	417958	AA767382	Hs.193417	ESTs	3.1
15	407426	AF129533		gb:Homo sapiens F-box protein Fblb (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	405548			Target Exon	3.1
	423595	R82826	Hs.220702	ESTs	3.1
	412533	AA679863	Hs.69608	ESTs	3.1
	434072	H70864	Hs.283059	Homo sapiens PR01082 mRNA, complete cds	3.1
25	405264			NM_030813*:Homo sapiens suppressor of po	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-004 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW886727	Hs.9914	ESTs	3.1
30	435021	AA922182	Hs.54709	ESTs	3.0
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.0
	450580	N40087		ESTs	3.0
	432319	AW510770	Hs.126386	ESTs	3.0
	453713	R20640	Hs.79133	cadherin 8, type 2	3.0
35	445784	AI253155	Hs.146065	ESTs	3.0
	416642	T98118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
40	404995			ENSP00000251890*:Monocytic leukemia zinc	3.0
	444794	AI419991	Hs.145225	ESTs	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	420133	AA426117	Hs.155643	ESTs	3.0
	407629	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449313	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CMO-CT0103-120899-037-g07 CT0103 Homo	3.0
	419622	AA452054	Hs.119338	ESTs	3.0
50	449746	AI688593		gb:y138a05.x5 Soares breast 3NbHbAt Homo	3.0
	428412	AA428240	Hs.126083	ESTs	3.0
	428200	AI039524	Hs.98388	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	431869	AA521136	Hs.190176	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
55	462959	AI933416	Hs.189674	ESTs	3.0

TABLE 668

60	Key:	Unique Eas probset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
65	Key,	CAT Number
	410790	1221131_1
	410869	1225123_1
70	411438	1245660_1
	411479	1247077_1
75	412988	1342150_1
	413081	1348563_1
	413625	1374635_1
	416009	1566379_1
	418948	180808_1
	420111	190755_1
80	420352	192979_1
	424200	236595_1
	424994	245786_1
	426002	285602_1



428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
430536	319843_1	AI092404 AI085630 AA731340
432765	353807_1	AW968485 AW968670 AA480922 BE350425
433523	368873_1	AJ003429 AJ003367 AA564825
434763	392847_1	H29882 AW655533 AW149901 AI572917 AA598500 AI886466 AJ336390 AW864390 AW864320
436295	41733_1	AA648618 AW974389 H51771
439082	468554_1	N73895 AJ001872
439306	47085_1	AA830149 AW978407 M85983 AW503637
440947	505904_1	BE220199 W01813 AF086118 N70760 BE221405
442481	543588_1	AA910403 AI815593 W58361 AW162520 AI816550
445432	63943_1	N99828 BE079873 AI110738 AF074645
448044	747196_1	AV653771 BE0889370
449570	81018_1	AI456682 H24240 R14537 R18426 AW867082
449745	814534_1	AA001793 AA001871
450317	831956_1	AI668593 AI820774 R86205 H39971 H22177 H26241
450560	83929_1	AI692689 R14223 R18395
450582	83933_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
450687	84327_1	AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
452462	918580_1	AA164518 AA730973 W00417 W65303
453682	977454_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
454037	996287_1	AA495800 AA495737 AA010736 AA654716 AA640726
454096	1007448_1	BE173515 BE173560 AI902860
454171	1048240_1	T79703 T96307 AL079725
454457	1207274_1	AW998716 AW022148 N68020
454665	1228599_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176828 AW176868 AW176892
454860	1237732_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
454968	1247029_1	AW753456 AW753036 AW854868 AW854862
455087	1252050_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
455276	1272541_1	AW835767 AW835537 BE180187
455446	1348557_1	AW849048 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
455710	1352368_1	AW854538 AW854418 AW854412
457374	328758_1	BE176479 BE176678 BE176357 BE176650 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
458912	823104_1	BE084420 BE084436 BE084429 BE084414 BE084400 BE084517
		BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
		AA493662 AW897396 BE154814
		AJ911066 AI933734 AI880888 AJ003599

TABLE 66C

Pkey: Unique number corresponding to an Eos probe set  
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
 Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7328328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11287-12511
403481	9965004	Plus	93496-93633
403510	7852047	Plus	81886-82027
403667	6850483	Minus	1344-1442, 1545-1697
404003	8655948	Plus	198349-199096
404561	9795980	Minus	59039-70100
404592	9843865	Minus	39067-39225
404848	8248647	Minus	23955-24034, 25143-25264
404987	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28568-28684
405321	3419846	Minus	44654-45210
405348	2814717	Minus	43310-43452
405510	7630909	Minus	101026-101174
405548	1532158	Plus	11562-11688

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile values amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probe set identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigenesID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292426	Hs.163484	ESTs	56.0
	446057	AJ420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.263946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424089	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400267	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52255	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301866	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	RA5175	Hs.117183	ESTs	24.5
	400296	AA306627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	426336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428852	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin)-prop	16.5
	413697	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5857	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	428501	AW043782	Hs.293616	ESTs	13.9
	428588	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW957646	Hs.23023	ESTs	13.3
	449519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	13.2
55	418848	AI820861	Hs.193485	ESTs	13.1
	426398	AI249368	Hs.98558	ESTs	13.0
	428220	AW207208		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M93119	Hs.89584	Insulinoma-associated 1	12.3
	450382	AA397668	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48378	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU 5	11.1
	412446	AI788015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99815	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI886489	Hs.83937	hypothetical protein	10.3
	430226	BE246562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11680	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449825	NM_014253		odc (odd Ozten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935862	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	UM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
10	432101	AI918960	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
15	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
	417333	AL167545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AJ076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	446100	AW967109	Hs.13804	hypothetical protein cJ462023.2	8.5
	400294	N95798	Hs.278695	Homo sapiens protein mRNA, complete cds	8.5
20	416182	NM_004354	Hs.79069	cyclin G2	8.5
	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothi	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
25	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0868 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.269014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
30	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
	428728	NM_016825	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	426905	AB032059	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	432586	AA668548		ESTs	7.3
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
45	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothi	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416816	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279450	Hs.86368	calmegin	6.8
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	6.8
	438982	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18984	Hs.1904	protein kinase C, iota	6.6
	450377	AB033091		KIAA1265 protein	6.6
60	451418	BE387790	Hs.26389	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isof	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A {	6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	438063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993087	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421586	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AJ297438	Hs.20166	prostate stem cell antigen	6.0
	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AJ572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189638	ESTs	6.0
	424036	AA770588		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410258	AA316181	Hs.61635	slx transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
5	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	5.8
	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-	5.7
10	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	5.4
20	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-B protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
25	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
30	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AI042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
35	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptojanin 2	5.0
	403046			NM_006656:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-tyrosine/alpha-amino acidipale aminotra	5.0
	450164	AJ239923	Hs.63931	ESTs	5.0
	417318	AW963937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	455088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AI378329	Hs.128629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
50	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGI-82 protein, PSOR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.105778	ATPase, Ca transporting, type 2C, member	4.7
60	431724	AA514535	Hs.283704	ESTs	4.7
	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.258301	hypothetical protein MGC13170	4.6
	414085	AA114018	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
65	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004805	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	448845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.5
75	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
80	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430284	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.3
5	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U86658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
10	442501	AA315267	Hs.23126	ESTs	4.2
	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436555	AI364997	Hs.7572	ESTs	4.2
15	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
20	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA687775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
25	432363	AA534489		gb:nf6g11.s1 NCI_CGAP_Co3 Homo sapiens	4.1
	447574	AF162666	Hs.18895	lousied-like kinase 1	4.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
30	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
	438825	BE327427	Hs.79953	ESTs	4.0
35	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
	415276	U88686	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.50790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
40	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
	432435	BE218886	Hs.282070	ESTs	3.9
45	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
	429259	AA420450	Hs.292911	Plakophilin	3.9
50	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
	410227	AB008284	Hs.61152	exocytosis (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.9
55	448826	AI580252	Hs.263246	ESTs, Weakly similar to putative p150 IH	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
	432875	AI791855		ESTs	3.8
	419713	AW968050	Hs.92391	nudix (nucleoside diphosphate linked mol	3.8
	427479	BE410082	Hs.178471	KIAA0798 gene product	3.8
60	443182	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249056	Hs.32793	ESTs	3.8
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419063	AI479580	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
65	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
70	418004	U37619	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AK33833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437957	BE277414	Hs.5947	mal transforming oncogene (derived from	3.7
75	417061	AI675944	Hs.186691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.7
	418838	AW385224	Hs.35198	eclonucleotide pyrophosphatase/phosphodi	3.7
	453468	AB014533	Hs.33010	KIAA0533 protein	3.7
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	3.7
80	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6

5	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24263	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
	422424	A186431	Hs.296638	prostate differentiation factor	3.6
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
10	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein OEC2	3.6
	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
15	429886	A1871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
20	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (Hs	3.5
	419168	A1336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
25	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
	452721	A1269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
30	443884	N20817	Hs.194397	leptin receptor	3.4
	403752			NM_002753:Homo sapiens mitogen-activate	3.4
	427723	A1356260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
35	426716	NM_006379	Hs.171921	soma domain, Immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
40	437617	A1026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
45	427871	AW992405	Hs.59822	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421882	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
50	420588	F08247	Hs.247735	protocadherin alpha 10	3.3
	435873	N23874	Hs.50477	RA827A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250628	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
55	443891	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409860	BE261944		hexokinase 1	3.3
	433891	AA813792		gb:nc97h03.s1 NCLCGAP_P12 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
60	419972	AL041465	Hs.182982	polg1-67	3.3
	445707	A1248720	Hs.114390	ESTs	3.3
	412628	A1972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
65	419879	Z17805	Hs.93564	Horner, neuronal immediate early gene, 2	3.3
	433345	A1661545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
70	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPIC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
75	401519			C15000476*gi12737279 ref XP_012163.1	3.2
	419577	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10325	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.2
80	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439583	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	A1249502	Hs.29868	ESTs	3.2
	445625	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW988504	Hs.123073	CDC2-related protein kinase 7	3.2
	425610	AI923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207188	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
15	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rbccc728	3.1
	433008	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
20	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	418974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty acid-Coenzyme A ligase, long-chain	3.1
25	423453	AW450737	Hs.126791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expressed	3.1
	436278	BE396290	Hs.5097	synaptophysin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	436705	AI049824	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181325	KIAA1073 protein	3.1
	431576	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	408767	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278862	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806593	Hs.125291	ESTs	3.1
	448607	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
45	427315	AA179949	Hs.175883	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	410082	AA061594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429538	AI816662	Hs.211577	kinectin 1 (kinasin receptor)	3.0
	452908	AB001451	Hs.30985	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W55321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE265822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408681	AW953853	Hs.282833	ESTs, Weakly similar to I38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
	412552	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10869	ESTs, Weakly similar to T00060 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78108	phosphodiesterase 8B	2.9
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420051	AW024937	Hs.29410	ESTs	2.9
80	431653	NM_016669	Hs.267182	TBX3-iso protein	2.9
	417822	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420944	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195822	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
5	446880	AI811807	Hs.108546	Homo sapiens cDNA FLJ14934 fs, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferm	2.9
	437395	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.9
	413125	BE244689	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*Homo sapiens keratin 15 (KRT1	2.9
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ecolunucleoside triphosphata diphospholhyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
15	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fs, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4995	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
	442202	BE272862	Hs.105534	hypothetical protein FLJ22625	2.8
20	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	2.8
	444367	HS4892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
	418166	AI754416		Cdc42 effector protein 3	2.8
25	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306981	MSTP043 protein	2.8
	426170	BE161055	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
	425320	U29344	Hs.83190	fatty acid synthase	2.8
30	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
35	453186	AK001708	Hs.32271	hypothetical protein FLJ10646	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
	450546	AA010200	Hs.175551	ESTs	2.7
40	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	449181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
45	452941	AL110947	Hs.31074	N-sulfoglucosamine sulfolhydrolase (sulfa	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434529	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA809200		gla:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015885	Hs.171731	solute carrier family 14 (urea transport	2.7
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
55	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452258	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	2.7
60	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA463208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW461449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X09635	Hs.1657	estrogen receptor 1	2.7
65	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*Homo sapiens Williams-Beuren	2.7
	441266	H16968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
70	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependent interferon response prota	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA480775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
75	409550	T08490	Hs.288869	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
80	438510	AL080220	Hs.6285	DKFZP585P0123 protein	2.7
	406527	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protela CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6



5	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BEG00150	Hs.48778	ribon protein	2.6
	422717	AJ557623	Hs.119475	cold inducible RNA-binding protein	2.6
	426110	NM_002913	Hs.186563	replication factor C (activator 1) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
10	401197			ENSP00000229263:HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
	447963	AJ452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU 6	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
15	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
	408157	AA047685	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulin 1	2.6
20	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AJ015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp59612022 (f	2.6
	428695	AJ356647	Hs.189999	purinergic receptor (family A group 5)	2.6
	431725	X66724	Hs.2839	Norrie disease (pseudoglioma)	2.6
	425174	D87450	Hs.154978	KIAA0251 protein	2.6
25	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
	428180	AJ129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439580	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	2.6
30	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449318	BE395253	Hs.30881	ESTs	2.6
35	445919	T53519	Hs.334592	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
	431472	AK001023	Hs.255649	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
40	434672	AW254020	Hs.117721	ESTs	2.6
	443016	R33261	Hs.6614	ESTs, Weakly similar to A43932 much 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor 1	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
50	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
	446237	AW270516	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE189641	Hs.270134	hypothetical protein FLJ20280	2.5
55	406789	AJ041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
	420460	AA262331	Hs.48378	Homo sapiens clone HB-2 mRNA sequence	2.5
	436185	AJ373544	Hs.331328	intermediate filament protein syncoilin	2.5
60	430542	AJ557488	Hs.119122	ribosomal protein L13a	2.5
	452827	AJ571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
65	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AJ720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
70	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW981400	Hs.333528	HER2 receptor tyrosine kinase (c-erb-b2,	2.5
	431615	AW295859	Hs.235800	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC067 protein	2.5
75	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
	450828	AW382884	Hs.204715	ESTs	2.5
	426783	X89867	Hs.172350	HIR (histone cell cycle regulation defec	2.5
80	431122	A267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
	408770	AW270608	Hs.170196	bone morphogenetic protein 7 (osteogenic	2.5
	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X55777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418549	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothet	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
	414566	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
10	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421966	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
15	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fls, clone NT	2.5
	443837	AI984625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
	435021	AA922182	Hs.73962	ESTs	2.5
	435750	AB029012	Hs.4890	KIAA1089 protein	2.5
20	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeast	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	425976	C75094	Hs.334514	NG22 protein	2.5
	449458	AI806078	Hs.208261	ESTs	2.5
	428013	AF151020	Hs.161444	hypothetical protein	2.5
25	424369	RB7622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
	433585	T85301	Hs.194397	gb:yd78d05.s1 Soares fetal liver spleen	2.5
	436682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.5
30	427515	T79528	Hs.179516	integral type I protein	2.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

35	Pkey	CAT Number	Accession
40	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AM89633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 AW341473 AA448195 AW207206 AI951341 AA969259 BC021735 AI669212 AL120184 AI769949 BE701002 BE184383 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF980859 AA987807 Z41449 BF908059 BF908053 BF908049 BE698424 BF908060 BF952832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617829 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AB040707 AW975518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32882 R54110 BF115783 F09044 BF808433 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D69344 BG966750 N45526 BG966917 T81382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360 BC009812 NM_003528 BI597616 AV781592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181626 BG210634 BG192999 AI253307 AA344186 AW952986 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AC037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336 AW959037 R42557 AI337047 AA948350 AI638005 AA450950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI93770 AI558211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 AI050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24708 AI379579 AA424899 AI884671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379562 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N35282 AA024987 N36887 BI919187 N49471 AA869970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW953972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D51278 BI756812 AA508234 R49885 BF850422 BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548 AF075009 R63109 R63068 AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW239378 AW444558 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041696 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE926699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812818 BF095731 BG212397 BF678766 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164 AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593 AK056315 AI015524 AA724079 BI712619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA768094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI358361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985584 AW263513 AA913892 AI93488 AW263502 AI808164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036997 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF953166 NM_033445 BC001193 AI885781 BF794032 AA476620 AA810905 AI291244 AI885097 AI359708 AI335629 H97395 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329098 BM045465 AL531028 BG437151 BE868021 AA179427 AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543182 AB032897 AI141878 AW978722 BE467119 AI761403 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW259901 BF057835 BE465977 AI621269 BE465983 N74056 AI817896 AA716567 AA934774 H62600 H08497 BF943762 BE395335 BE863333 AW970240 AA534489 AW970323

5	422890	61426_1	AK057805 AW162343 AI190479 AI083318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964435 AW004030 AI632565 BE026300 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI368013 AI867923 BG911906 D81142 C15616 AL538687 Z25032 Z43784 R13382 AV746824 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603 AA196390 AA507837 AA196468 AK056626 AI800896 BF939022 BE844718 AI954754 BE218177 BE348667 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185 AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW863548 AI139947 AA514302 AA848232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE705539 BE153177 BF084925 AI133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE170736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826 AW973834 AI791932 AI791855 AI732640 AA558833 AA558987 AI821610 AI973061 AI400921 AI796154 AW241817 AW260951 NM_004892 AF047442 BE275338 BF724663 BI917206 BE276993 AI602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993263 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI802726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435620 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R58565 R80136 AA484577 BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296858 AI268977 AI168133 BM352055 AI262769 BF941976 AI056920 AA481861 BF763697 AL565888 BM352383 AA427768 AA385348 AI186988 AA931831 AA134972 BF217480 BF111012 AI908246 AA319949 AA318136 AL514721 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945360 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257 AW182329 AA613792 T05304 AW868385 BG107484 AA632009 AI432670 AI656560 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434869 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952801 AI581363 AA557165 AI656577 AL562079 AI700926 AI470561 BF083058 AW196387 AI132984 BI064046 AI970157 R02122 H56924 AI521721 AA808206 AA725223 AI768003 AW339621 AA805851 AI287969 AW654627 BC021085 AL527872 AL526298 AI557087 BI255090 AU143499 AI560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141430 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BI7632690 BG430761 BE792868 AW326267 AI135173 AA102674 BF726986 AL564735 BE155862 BE155979 BF741679 H67776 H59234 H86665 AW117774 AW274435 L20008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW059877 AW015214 AI948718 BE219706 AI953805 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI204449 AW275385 AA336950 BE501521 BF740688 AA311404 AA384639 BI772535 BG473076 BE891298 BE246926 BM012886 BE242693 BE901342 BG745358 BF374053 AL564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158954 AU158917 AI282616 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857928 BF372588 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N65172 AW013929 AI262274 AI871237 C75260 AA934848 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA405317 AI285043 N53050 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AA115336 BE812876 BE812972 BE812982 BE813008 BE813018 R43883 BE812881 AK055109 BC019085 AA187684 BG658226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129680 AW262782 AI134107 BM023515 AA977504 AI858222 AI348454 R69725 AA975268 BM021207 AL080074 AI129218 AW207842 N50581 AA771919 AI092259 AI028416 AI074114 BG656536 BE001677 AW193419 AA917040 W90430 AI342884 AI378957 AL036486 AW020058 BI491093 BF476021 R41226 R99631 F04125 C02343 AA115589 R56480 AI00988 R54266 R31422 AK056915 BE887252 AI523348 AA765350 BF446858 Z43675 R19529 AI133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE836308 BE835295 AA376302 BE645790 AA375690 AA376892 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI098810 AW183016 AI635738 N27524 BE45916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680080 AW953889 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA248732 AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654208 F27874 AK074291 AW293424 BE676135 AI832126 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF824261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019369 BF928776 AW813409 AV726804 AW077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF694155 BE205787 BF063513 N35828 AI948557 AI438839 AI379879 BG056182 AI589094 N23123 AA588805 AW318581 AI080272 AI421980 AI493318 BF194630 N87590 AA495993 N32996 AA698444 H96845 H96592 N26741 BI035539 BF747723 BF171055 W01350 H05495 AI243785 Z39522 AA887432 AI350669 R48102 AA602964 AA609200 AW976537 AI033582 AA837085 AA745281 AA648395 BC013939 BI494690 BI491211 AI928393 AA843546 BG938644 AI185828 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA828759 AW116737 BF513970 AW707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA502308 AA428261 AI460355 AW652760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA462120 AI150479 AI016166 AA775515 AA661791 BM474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI862893 AI989289 Z42328 BF028504 T35668 BG402602 AI185770 AI023271 AA147719 AI434079 AI568000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA326941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI363586 AA827189 BI494972 AW021094 BI494871 AA605500 AA460923 BI492041 AW028965 AI824611 BG271780 AI497723 H88862 D59658 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370863 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R81003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954388 NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530064 AL525377 BG474566 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF080526 F12128 AL568773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529841 AA324163 AI523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BE528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL522884 AL568203 AL534419 BF981162 BE257148 AL561833
	417379	1610005_1	
	407819	7392_2	
10	419733	7612_3	
	432675	1237917_1	
	447820	687223_1	
15	409151	4123_1	
	409960	39576_1	
20	433891	647290_1	
	414922	1563_2	
25	414222	18695_1	
	426991	29771_1	
30	434194	62680_1	
	432908	452541_1	
35	412652	18658_2	
	437179	12239_1	
40	418166	18858_1	
	431416	120918_1	
45	447881	44623_1	
	407192	2200202_1	
50	434747	117643_1	
	410297	2990_1	
55	424339	50559_1	
60			
65			
70			
75			
80			

445636 B561\_5 BF339386 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310  
AA090672

419175 35068\_1 AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF098162 BF096132 AA744972 AI961988 AI858339 BE076331  
AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626  
Z44671 BI062776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80662 AA360728 F10618  
AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA634314 BE814964 BE973713 N49493 BE006634  
BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA256424 AW008334 AA847572  
AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403  
F02090 AI187299 AI609644 Z40516 AW952314

441128 20932\_1 BC014072 BE328850 AI355557 AI148171 AI022165 BG149661 BF000571 AA233101 AA573721 AA447991 AW016855 AI006058 AA554071  
BF478215 AA906902 AW014761 BE905661 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706  
N90525 AW973623 AI359627 BG674574 BE903322  
AI041403 Z49148

405789 0\_0 AK057700 BC015899 BE857108 AL526926 AL527436 BG13023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161  
421091 24941\_2 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396  
AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AI568301 AL567278 BI522445 BI754384  
BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AI536876 AI574332 BF834531 BF340116  
BF836954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148696 AL569234 BG034270 BI913839 AL581327 AL565842  
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Z11692 X61466 NM\_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI888869 BG337218 AW629935  
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BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869852 BG998348 BI011834 BF888337 BF998627 BF092380 AW803215 F01241  
BF805719 BG076487 AW498536 BF988866 BG988849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685  
BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF568947 BF154671  
BM007368 BF669385 BE772007 BI199487 BF761700 BI261519 BF944452 BF698506 AI038390 BM044934 AW381142 BG743618 BE769206  
BE893973 BI018047 BF886479 BF761350 BE769768 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180984  
BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Key: Unique number corresponding to an Eos probeset  
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA  
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.  
Strand: Indicates DNA strand from which exons were predicted.  
NL\_position: Indicates nucleotide positions of predicted exons.

Key	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8178894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9785672	Minus	118596-118816, 119119-119244, 119509-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006248	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165996, 166189-166314, 166408-166556
401866	8018105	Plus	73128-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Key: Unique Eos probeset identifier number  
ExAccn: Exemplar Accession number, Genbank accession number  
UnigeneID: Unigene number  
Unigene Title: Unigene gene title  
R1: Ratio of tumor to normal body tissue

Key	ExAccn	UnigeneID	Unigene Title	R1
448889	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.6
426747	AA536210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	AJ420227	Hs.149358	Trp-pB transient receptor potential cat	66.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AI821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424069	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.61635	slx transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

5	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
	400292	AA250737	Hs.72472	BMP-R1B	31.4
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL136623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog	30.3
10	407168	R45175	Hs.117183	ESTs	29.6
	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	AI733861	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
15	423073	9E252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002125	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
20	407709	AA456135	Hs.23023	ESTs	24.7
	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI257700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
25	437052	AA861697	Hs.120591	ESTs	22.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	20.8
	419743	AW408752	Hs.6957	Homo sapiens clone 24416 mRNA sequence	20.5
30	427956	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
35	428662	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (oa	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
40	418961	AW967646	Hs.23023	ESTs	17.3
	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98568	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
45	449625	NM_014263		odz (odd Ozten-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AIJ076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
	448619	AW175885	Hs.278695	Homo sapiens protein mRNA, complete cds	14.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820961	Hs.193465	ESTs	14.3
	428918	AW873986	Hs.119383	ESTs	14.2
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
55	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bulous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004398A chromos	13.3
	432101	AI918960	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
60	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU 5	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	439927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA428834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
80	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277852	Hs.54578	ESTs, Weakly similar to I38022 hypothesi	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S61797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
10	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
15	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalus	9.8
20	432674	AA641092	Hs.257339	ESTs, Weakly similar to 138022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.180044	ESTs	9.6
	443180	R16875	Hs.258576	claudin 12	9.5
	406864	M21305		FGFES predicted novel secreted protein	9.5
25	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456860	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
	451684	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
	437124	AA654458		KIAA0665 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
35	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431892	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AI655499	Hs.161712	ESTs	8.8
40	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
	418260	U29928	Hs.83918	adenosine monophosphate deaminase (isofo	8.7
	425905	AB032959	Hs.318684	novel C3HC4 type Zinc finger (ring finger	8.7
45	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-lysine/alpha-amino adipate aminotra	8.7
	425465	L16964	Hs.1804	protein kinase C, iota	8.5
	416239	AL038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP564I052 protein	8.4
50	450164	AI239923	Hs.63931	ESTs	8.4
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AI420511	Hs.153934	ESTs	8.3
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
55	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
60	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.183145	metallothionein 1E (functional)	7.9
65	447476	BE293456	Hs.20880	ESTs, Weakly similar to 138022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	7.7
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
70	451962	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (	7.6
75	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE484341	Hs.21201	nectin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
	421588	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
80	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AI548502	Hs.55468	ESTs	7.4
	442692	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AI623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.1
	431958	XG3628	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	438063	AK000028		ribosomal protein S24	7.0
10	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA328108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195814	splicing factor 3b, subunit 3, 130kD	6.6
	422486	BE614492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
20	410227	AB009284	Hs.61152	exostases (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
25	448148	NM_016578	Hs.20509	HBV pX associated protein-B	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415058	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
30	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410782	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
35	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75285	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
40	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183181	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
45	449845	AW971183	Hs.8019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016888	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone Z3948 mRNA sequence	6.0
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
50	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocytes (homolog Droso	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446418	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW246508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyl	5.9
	429165	AW008886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266559	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.8295	ESTs, Weakly similar to T17248 hypotheti	5.8
	418795	AA497778	Hs.20509	HBV pX associated protein-B	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.283663	ESTs, Moderately similar to I38022 hypot	5.7
65	433852	AJ378328	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GLD04 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
70	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AM33833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429838	AI916662	Hs.211577	kineclia 1 (kinesin receptor)	5.5
75	403046			NM_005656:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49851	Hs.9028	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
80	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23058 fis, clone L	5.4
	440145	AW014231	Hs.90780	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	DZ6067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306106		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
5	417318	AW953937	Hs.240845	ESTs	5.3
	429467	NM_004477	Hs.203772	F5HD region gene 1	5.3
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004805	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443866	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
15	450832	AW970602	Hs.105421	ESTs	5.1
	448807	AJ571940	Hs.7649	ESTs	5.1
	420568	F08247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
20	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	452678	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
25	407103	AA424861	Hs.256301	hypothetical protein MGC13170	5.0
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83983	transmembrane, prostate androgen induced	4.9
30	446880	AB111807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R56784	Hs.140842	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479660	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.2255	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032987		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
45	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
	432363	AA534489		gb:mf76g11.s1 NCL CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.296039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080236	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA: cDNA DKFZp58401763 f	4.7
50	447574	AF162666	Hs.18896	tousled-like kinase 1	4.7
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zp99b10.s1 Striatogene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
55	431725	X85724	Hs.2839	Nonie disease (pseudoglioma)	4.7
	441224	AJ076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA653045	Hs.10689	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI638226	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA180000	Hs.137396	ESTs, Weakly similar to J05238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80668	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154878	KIAA0261 protein	4.7
65	420360	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132582	Hs.69757	zinc finger protein 281	4.7
	440300	N39780	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5630	4.6
	436761	AB17776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWWSNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AJ076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypol	4.5
75	407894	AJ276313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272806	putative transcription regulation, nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.26482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5



	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416855	AW988613	Hs.79428	BCI2/adenovirus E1B 19kD-interacting pro	4.4
5	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
10	417958	AA767382	Hs.193417	ESTs	4.4
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW506076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp782O076	4.4
	425810	AJ923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.3
	429269	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	met transforming oncogene (derived from	4.3
20	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW568058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
	427369	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	426055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
30	432676	AI791855		ESTs	4.2
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AJ248720	Hs.114390	ESTs	4.2
	410297	AA148710		kumikan	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430265	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW280951		ESTs	4.2
	428647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
40	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ276120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AJ355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AJ918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calcisarin-1	4.1
	407192	AA609200		gb:af12e02.s1 Soares_Jesús_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0788 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4096694, mRNA,	4.1
	449459	BE546848	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614589		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433847	AA803967	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108842	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL380204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014633	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47166	HT021	4.0
	448791	AF632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	tepin receptor	4.0
	418857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476*.g  12737279[ref]XP_012163.1]	4.0
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267686	UDP-Gal:beta-GlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW106663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240846	DKFZP434D146 protein	3.9
	432278	AL137508	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubiquitin 1	3.9
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	A1878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
5	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432852	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	A1681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	A1249502	Hs.29669	ESTs	3.8
	425910	AA830787	Hs.184760	CCAAT-box-binding transcription factor	3.8
15	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA776483	Hs.288938	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426891	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	A1186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE378758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440595	AW088363	Hs.246240	ESTs	3.8
	429586	A1871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159482	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	A1861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	ALD41465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	A1806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*HSPC213.	3.7
	420081	AW024937	Hs.28410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284182	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulon 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dvt-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
	405387			NM_022170*Homo sapiens Williams-Beuren	3.7
55	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451845	BE504066	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
60	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
	416974	AF010233	Hs.80687	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440484	BE518768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079408	Hs.38176	KIAA0606 protein; SCN Circadian Oscilla	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFRA_HUMAN SPUC	3.6
	408096	BE250162	Hs.63765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272289	Hs.121429	zinc-binding protein Rboe728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452280	AA453208	Hs.330994	RAB9, member RAB oncogene family	3.6
75	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
	427716	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17806	Hs.93584	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	A1049624	Hs.283390	ESTs, Weakly similar to 2108260A B cell	3.6
	443960	A1093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

5	428695	AJ355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.6
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gb:nc97h03.s1 NC1_CGAP_Py2 Homo sapiens	3.5
10	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
15	417183	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	448943	AW698533	Hs.181574	ESTs	3.5
	412628	AI972402	Hs.306061	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
20	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW802312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
25	436087	BE300296	Hs.5054	CG1-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty acid-Coenzyme A ligase, long-chain	3.5
	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21388	ESTs, Moderately similar to A Chain A, H	3.5
30	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW018669	Hs.29190	ESTs	3.5
35	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE816633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
40	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF181455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
45	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
	438279	AA805168	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoonCrisp	3.4
50	419749	X73808	Hs.93029	sparcosteonecin, cwcw and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
55	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14632 fis, clone OV	3.4
	452295	BE378935	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
60	439593	BE073597	Hs.124883	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
65	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412662	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.88644	Homo sapiens microsomal signal peptidase	3.3
70	426010	T18837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_018569	Hs.267182	TBX3-iso protein	3.3
75	412926	AI879076	Hs.75081	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
	408681	AW963853	Hs.282833	ESTs, Weakly similar to 138022 hypotheti	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
80	424560	AA158727	Hs.150565	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418188	AI754416		Cdc42 effector protein 3	3.3
	434629	AA769081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW380020	Hs.20416	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase 1	3.2

5	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035289	Hs.17752	phosphatidylserine-specific phospholipase	3.2
	422522	A023428	Hs.34549	ESTs, Highly similar to S84541 1 clone 4	3.2
	423396	A1382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275: Homo sapiens keratin 15 (KRT1	3.2
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA480775	Hs.6295	ESTs, Weakly similar to T17248 hypothe	3.2
	422173	BE385828	Hs.250619	phorboln-like protein MD5019	3.2
10	452099	BE612992	Hs.27831	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
	419829	A924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	405214			NM_016371: Homo sapiens hydroxysteroid (1	3.2
15	416292	AA179233	Hs.42380	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
	433213	AW685130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein M3C2771	3.2
20	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
	437179	AA393508		serologically defined colon cancer anti	3.2
	418700	A1633808	Hs.86970	ESTs, Moderately similar to ALUS_HUMAN A	3.2
	438361	AA805566	Hs.146217	Homo sapiens cDNA: FLJ23077 fs, clone L	3.2
25	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
	408739	W01555	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638: Homo sapiens hypothetical prot	3.2
30	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
	423044	AA320829	Hs.97286	protocadherin 18	3.1
	429716	R25885	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
	423551	AA327598	Hs.89633	ESTs	3.1
35	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
	413560	W03011	Hs.305881	MSTP043 protein	3.1
	431933	A187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99384	putative transmembrane protein	3.1
40	446044	AA58682		gbcl13e01.x1 NCI_CGAP_LJ24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
	421254	AK001724	Hs.102950	coat protein gamma-coo	3.1
	424339	BE257148		antibody	3.1
	446109	AF039916	Hs.12330	ecolnucleoside triphosphate diphosphohyd	3.1
45	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE181085	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	3.1
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.108534	hypothetical protein FLJ22625	3.1
	417622	AW298183	Hs.82318	WAS protein family, member 3	3.1
50	439864	AJ720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433038	AA574091	Hs.105854	ESTs	3.1
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
55	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437295	AA350994	Hs.20281	KIAA1700	3.1
	452827	AJ122843	Hs.184319	ESTs, Weakly similar to KIAA1005 protein	3.1
60	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
65	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
70	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183558	solute carrier family 1 (neutral amino a	3.0
	428657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
75	426110	NM_002913	Hs.168563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
	431416	AA532718		ESTs	3.0
	431631	AA548908	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
80	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypothe	3.0
	450937	R49131	Hs.26267	ATP-dependant Interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC057 protein	3.0

5	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
10	438209	AL120559	Hs.6111	aryl-hydrocarbon receptor nuclear transi	3.0
	434392	AW963709	Hs.250824	Homo sapiens cDNA: FLJ23436 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445586	R89543	Hs.12942	vesicle trafficking protein	3.0
15	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439880	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	3.0
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ27785 fis, clone K	3.0
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
20	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409827	T69881		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
	447681	BE620886		GCM1 (general control of amino-acyl synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
25	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
30	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447953	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43832 mucin 2 p	2.9
	429351	AK001490	Hs.200016	hypothetical protein FLJ10528	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
35	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	446911	N27605	Hs.16492	DKFZP584G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
40	430482	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
	418222	AI675881	Hs.86538	ESTs	2.9
	433009	AA761688		gb:ncz24c08.s1 NCL_CGAP_GCB1 Homo sapiens	2.9
45	432140	AK000404	Hs.272888	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
50	452258	AK000933	Hs.28861	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371049	Hs.93758	H4 histone family, member H	2.9
	409660	T08490	Hs.288969	HSCARG protein	2.9
	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
55	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AI200281	Hs.123910	ESTs, Highly similar to B34087 hypotheti	2.9
	437050	AA766420		ESTs	2.9
	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
60	416841	BE000150	Hs.48778	riban protein	2.9
	421694	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	438213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
	435823	AW749885		ESTs, Weakly similar to I38022 hypotheti	2.8
	441266	H15868	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
65	428761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp58612022 (f	2.8
	413748	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
	400860			Target Exon	2.8
	438185	AI373544	Hs.331328	Intermediate filament protein syncoilin	2.8
70	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNAR	2.8
	431604	AF176265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	436703	AW630133	Hs.83313	GK003 protein	2.8
75	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
	418196	AI745649	Hs.26548	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
80	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	415762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AI557623	Hs.119475	acid inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235518	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4616	2.8
	417517	AF001175	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266519	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
15	440080	AW051597		ESTs	2.8
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AA36124	Hs.294089	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506856	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (tr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41680	desmocollin 3	2.8
	442013	AA506476	Hs.10500	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
25	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
	419175	AW270037		KIAA0779 protein	2.8
	426788	U68816	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75380	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.80572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975053	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.296258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AI050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (tr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gbnt7895x5 NCL-OGAP_Pr3 Homo sapiens	2.7
50	409299	AA045850	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3 (tr	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T48395 hypotheti	2.7
55	408263			Eos Control	2.7
	436750	AB029012	Hs.4890	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107058	CED-5 protein	2.7
	421077	AK000081	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW208942	Hs.253594	Intron of trichorhinophthalangeal syndro	2.7
	420223	NZ7807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AI823987	Hs.182285	ESTs	2.7
	411980	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613418	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.298141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411552	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA808184	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCTAC0142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334682	hypothetical protein MGC14141	2.7
	423116	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.28630	ATP-binding cassette, sub-family A (ABC1	2.7
	431815	AW295859	Hs.235860	ESTs	2.7
5	418549	AK06485	Hs.189341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	438882	AA354489	Hs.222103	EBP50-PDZ Interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW878811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
15	441094	U33819	Hs.7647	MYC-associated zinc finger protein (pur	2.7
	451356	AA748418	Hs.164577	ESTs	2.7
	408481	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_005218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL036633		Human DNA sequence from clone RP6-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain Interacting p	2.7
	404913			NM_024408*:Homo sapiens Notch (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	UG snRNA-associated Sm-like protein LSM8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AA58179	Hs.41628	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.8551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	428797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410835	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
35	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibitor	2.6
	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297667	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420184	AW339037	Hs.24908	ESTs	2.6
	443444	AW562619	Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AI337316	Hs.147998	ESTs	2.6
	428925	NM_000786		cytochrome P450, 51 (lanosterol) 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
	417327	NM_004822	Hs.81954	SEC24 (S. cerevisiae) related gene famil	2.6
50	420937	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110248	Hs.47367	KIAA1785 protein	2.6
	434011	AW853437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL113745	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	448258	AI283476	Hs.283478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI181383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	UB3460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	426960	AW410845	Hs.164649	hypothetical protein DKFZp434H247	2.6
	458161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	455236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaap1, yeas	2.6
	416751	T48130	Hs.6897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
75	458948	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425983	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	428809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476956	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
15	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	458050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalin	2.5
	406795	AA688282	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62820	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synth	2.5
	415852	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15673	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.5
35	449500	AW556345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	418430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R08859	Hs.193172	ESTs, Weakly similar to I38022 hypotheti	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Sta-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W09856	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437782	T78028	Hs.154579	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fls, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4548	2.5
	424959	NM_005781	Hs.153537	activated p21cdc42hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [Hs	2.5
	446054	AB014537	Hs.13804	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101057	GCM5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433883	AI617723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probaset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469533 AW958465 AW953397 AA172056 BE940298 BF090208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355088 AA172236	
	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259	



449625	249224_1	B1918168 AW779780 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG986760 N45526 BG986917 T61362 R49381 R45432 A1203107 R35004 F07491 R25094 R35360	
121446	63467_1	8C021735 A1668212 A1120184 A1769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 A4934514 A151245 BF960659 AA987907 Z11449 BF908059 BF008053 BF908049 BE699424 BF908050 BF962832 BF962020 BF963134 B1035538 BF908052 BF908057 BF090025 BF943158 A1632924 BF512340 BF952021 BF980776 BF943437 BF942847 A1768015 F09778 F04816 F02721 AA102645 A1633838 AA817829 BF947001 B1035448 BE335876 AW980837 AW988604 BF957405 BF963433 BG704816 BC022980 BF224081 BG149908 AW672842 BE570687 A1702161 AW341832 BE222503 N71836 A1026081 AW953116 AW083132 A1979261 AV725377 A1423298 A1640707 AW675518 A1032611 A1818044 A1299508 A1911386 A1270418 BE219257 BM141626 AA26491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433	
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15	420218	191547_1	AW958037 R42557 A1337047 AA948360 A1638005 AA459950 A1624915 A1638047 A167856 A1521826 AA860305 A1932315 AW003082 AW271756 AW779380 AA609879 A1634791 A1493770 A1565211 Z11145 A1627952 AA303734 BE349457 AW156765 AA256527 BE089727 AL050013 BG939500 AW969191 AA769925 A1377973 A1625545 AA811385 AA521114 N24705 A1379579 AA424899 A1684671 AA829715 A1463010 N35401 AA877452 AA504340 A1209149 AA883574 A1379052 A1084455 A1280147 AA644327 BF432508 N27873 N47364 N34880 A147024 T86860 A1219716 AA960626 H25544 B1857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 A1929238 AA829886 N95742 A1218758 H25588 N36282 AA024987 N36687 B1919187 N49471 AA889870 AW166152 AA468546 A1626204 A1452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 A1016509 AW863972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108638 N49381 R49888 D81276 B1756612 AA508234 R49885 BF850422
20	438869	52134_1	AF075009 R63109 R63068
25	428342	6712_1	AK056315 A1015524 AA724079 B1713619 A1377728 AW293682 A1928140 A1092404 A1085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 A1332765 AW500888 AW676556 A1659571 AW499664 AW614573 AW829495 AW505314 W174704 A1356361 A1923640 AW070509 A1521500 A1042095 AA609309 AA781319 A1381489 H45700 AA761333 AW255424 AA908524 AA835311 AA649040 A1392620 Z40708 A1985564 AW263513 AA913892 A1693486 AW263502 A1806164 AW291137 B1081872 B1059498 AA134476 AW084688 AA036967 AW370823 T65263 B1002756 AA489664 BF827261 W74741 BF963166
30	450203	19008_1	AK056352 BG182168 BG220105 BG181659 BG188954 BG187388 BG220104 BG183714 BE645998 A1819354 AW974068 A1393635 A1580846 A1024788 AW020098 B1491127 A1393644 N74993 AW472959 BM478854 B1597437 H12165 B1458612 BE543192 BC022881 A1150944 BG750783 AW754175 AW857737 A1911659 A1050036 AA554053 A1826259 AA568548 AB033081 A1520743 BE811813 N53332 N99716 A1561910 AA280656 BE710392 AV705100 AW259378 AW444556 AA281459 A1679751 A1873695 BG700891 B1553517 R80518 BG779771 BG534451 AA794042 AW961580 BF061430 A1857643 A1768486 AW512118 AA479302 AW770384 AW072470 A1041586 A1049699 AW592855 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF353375 BE925699 AL050294 BC010371 BF882270 A1042656 BF085732 AW812618 BF085731 BG212397 BF678765 BG136692 BG398564 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 A1693720 AA743364 A1915793 N48185 A1573107 AA043474 A1351615 A1969490 A1810783 R50866 A1699181 N73808 H08164
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45	407819	7392_2	AK056628 A1800898 BF939022 BE447118 A1954754 BE218177 BE348557 A1852405 AW293122 A1988798 A1457321 BE327228 BG913531 AW939055 T30280 R54466 Z43386 BG919163 BF003119 BE546274 BF940881 R18246 R42185
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55	422890	61426_1	AK057805 AW162343 A1190479 A1083318 BE048820 A1196397 AA654667 BE218303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964438 AW004030 A1632656 BE602530 B1792363 BF058928 AA449241 A1651825 AA805324 A1264883 AW196918 AA948257 A1953736 A1263703 BF056387 AW594711 A1867447 AA319159 A1903440 AW958110 A1366013 A1867923 BG911906 D81142 C15616 AL536697 Z25032 Z43784 R13382 AV745924 AA449368 AA318816 BF964265 H17038 H10084 F04161 T87230 R40898 AW204071 B1819428 AA683393 AA683376 Z43182 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
60	451752	10408_5	AB032987 A1141678 AW978722 BE467119 A1761408 BF727385 AW237035 A1934521 BF436248 A1479668 Z40632 AA832081 AW295801 BF057835 BE465977 A1621269 BE465983 BF766369 N74056 A1817895 AA716587 A1934774 H82600 H09497 BF943762 BE395335 BE883333 AW970240 AA534488 AW970323
65	432363	1234917_1	AA196390 AA507837 A1196468
70	417379	1610005_1	BG107484 AA632009 AA32670 A1656650 A1650884 A1521919 A1264653 AW150793 AW611894 A1917098 B1091245 A1651454 BF434889 A1580286 A1880735 BE301995 A1392959 AW613965 BM023628 AW515374 A1480102 BM023318 BE328188 A1952820 A181383 AA557165 A1695677 A1582079 A1700926 A1700561 BF063058 AW196367 A132984 B1054046 A1870157 R02122 H55924 A1521721 AA808206 AA725223 A1768003 AW339821 AA805951 A1287969 AW654827
75	419733	7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE846183 BM126230 AW044233 A1951970 AW663548 A1139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW108870 BE706664 BE709539 BE153177 BF084925 AL133779 AW951788 AA658688 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710738 BF687723 H28581 AA249370 BF726698 BE841554 B1045059 T84625 AW128678 BG770826
80	447820	687223_1	AW973834 A1791932 A1791855 A1732640 AA558833 AA599897 A1821610
	407192	2200202_1	BC013939 B1494690 B1491211 A1928393 AA843640 BG938644 A1185628 B1495842 AW173256 BM052709 A1743999 A1690144 A1922209 A1740907 AW340368 AA828758 AW118737 BF513970 AA707807 BF436296 A1339463 A1373842 A1433808 BE222392 AA602308 AA428261 A1460365 AW682760 A1888087 A1342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 A1150479 A1018168 AA779515 AA661791 BM474307 B1911169 BG575154 AW953303 T33604 D69141 AA385785 AA148848 BM461981 BG681169 B1602483 BE889592 AW954311 BM052986 B1962893 A1889299 Z42328 BF029504 T35668 BG402802 A1918770 A1023271 AA177119 A1434079 A1589000 A1276488 AA992453 AA342821 AA848303 A1349364 A1051008 AA925941 AA350894 AW071451 N22249 A1784138 AA083847 N22258 AW440825 AA661570 AA376687 AA669125 A1356239 R70463 A1383588 AA827189 B1494872 AW021094 B1494871 AA905500 AA460823 A1482041 AW028965 A1626411 BG271780 A1497723 H88862 D58858 N89979 AA658425 N81154 D62341 A1274437 N66697 H96993 A1370663 AA728850 H05232 R59374 H12223 A1935759 A1562553 D8006 N29572 A1916833 N75273 AA148710 B1597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG823469 AA452342 AW965441 W19723 R32966 BE883841 R81003 A1910374 A1865262 R56325 A1468827 R34681 H96211 Z39807 BF954386
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	434194	62680_1	AA602964 AA809200
	448653	16112_4	AF119847 AA437261 AA436987 A1132965
	429163	1238297_1	BE868763 AA659765 A1961658 A1520818 AA761743 AA261477 N66431 BE463652 AA281329 AW272944 AA058687 BM145087 AA045516 AW341820 AA112515 AA258786 A1866593 AA714133 AA768245 AA035533 AA530459 T20165 AW971268 BE965269 AA522722 AW974271 AA592975 AA447312 AA884766



			AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 A1334004 BF057178 A1857450 A1341191 A1634143 A1917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 A1580157 A1364363 AW242357 AW235291 N56645 AA319869 R36911 AA256551 AW044186 A1203159 N49403 F02090 A187299 A1609644 Z40516 AW852314
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10	441128	20932_1	A1041403 Z49148 AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 B1917678 BG819395 BG911971 BG820167 A1174254 AA348720 AA364503 BG714279 AW993230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 A1563737 BG022908 W52892 A1395658 BE551237 AA283724 BF109530 A1457096 A1085992 BE467736 AA693467 A1697583 A1887863 A1167419 AW801980 AW901788 BE702179 AA484549 Z23811 BE327043 AA716027 AA917004 AA167714 BF338675 AA084618 A418634 T31586 AA436630 A1368472 AA706191 A1422304 A1204899 A041169 AA211402 AW827081 A1788593 T32736 A1767935 AA747914 T09634 AW959843 A1119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60900 N79908 D52685 T07735 BE702069 BE702172 T08671 BE767112 BE767113
15	406789 410099	Q_0 16732_1	AA658826 A1821926 A1791191 AA635129 AA564482 Z11692 X51466 NM_001061 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE868804 B1868669 BG337216 AW629935 BMD16525 A1580409 AL582866 A1909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF868862 BG998348 B1011834 BF888337 BF898627 BF092380 AW803216 F01241 BF805718 BG876487 AW498536 BF988666 BG998849 AA248724 BG829202 BG756456 BG032392 B1859287 BMD16990 BG332369 BE933685 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569847 BF154671 BMD07368 BF569385 BE772007 B1199487 BF761700 B1261519 BF944452 BF888506 A1038390 BMD44934 AW381142 BG743618 BE769206 BE893973 B1015047 BF886479 BF761350 BE769789 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 B1000274 BG255503 BG874499 BG774174 B1015084
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25	445836	8561_5	NZ7807 AA258634 BE276324 AF263306 BF951698 T66089 F11794 H29379 R19493 H18042 AL133995 AW134660 A1299437 AA057405 AA817450 A1002692 T09262 R43839 H29280 T66008 N78357 A1221207 A1659856 AA013581 A1220302
30	441606	10026_3	NM_000786 U23942 B1601050 BG771947 BG773455 B1581558 B1480208 BG714348 BM126447 AU129411 AU129401 AL119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149681 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 A1217688 AA399409 BE182318 BM128040 A1899988 AW616411 AW070426 AL124550 AW778736 AA477781 AW263013 A459819 AA860513 BF809648 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 B1918393 BM470755 B1332311 AA095636 B1256415 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H47580 R48658 T91611 H42019 B1889421 BG502073 BG425943 W37220 W31363 BE004451 BF208311 B1048717 N78122 AA228597 A1525334
35	420223 423476	191648_1 32437_1	A1953821 AA657925 AA935436 AW976088 BC000222 AL136871 NM_032261 BC008497 BM461705 BG470749 BG826905 BG285127 B1253235 BE397026 BG704967 AW961225 BM352817 B1227161 BG820180 AA454463 AA256885 N31549 AA326504 BC019924 BG257230 B1082368 B1869896 BG251883 BF034444 BC286577 BE260391 AA599912 BF666779 A1755222 W24241 A10156565 F28259 T16319 AA362506 N64153 BMD16416 BM458863 BG739972 AV729565 BE288285 BE867433 BMD11110 BG285856 A1922439 BE270975 AL119339 BF959085 A1565178 AL554305 AL573240 AL572817 A129627 AL548640 BE392285 A092843 A1371057 BE302410 A1087653 AW874261 A1750057 A1052649 N47822 AL516249 A1589903 BG258439 A123662 A126014 AA778101 AA243218 AW498837 A4748311 A1754395 T15728 AA776369 AA858195 W73625 AA216784 AW513778 AW243958 A051112 A1783806 AL569622 A070466 BF229336 N58159 H80288 N32598 H02893 H0279 AL581253 AW571884 A1361698 AW073321 AA878464 H95640 T34421 AA331419 N59897 H0274 B126120 AA205826 AA070716 AA653206 AA653483 BG388811 W20432 AA670295 AA653197 D51888 AA382527 BG056668 AW118162 AW073071 BE293888 BF792321 BF792258 BG107176 T66604 BM193556 H03238 AA818045 AA908004 B1086886 AA664566 A1221630 D52045 C14510 AA029390 W60153 H88743 A1882641 H28485 AA723093 A1081730 AA641309 AA687083 B1224818 AW204722 A1309186 A1216122 A1200785 BE457373 BM352502 A104440 A1193071 A1742463 AW003408 A1400201 A1585740 A1474637 A1284448 A1699509 BE704420 AA989278 AA918266 AA830866 AA989425 AA911829 AA282588 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94853 N69544 AA181782 D20132 T55734 T60692 R76888 AA022948 AW770291 R50934 AA206816 R97811 H40328 R85252 AA936029 A1813809 AA933607 AA129695 AA548261 AA714393 AA776006 AA853439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51695 D55942 D52740 A1000118 AL516304 AL534258 N54940 AL579194 A1689399 A1342925 BE938201 AA633000 B1222963 A1619676 AW190306 BF035010 AW087897 A1864989 T57243 R48211 AA113880 R26594 C14467 C14444 A184549 BE896346 BE270780 AL580073 BG389833 BE891549 B1223147 AW381001 AA448464 AW709744 AA412194 AA848107 AA927157 AA883841 BF752671 BE731304 A1380443 A1240179 AA877516 AA884643 AW079380 AW294316 A1913755 A1884320 A1685770 H25135 A1972654 A1538592 A174783 R12271 R83569 A1274757 A1559500 AW022182
40	441064 429925	2641490_1 33135_1	AW970134 AA516420 AA543007 BG057526 B1001430 A1498371 D50181 D81004 D60382 C16876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656
45	434976 440191	121716_1 MH790_2	Z11692 X51466 NM_001061 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE868804 B1868669 BG337216 AW629935 BMD16525 A1580409 AL582866 A1909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF868862 BG998348 B1011834 BF888337 BF898627 BF092380 AW803216 F01241 BF805718 BG876487 AW498536 BF988666 BG998849 AA248724 BG829202 BG756456 BG032392 B1859287 BMD16990 BG332369 BE933685 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569847 BF154671 BMD07368 BF569385 BE772007 B1199487 BF761700 B1261519 BF944452 BF888506 A1038390 BMD44934 AW381142 BG743618 BE769206 BE893973 B1015047 BF886479 BF761350 BE769789 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 B1000274 BG255503 BG874499 BG774174 B1015084
50			
55			
60			
65	440409 444810 446091 431843	586375_1 2145282_1 519091_1 445334_1	
70	400262	18977_1	
75			
80			

TABLE 88C

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.  
 Nt\_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	403047	3540153	Minus	59793-59968
	401424	8176894	Plus	24223-24428
	401451	6634068	Minus	119926-121272
10	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	404632	9796868	Plus	45095-45229
	403046	3540153	Minus	55707-55859,56369-56511
	404922	7341893	Plus	13248-13428
	401519	6649315	Plus	157315-157950
15	401197	9719706	Plus	176341-176452
	401866	8018106	Plus	73126-73623
	405387	6587915	Minus	3769-3833,5708-5895
	403752	7678857	Plus	33704-33828
	404210	5006246	Plus	169926-170121
20	401785	7249190	Minus	165778-165996,166189-166314,166408-16656
	406214	7342036	Plus	86320-86523
	403632	8076842	Minus	81750-81901
	400860	9757499	Minus	151830-152104,152649-152744
	404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number  
 ExAccn: Exemplar Accession number, Genbank accession number  
 UnigeneID: Unigene number  
 Unigene Title: Unigene gene title  
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	424806	AA382523	Hs.105689	MSTP031 protein	1.51
	418036	Z37978	Hs.83337	latent transforming growth factor beta b	1.94
45	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet	1.60
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
	417944	AJ077198	Hs.82885	collagen, type V, alpha 2	1.48
	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
	452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.89
50	425139	AW630488	Hs.25338	protease, serine, 23	1.63
	402483			NM_014624: Homo sapiens S100 calcium-bind	1.50
	423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
	412568	AJ878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
	419948	AB041035	Hs.93947	NM_016831: Homo sapiens NADPH oxidase 4 (	2.08
55	447526	AL048763	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
	448500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
	441457	AW986651	Hs.43838	ESTs	1.30
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
	418994	AA298520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
60	413795	AL040178	Hs.142003	ESTs	1.64
	441689	AI123705	Hs.289068	ESTs	1.44
	412567	AJ750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
	424432	AB037821	Hs.146858	protocadherin 10	1.65
	432673	AB028859	Hs.278805	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
65	418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
	453085	AW854243		KIAA0251 protein	1.47
	438887	R68867	Hs.265499	ESTs	1.49
	436729	BE621807		transmembrane 4 superfamily member 1	1.91
	400494			ENSP00000238970:CIG30 (Fragment).	1.34
70	442506	BE366411		ESTs	1.54
	425023	AW956889	Hs.154210	endothelial differentiation, sphingolip	1.55
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	2.65
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
	422389	AF240635	Hs.115897	protocadherin 12	1.38
75	417124	BE122762	Hs.25338	ESTs	2.13
	433681	AJ004377	Hs.200350	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
	419963	W55955	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
	450534	AJ570189	Hs.25132	KIAA0470 gene product	1.43
80	449618	AJ076459	Hs.15978	KIAA1272 protein	1.42
	446098	AW072215	Hs.208470	ESTs	1.53
	413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
	448574	W31178	Hs.154140	ovary-specific acidic protein	1.47
	407061	X97748		gb:Haapiens PTX3 gene promoter region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628617	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.82
	401234			mitogen-activated protein kinase 8 Inter	1.48
	420174	AI824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.289592	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
15	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA168022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	446119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF161073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1962 protein (Homo sapien	1.78
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	425828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T69538		gb:gb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AI821409	Hs.304471	EST	1.45
40	429113	D28235	Hs.195384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.62
	453983	HS4997	Hs.16450	ESTs	1.94
45	406506			Target Exon	1.97
	424603	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW560899	Hs.97199	complement component C1q receptor	2.36
	426596	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452870	Hs.239527	ETB-55kDa-associated protein 5	1.41
50	450152	AI138635	Hs.22968	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptotagmin 2	1.61
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407882	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412584	X83703		cardiac ankyrin repeat protein	1.51
	414786	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiotensin-2	1.91
	405627	T64904	Hs.163780	ESTs	1.78
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
70	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.85
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478766	Hs.184477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL035658	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.78067	MAD (mothers against decapentaplegic, Dr	1.71
	450589	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412765	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000262	Hs.169758	hypothetical protein FLJ20245	1.81
	456977	AK000262	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	1.74
	444409	AI792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1359	decay accelerating factor for complement	1.74
5	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AI380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	418940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AI834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453457	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219691	Hs.73625	RAB8 interacting, kinesin-like (rakines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.59
	405121			mitogen-activated protein kinase 8 inter	2.98
30	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AI878857	Hs.108706	hematological and neurological expressed	1.65
	408669	AI93591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	418815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA160797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.33
45	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
	432128	AA127221	Hs.298502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439285	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
50	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to 841044 chromosom	2.37
	442573	H93366	Hs.7587	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE260074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422803	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
	406954	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AI701916	Hs.202509	ESTs	2.27
	409989	AW381666	Hs.49500	KIAA0746 protein	1.43
60	429653	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW386633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418186	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	XB9426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400668			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288767	v-rel simian leukemia viral oncogene hom	2.25
	413132	NM_008823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
70	451979	FD6972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	416138	C18355	Hs.295844	tissue factor pathway inhibitor 2	3.11
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI697655	Hs.49265	ESTs	3.08
	422424	AI186431	Hs.296538	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B

Pkey: Unique Eos probasel identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI339138 AI273442 AW102617 AA831177 AA745642 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI026328 AI298436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AI445481 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 AI494958 AA088439 AA708057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI795814 AA129575 AI671727 AM70033 BE648195 AW779726 AA903050 AA147228 AA404570 AI075878 W38161 AI927239 AW673152 AA723200 C06123 BF057147 AAG27688 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823468 AA562397 AA135658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692848 AI061086 H80983 F79933 AI950693 AI245632 AI349380 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872828 AI927217 AI453453 AI189366 AW338678 AI261369 AI500576 BF477735 AK032569 AI972899 AI985583 Z28771 AI353829 AI693030 AA603566 BE773488 AW339301 BE773489 BE773482 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI585439 AI918453 AI472527 AA46740 AA035576 AA191414 AW674145 C05782 AI589264 D67658 AI468237 AI432033 AA989682 R21752 BF002457 AA988297 AL574085 AI576200 AL571074 AL574525 AL578810 BC498381 AI282364 BE879732 AA479934 AA479712 CT17732 BM091258 BF843901 AW620230 C17476 BE327120 AA129574 AA136645 BF843900 AW805193 AA502832 AA549494 AI688520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377598 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE814379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI246307 BE773483 AI567995 W60075 BF941183 AI738944 BE811458 BE773481 AI262930 AA948565 BE706942 BE156380 T65026 AW242658 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE521857 BE156280 AA454099 AA037722 BF843897 AW805183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE166214 AA190427 T91762 AA035067 AA837326 T10930 BF908587 BI755027 BG056731 BC008442 BC010166 AI550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118527 AL601379 BI259821 BG741786 BI888522 AU135868 BI552770 BI259210 BI255620 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF891383 BG721129 BG541678 BE906666 BG761068 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392485 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088644 AI815867 BG528531 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA378800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343759 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF822148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA653496 AA360401 AW955168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882 AA166151 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 XB3703 NM_014391 BC018667 AU139209 BE924924 BE824899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA989184 BE924898 BF229086 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943778 AA488072 AA488364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787
442506	29197_1	TABLE 69C Pkey: Unique number corresponding to an Eos probaset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. Nt_position: Indicates nucleotide positions of predicted exons.
436772	1239464_1	Pkey Ref Strand Nt_position 402463 9795895 Minus 8818-8952 400494 9714719 Plus 169845-170272 401234 9926542 Plus 120173-120337 406506 7711374 Minus 6843-8077 405025 7107727 Plus 105267-105343,106184-106294,106387-10653 405121 8102330 Minus 35816-36004,36587-36684 400666 8118496 Plus 17982-18115,20297-20456
442006	1238046_1	TABLE 70A: Pkey: Unique Eos probaset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigenelD: Unigene number Unigena Title: Unigene gene title R1: Ratio of the mean of the vessel A1's to the mean of the HUVEC A1's
428928	BE408838	UnigenelD Unigena Title R1 Hs.194857 cadherin 1, type 1, E-cadherin (epitheli
439180	A1393742	Hs.195057 v-erb-b2 avian erythroblastic leukemia v
412636	NM_004415	desmoplakin (DPI, DPL)
428158	NM_001982	Hs.199087 v-erb-b2 avian erythroblastic leukemia v
414320	U13816	Hs.75893 ankyrin 3, node of Ranvier (ankyrin G)
417878	U90916	Hs.82845 Homo sapiens cDNA: FLJ21830 fs, clone H
414572	AU077174	Hs.288181 cathepsin H
415314	N88802	Hs.5422 glycoprotein M6B
431103	M57389	Hs.44 pleiotrophin (heparin binding growth fac
408973	M34896	Hs.198253 major histocompatibility complex, class
456974	M12529	Hs.169401 apolipoprotein E
430560	Z28942	Hs.243960 N-myc downstream-regulated gene 2
406828	AA419202	Hs.84298 CD74 antigen (invariant polypeptide of m
422048	NM_012445	Hs.288125 spordin 2, extracellular matrix protein

5	406826	AW516005	Hs.84298	CD74 antigen (Invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AJ232328	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
	406824	AW516981	Hs.84298	CD74 antigen (Invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	2.17
10	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.28
	446945	AI93115	Hs.16611	tumor protein D52-like 1	2.27
	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
	427451	AI690816	Hs.178137	transducer of ERBB2, 1	2.31
15	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	2.38
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.39
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415894	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
20	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23166 fls, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB class II histocompatib	2.51
25	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (	2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
30	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	pB protein (candidate of metastasis 1)	2.62
	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylphosphatase amidohydrolase (acid c	2.63
35	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AI684911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410577	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
	452685	AI634851	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXRD domain-containing ion transport reg	2.73
40	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453787	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24396	small inducible cytokine subfamily B (Cy	2.86
45	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plekophlin 4	2.94
	428123	AB011099	Hs.196847	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fls, clone NT	3.01
50	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fls, clone L	3.01
	425622	AW390847	Hs.18578	ESTs	3.01
	420195	W4348	Hs.251385	Homo sapiens cDNA FLJ11177 fls, clone PL	3.04
	445584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	AI827976	Hs.24391	hypothetical protein FLJ13512	3.06
55	423815	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	caldesmon 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
	414940	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	3.14
	424651	AW93208		ESTs	3.17
60	443932	AW688222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
	421834	BE543205	Hs.288771	DKFZF586A0522 protein	3.20
	423961	D13666	Hs.136348	periostin (OSF-2os)	3.24
65	447384	AI377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.25
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
70	410132	NM_003460	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	Indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipin)	3.29
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	AI081195	Hs.65029	growth arrest-specific 1	3.35
75	451529	AI917901	Hs.208641	ESTs	3.36
	430310	U60115	Hs.235069	four and a half LIM domains 1	3.37
	424997	D63216	Hs.153684	fizzled-related protein	3.37
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
80	421913	AI934385	Hs.108439	osteoglycin (osteoclast-inductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fls, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
	407938	AA905087	Hs.85050	phospholamban	3.48
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L35531	Hs.91295	integrin, alpha 8	3.52
	404277			NM_019111*Homo sapiens major histocompa	3.54



5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (poussin)	3.64
	447111	AJ017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV857778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (mdulin)	3.86
	428957	NM_003861	Hs.194679	WNT1 inducible signaling pathway protein	3.89
15	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82225	glycoprotein (transmembrane) numb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
	449925	AJ342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
20	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245168	tissue inhibitor of metalloproteinase 3	4.09
	418223	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.6944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW939251	Hs.25847	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78085	complement component 7	4.37
30	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22887	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI588801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276853	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416794	AA334592	Hs.79914	tumican	5.20
45	453356	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.85
	430223	NM_002514	Hs.235835	nephroblastoma overexpressed gene	5.87
	416585	X54182	Hs.79385	leiomyodin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426405	AI742501	Hs.189756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (nast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
60	412636	1438_1
65		M77830 NM_004415 AF139085 BG681115 BG740377 B1712954 BG000856 AA128470 BM438324 H27408 BE316330 BE167165 AW370827
		AW370813 J05211 BG68865 BG740734 BG680618 BG739778 B1705807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592
		BE182184 BF149266 BE940187 BE060445 BE060444 BF360983 BE720095 BE720089 BE715154 BE082584 BE082578 BE004047 AA857316
		BI039774 BE713818 BE713548 AW170253 BE160433 BI039776 AW888475 BM462504 BE931734 BF149284 AA340777 BF381183 BG621737
		AU127260 AW364859 BF983352 BG223489 BE819009 BF381184 BE715956 R68704 AA852212 AW366566 BI090356 BF087707 BE819046
		BE819005 AA377127 BE073467 BE819069 BE819048 BI036308 BG990973 BI040954 BF199111 AU140165 AI851768 AI434518 AW804874
		BF752969 BE637009 BE925826 BF149265 AW995815 BE814264 BI039782 AU140407 BE144243 BE709883 BF085642 BE001923 BF933510
		AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873579 AW178000 BE082526 BF476868 BF086594 BF592276
		BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813830 BE002030 AW365153 BE184941 BF749421
		BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE155646 BE714632 BE184948 BG886845
		AA131128 AA099891 W39488 C04715 BF096124 BE88341 AW799304 AI803116 BE149760 BE705967 BE705966 BE705968 AW848723
		AW376699 AW376817 AW376697 BG005097 BF761115 BE688084 AW848371 AW376782 AW848789 AW849074 AW381413 BF927725 BF094211
		AW997139 BE865474 BE185187 BE156621 BE715089 BE713287 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599
		BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831180 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583
		AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU158919 AI760816 BF082516
75		AI439101 AA451923 AI340326 AI590975 BI791653 AI700963 AI142882 AA039975 AA946936 AA544381 BM344884 AA702424 AI417812
		AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI345078 W95070 AA149191 AA026864 AI830049 AW780435
		AI078449 AI819984 AI858282 BI468588 AI860684 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI827207
		AI205263 BF082491 AW021347 AI588096 BE938862 AA088888 D12062 AA066527 AA782109 W19287 W02156 AW150038 AA022701 T87181
		HA4405 AI910434 BF082513 AI494069 AI270027 AI35878 AI128330 BG681425 BE708078 R20904 BG880058 BG676647 BF764409 AA026654
80		AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW798118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320
		AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686889 AI588892 AI915596 AW105614 AI887258 AI536577 BE926474
		BE067737 BG319486 AA247685 AW798883 AW103621 BF989173 AW880878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763
		BG950164 BE713810 AW365151 BG955489 BE006272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679408

5	454042	30254_1	BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705959 BG877157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI068659 BE813665 W95048 W25458 AW177788 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284080 BE664323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF878726 H90899 AW365145 W38382 AI498487 AJ420458 AI018523 AA708686 BF949633 AL119553 BF945960 AI081305 AA041432 AI821013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF963052 H45928 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549781 R63955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358884 AW137298 AI366488 N64360 AA779107 AW025989 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494438 BF856114 H22570 AW954381 BG007409 BM314056 AA465642 T30881 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 AI267360 N64249 W67500 F07962 AA322394 BI489987 BE644865 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BI141766 AI742325 AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648364 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383 AI694152 AA226536 BE467282 N47808 BE348825 BE830561 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280 BG435302 BM083687 AA904035 AA488889 W76175 AA761874 H28767 AA910081 AA837086 AI521825 BG986378 AI478562 AA743152 AA746092 H88863 BG986375 AA635644 AI493206 AA699979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495
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## TABLE 70C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404277	1834459	Minus	91655-91946

## TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	75th percentile of ewing sarcoma to 85th percentile of body map

  

Pkey	ExAccn	UnigeneID	Unigene Title	R1
104659	AW968769	Hs.105201	ESTs	70.3
101447	M21305		gtxHuman alpha satellite and satellite 3	64.7
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
101104	AW882258	Hs.169268	neuropeptide Y receptor Y1	48.8
110278	AF061573	Hs.19452	protocadherin 8	46.1
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
116752	AL008683	Hs.91622	neuronal pentadactin receptor	40.9
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9
110728	AA737106	Hs.32250	ESTs, Moderately similar to T78885 serin	35.5
121362	AF060147	Hs.97932	chondromodulin 1 precursor	34.7
131291	NM_004350	Hs.170019	nunt-related transcription factor 3	33.0
101063	D54745	Hs.80247	cholecystokinin	31.7
121619	AA528339	Hs.178052	ESTs, Weakly similar to phosphatidyseri	28.7
122651	AW975398	Hs.293836	ESTs	28.0
100299	D49483	Hs.2171	growth differentiation factor 10	26.5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2
123619	AA802984		gban07c02.s1 NCL CGAP_Pt2 Homo sapiens	26.1
124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	23.1
116301	AW968706	Hs.293332	ESTs	22.6
121231	AA814948	Hs.98343	ESTs, Weakly similar to ALUC_HUMAN IIII	22.3
106533	AL134708	Hs.145998	ESTs	22.3
109166	AA219581	Hs.73625	RAB6 interacting, kinesin-like (retikines	21.3
131313	RS6250	Hs.75874	ribosomal protein L44	20.8
116790	AW181357		microtubule-associated protein tau	18.7
105316	AI671245	Hs.24835	hypothetical protein FLJ14594	18.2
102123	NM_001809	Hs.1594	centromere protein A (17kD)	17.8
126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	17.8
119791	AA554907	Hs.58291	ESTs	16.7
113003	AW282315	Hs.7215	ESTs	16.3
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
126799	AW753865	Hs.74376	olfactomedin related ER localized protei	16.3
105298	BE387780	Hs.28369	hypothetical protein FLJ20287	15.5
107160	AA314480	Hs.27669	KIAA1563 protein	14.8
115313	AA808001	Hs.184411	albumin	14.6
123308	C14187	Hs.103538	ESTs	14.2

	126077	M7B772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	108821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
5	110288	H40665	Hs.31564	ESTs	13.8
	106498	AJ221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;calyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	126639	AW582562	Hs.102897	CGL-47 protein	13.2
10	125598	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119458	AA248897	Hs.48784	ESTs	12.2
	135155	AJ207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
15	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
	132988	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
20	104988	AJ249502	Hs.29669	ESTs	11.1
	123532	AA608733		gb:ae56106.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125558	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
25	123049	BE047880	Hs.211859	diclkopf (Xenopus laevis) homolog 2	10.6
	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein Interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
30	110730	N67655	Hs.26411	ESTs	10.3
	119186	A979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (Importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133161	X91662	Hs.86744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000026	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA467211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22895	9.6
	106148	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.6
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AJ204600	Hs.96978	hypothetical protein MGC10784	9.2
	130625	AF176012	Hs.280720	J domain containing protein 1	9.2
	129756	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247629	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	A940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA882257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-link	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	A085153	Hs.143764	ESTs, Weakly similar to unknown ji.sapie	8.8
55	113903	AJ368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159158	protocadherin 11	8.5
	130298	A1347487	Hs.132761	class II cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106576	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119498	AJ918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244830	Hs.166895	ESTs	8.0
70	107088	AJ823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894538	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, act	7.9
75	133083	AJ654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	105730	AW377314	Hs.6364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82285	phosphatidylglycerol kinase formyltransfer	7.8
	115082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP566D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AJ608657	Hs.95097	ESTs	7.7
	129075	BE250182	Hs.83765	dihydrofolate reductase	7.6

5	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypothet	7.6
	132438	AW363587	Hs.82916	chaperonin containing TCP1, subunit 6A (	7.6
	118036	AA71882	Hs.196008	Homo sapiens cDNA FLJ11723 fls, clone HE	7.6
	131170	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
10	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE588452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
15	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked mol	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
20	110458	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gb:nc06a07.s1 NCL CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc06a07.r1 NCL CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 fami	7.0
25	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	NA5018	Hs.8769	hypothetical protein DKFZp781J17121	6.9
	118013	AI674128	Hs.94031	ESTs	6.9
	120147	AI917116		hemoglobin, beta	6.8
30	118257	N34905	Hs.44853	Homo sapiens cDNA: FLJ22668 fls, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195551		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
35	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIC, polyp	6.6
	121553	AA412468	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
40	115197	R18858		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	125967	AA205876		gb:cg48a10.r1 Stragene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
45	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fls, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
50	115844	AI373082	Hs.332938	hypothetical protein MGC5370	6.3
	121886	AA934683	Hs.96467	ESTs, Highly similar to AF257737 1 clla	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
55	106383	AA447453	Hs.27860	Homo sapiens mRNA: cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fls, clone PL	6.1
	114357	R41877	Hs.6107	Homo sapiens cDNA FLJ14839 fls, clone OV	6.1
60	128501	AL133572	Hs.196009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-53015	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
65	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121850	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypothet	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:bj32h01.s1 Soares placenta Nb2HP Homo	5.9
	115822	AI088601	Hs.208414	Homo sapiens mRNA: cDNA DKFZp564D0472 (f	5.8
70	122969	AW821262	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28853	ESTs	5.8
	114208	AL049468	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
75	129300	W94187	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01656	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
80	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI488004	Hs.278958	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
	102745	AW763865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gb:yx98h12.e1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
5	100439	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	R49390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone FL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
15	131185	BE280074	Hs.23960	cyclin B1	5.4
	111227	T05701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
20	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
	115121	AI634549	Hs.325422	ESTs	5.3
	125484	N71807		gb:yz29d09.r1 Soares multiple sclerosis	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4288026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (	5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040684	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	NA1367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	5.2
30	120830	AI568170	Hs.96896	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (	5.2
	103318	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49183	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3882	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW181885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
40	110799	A089860	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW976988	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102827	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	118814	H50834	Hs.77899	gb:yp88a10.s1 Soares fetal liver spleen	5.0
50	130622	AI582291	Hs.16846	ESTs, Weakly similar to C4H1UD1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA071146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU28	4.9
	120484	AA253170	Hs.98473	EST	4.9
55	114618	AW163257	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.8
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 sarineth	4.9
	124648	AA248086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fs, clone H	4.9
	130637	AA356764	Hs.17109	Integral membrane protein 2A	4.8
	125769	AA083456		gb:zn05g08.r1 Stratagene hNT neuron (937	4.8
	128086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100168	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D83218	Hs.153684	fizzled-related protein	4.8
	109260	AW878615	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H88261	Hs.40568	ESTs	4.8
70	126802	AW805510	Hs.97056	hypothetical protein FLJ21834	4.8
	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129708	AA443241		ribosomal protein L44	4.7
	128588	N30435	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL096739	Hs.107260	hypothetical protein DKFZp586I0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF294887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW362149	Hs.102314	ESTs	4.7
	128521	AI475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.8
	102963	X02404	Hs.274534	calthionin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

5	113974	AW959756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743503	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.148377	hypothetical protein DKFZp761L0424	4.6
10	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependant kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
15	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33458 hypotheti	4.5
	104912	AAB13192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
20	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
	106489	AA452054	Hs.118339	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
25	112651	AA585802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
30	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334642	tubulin alpha 1	4.4
	127498	AI031650		ESTs	4.4
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA, seque	4.4
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
35	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
	115167	AA749209	Hs.43728	hypothetical protein	4.3
40	102407	AW802154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PR00659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
	103616	NM_002847	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
45	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	136098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
	133571	BE515037	Hs.177956	melanoma antigen, family D, 1	4.3
	106248	AL036917	Hs.288821	KIAA1638 protein	4.3
50	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
	129550	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
55	108073	AL157441	Hs.17634	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankryn-rela	4.2
	118041	AA252457	Hs.88543	ESTs, Moderately similar to T00258 hypot	4.2
60	106012	AI240685		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130632	AW838005	Hs.20082	zinc finger protein 3 (A8-51)	4.2
	125960	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
65	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-IRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101286	L36845	Hs.73964	EphA4	4.2
70	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to 6	4.1
	118133	AW448597	Hs.913652	EST, Weakly similar to I38022 hypotheti	4.1
	128001	AA443323	Hs.107812	BPOZ protein	4.1
75	119271	AI081118	Hs.85328	Fanconi anemia, complementation group F	4.1
	114767	AI858865	Hs.154443	minichromosome maintenance deficient (S,	4.1
	126107	H75477	Hs.93361	ESTs	4.1
	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
80	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
	129948	AI537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW068276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AK038201	Hs.283316	ESTs	4.1

	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retroviru	4.0
	127153	AI732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
5	124105	H11484	Hs.79133	ESTs	4.0
	100031			AFFX control - DepX-M	4.0
	106997	AF038023	Hs.167495	RAM binding protein 6	4.0
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
10	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.0
	126985	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.0
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	116751	N74210	Hs.50454	ESTs	4.0
15	128797	NM_002975	Hs.105927	stem cell growth factor, lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
	116676	N45312	Hs.48506	ESTs	4.0
	107348	AW973763	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
20	115652	BE083589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M62843	Hs.76236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gbcy54c08.s1 Soares_multiple_sclerosis_	4.0
25	126522	W31912	Hs.21168	gbzcd76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
	102507	U62164	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
30	105908	AI133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112896	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
35	118967	A568670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U25725	Hs.3080	mitogen-activated protein kinase 7	3.9
40	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AJ077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	3.9
	131971	BE567109	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179969	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.105965	ESTs	3.9
45	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149868	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
50	106476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
	122682	AA884531	Hs.159293	ESTs	3.8
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
55	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gbzbd80d09.s1 Soares_senescent_fibroblas	3.8
	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H80720	Hs.81892	KIAA0101 gene product	3.8
60	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA256674	Hs.77494	deoxyguanosine kinase	3.8
65	127282	AA828125		gbzcd71a08.s1 NCL_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UL-H-BI3-sla-a-12-O-ULs1 NCL_CGAP_Su	3.7
	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
70	116203	AW137166	Hs.87305	ESTs	3.7
	123377	AW988183	Hs.271297	ESTs	3.7
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123854	PCF11p homolog	3.7
75	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
	126708	AW962593	Hs.136280	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
80	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434F0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109250A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W98141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
	103163	AU077018	Hs.3235	kerafin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	A1300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB036598	Hs.150587	Winesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	141118	F01598	Hs.176930	ESTs	3.6
15	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.6
	125174	W61835	Hs.231082	EST	3.6
	104799	AA029703		gb:ze95n08.s1 Soares fetal_heart_NbHH-119W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X18868	Hs.333497	cytochrome P450, subfamily 1D (debrisoq	3.6
20	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113998	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AF738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	116691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23626	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zr82n12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50861	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AI484372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE181065	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:zh16c10.r1 Soares Infant brain 1NIB H	3.5
	117265	AA451966		RA89-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
45	109482	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117813	AW028607	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc68d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like protein	3.5
	118443	AW982198	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fs, clone HE	3.5
	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	Insulin receptor substrate 2	3.5
	111223	AA652773	Hs.334838	KIAA1886 protein	3.5
60	104867	AI920802	Hs.19058	ESTs, Moderately similar to 585657 alpha	3.5
	105395	AI580880	Hs.288149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504683	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	105367	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94683		gb:H.sapiens dbbactbp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fs, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp596L1121 (f	3.5
70	114098	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
	109734	AI927212	Hs.3734	ESTs	3.4
75	132788	BE083422	Hs.58851	hypothetical protein MGC2688	3.4
	106685	AU078617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
	108687	BE544475	Hs.54347	ESTs	3.4
80	113115	AF141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486258	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4



5	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMT1_HUMAN REGUL	3.4
10	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122385	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
15	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037766	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE246284	Hs.180789	S164 protein	3.4
20	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126636	AA849257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
	108650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
25	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal affect	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
	132994	AA112748	Hs.278905	clone HQ0310 PRO3310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
30	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Scores Infant brain IN1B H	3.3
	133363	AB68286	Hs.71962	ESTs, Weakly similar to B36298 prolina-r	3.3
	107908	AF087999		ESTs	3.3
35	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC15887, mRNA, com	3.3
	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21901	3.3
40	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	3.3
	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
45	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133180	N54988	Hs.66309	hypothetical protein MGC11061	3.3
	134076	AF086215	Hs.78980	gb:homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
50	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76057	ribosomal protein L10a	3.3
	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648986	Hs.151999	ESTs	3.3
55	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW981605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
	121292	AA401807		gb:zv65f1.1.s1 Scores_totat_fetus_Nb2HFB_	3.3
	123284	AA488988	Hs.293796	ESTs	3.3
60	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	106014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
	114988	AA251089		gb:zst0405.s1 NCL_GCAP_GCB1 Homo sapiens	3.3
	132967	AF226867	Hs.58553	CTP synthase II	3.3
65	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
	111520	AI865359	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
70	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129519	AA208534	Hs.264243	tetraspan NET-6 protein	3.3
	126770	AI282320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
75	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
	129284	AA318224	Hs.288141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
80	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	116397	BE139479	Hs.161492	ESTs	3.3
	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.225795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113628	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
5	123808	AA620552		gb:ae5Bg11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein I3	3.2
	110661	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29882	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
10	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
15	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
	109617	A1631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
20	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AJ769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN III	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA926960		CDC28 protein kinase 1	3.2
	130553	AF082649	Hs.252587	pituitary tumor-transforming 1	3.2
	126394	BE178502	Hs.173772	ESTs, Weakly similar to I76885 serine/th	3.2
30	132305	AJ806090	Hs.44344	hypothetical protein FLJ20534	3.2
	131136	AB033089	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117638	AA377165	Hs.44833	ESTs	3.2
	127076	AJ422951	Hs.146162	ESTs	3.2
35	126153	H05692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.281038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	cardioembryonic antigen-related cell ad	3.2
	122110	AJ123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
40	109442	AW298134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.82180	anillin (Drosophila Scars homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108612	hypothetical protein FLJ22004	3.2
45	134984	AJ803516	Hs.272891	hippocalcin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease H1, large subunit	3.1
	119750	AJ538880	Hs.94612	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group 1, m	3.1
50	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	118429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	123721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
55	129179	AW959025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AJ652236	Hs.49376	hypothetical protein FLJ20844	3.1
	133461	NM_000782	Hs.334345	cytochrome P450, subfamily 11A (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
60	134937	AJ251448	Hs.171939	ESTs	3.1
	125766	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW956243	Hs.4243	hypothetical protein FLJ12850	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
65	117121	H95044	Hs.321386	EST	3.1
	128556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AJ908008	Hs.295382	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA609672	Hs.123304	ESTs	3.1
	114250	AJ914699	Hs.13297	ESTs	3.1
70	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:u57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R58878	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
75	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nuclear protein NOP5/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
80	123485	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	100416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LIM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hm88a05.x1 NCI_CGAP_Kid11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AAA43473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ120212	3.1
	129707	AF572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336535	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
15	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	108651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824288	Hs.21331	hypothetical protein FLJ10036	3.0
	128660	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128804	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126598	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypothe	3.0
	133966	BE280478	Hs.182895	hypothetical protein MGC3243	3.0
	119165	R81715	Hs.310558	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26866	KIAA1171 protein	3.0
30	100237	D30715	Hs.23038	Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.105652	HSPC071 protein	3.0
	123073	AA485061	Hs.252692	ESTs	3.0
	111375	H56499	Hs.44143	ESTs, Weakly similar to I38022 hypothe	3.0
	130724	AK001507	Hs.134535	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129828	AI388993	Hs.134535	ESTs	3.0
	118922	AW206193	Hs.34348	hypothetical protein DKFZp76182423	3.0
	131902	AA180146	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350	Hs.183161	gb:acc81h08.s1 Pancreatic Islet Homo sapi	3.0
40	122219	AA438002	Hs.183161	ESTs	3.0
	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
	126997	AI377160	Hs.150914	ESTs	3.0
45	128902	AA036637	Hs.107052	ESTs	3.0
	117188	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ121891 fls, clone C	3.0
50	135028	H58818	Hs.301824	hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.337778	hypothetical protein PRO1331	3.0
	105735	R77698	Hs.170994	ESTs	3.0
	126828	N49776	Hs.71573	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.11896	hypothetical protein FLJ10074	3.0
55	110312	BE258986	Hs.87829	hypothetical protein FLJ12089	3.0
	125659	T67693	Hs.115726	Homo sapiens cDNA FLJ13707 fls, clone PL	3.0
	128601	AB032984	Hs.101299	KIAA1138 protein	3.0
	123423	AA588494	Hs.101299	gb:acc38f04.s1 Gessler Wilms tumor Homo s	3.0
	126595	NM_003478	Hs.101299	cullin 5	3.0
60	123470	AW303285	Hs.85944	Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259	Hs.78561	gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.334812	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.12835	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.1857	A kinase (PRKA) anchor protein 7	3.0
	103108	W27172	Hs.18910	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.25780	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fls, clone MA	3.0
	126887	H20832	Hs.47044	gb:ym48d03.s1 Soares infant brain 1N18 H	3.0
70	117980	AA310417	Hs.75277	ESTs	3.0
	133826	AW836130	Hs.152571	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.26484	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	105968	H09232	Hs.81685	HIRA-interacting protein 3	3.0
	125770	AA143045	Hs.81685	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

Pkey: Unique Eos probe/identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Pkey      CAT Number      Accession

108451	13766_2	AA079196 AA084955 AA126308 AA084956
107908	46987_1	AF087999 N26296 A1928858 AA846757 N20229 AA026894 D80634 AW388923 AW388082 AW388957 AW571771 AW388838
5	123619	AI686662 AW389079 AA602099 AW134567 AW517843 AI682674 AI474874 AA374167
	131495	AA602964 AA609200
	371681_1	AA812434 AI831542 AW766261 AI769894 N63378 AA214392 AA135833 AW605017 AA135965 AW450072 H04612 AA446459
	124006_1	AW439151 AA426273 AI061423 AA598549 Z4D087 AI753216 AA743075 AA854288 AA458920 AA843893 AI566616 AI864957
		AI566634 AW971760 AA211796 AA430089
10	101445	M21259
	100944	L07518 AW815215
	117265	AA451966 NM_016370 AB036693 AI139228 R58124 AI634847 AL119333 W07356 AI334284 H29050 AI192685 AA662438
		AW172843 W19794 N21460 AI743862 AW130622 AA991348 AI204553 AA992664 N80848 AA699329 AI824676 T26624 R49653
		AW779829 N22494 AI248120
	117287	AL121500 AW291763 AI732432 AA129708 AA133309 AI733750 AI225224
15	108859	W45350 W45406
	125165	AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671
	116790	AA476718 AW772454 AI807703 R44253 AA976657 AI985186 AI650254 H38942 R84829 AA018724 AA001000 H85934 AA019126
		H85609 AA017000 AA339355 AW950566 D51397 AA213981 BE548002 AA066359 AA001560 AW852113 AA317769 AI857477
		AI857475 AW248771 AW162661 H38943 AA018628 R85885 AI984613 AI934765 AI766172 AW157489 AI929181 R85523 D51221
		D53851 H85610 AI748674 F21582 AA323145 AA019127 AA887444 T06745 AI699293 H29532 AA214029 AA223656 NM_010834
		X14474 R19697 H06965 R17456 R13812 R19056 AI881231 AI590200 R37671 AI928128 AI990023 AI935569 AW005921 AA324581
		H17335 R37659 R42802 R46242 R60936 R59371 H28993 AA479907 R44570 AI890695 AA306884 AA507078 R41274 AI365507
		T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045
20	103038	AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267638 H83186 AA469909 N88396 AA001348 BE535736 AA081745
25	15024_1	BE566245 AA082436 H72525 H75755 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE278271 AW960304 T29612
		AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314368 AA908783 AI719075 BE270172 BE269819 AA889955
		AI204630 W26243 AI935150 AA872039 W72395 T99630 AI422691 H86460 N31428 BE258916 H03285 AI857576 AA776920
		AA910844 AA459522 AA293140 AW154667 H75953 AW662396 AA662522 AH865147 AI231553 AW252230 AA584410 AA583187
		AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100826 AA772418
30		AA594628 AI033892 W86098 AI034317 AA398727 AI085031 N95210 AA59432 AI041437 AA932124 AA627684 AA835829
		AI004827 AI423513 AI094587 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI637692 AI090262
		AA740817 AI312104 AI911822 AA416871 AI185409 AA128784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880
		AA399229 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI942230 AI278887 AA962596
35		AI492800 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA458292 AA037114 AA129785 AI494211
		AW959601 AW886710 R92790 N59756 AI361128 AW589407 H47725 H97534 H48076 H48450 T98931 AW300758 H03431 R76789
		AA954344 H77576 R96823 AA57100 N92845 N49862 H42038 BE220898 BE220775 H99562 AW01624 N74173 H54704 H79520
		H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 AW104725 W25611 W25071 T86960 H03513
		T77589 R99156 W95096 R87470 AA702275 T77551 AA911952 H82956 N83673 AA283672
40	126086	H75881 H70795
	126098	M79088 N88221
	125454	N71807 AA203399
	126127	N95428 W24040 AW751366 H81987
	125558	R59305 R19748
	126426	AA125984 AA127169 AA065075 AA070377 AA100017 AA079891 AA113255 AA075186 AA082764 AA083380 N04829 AA084752
45	118644	AA076512 AA085119 AA085208 AA085040
	81501_1	AA443241 R23784 R87255 R00047 AA547612 R63254 R28645 R27618 HD1310 R78329 R76046 R76055 AA369734 N57914 H94864
		AI953638 R31869 AW769278 R82398 AA131925 R21776 R79031 AI129559 N70340 AI276116 AA709381 N63734 AI342605
		AA327133 AI805980 AA05377 AW611716 T86946 AA369083 R67250 H02040 R32578 W66279 R80248 R23734 H00977 R21732
		R78932 AA366675 R16780 R26523 H40161 W93671 R99823 R77956 H81801 R88785 R897

106012	95214_1	A1240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AJ095755 T49804 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 A1803329 R27528 R36203 A1809932 A1808765 R78948 AA411449 AA976929 A1378760 A1378620 T48870 R73908 R75632 H03612 AA909584 N50695 H02580 H12839 N58761 AA742532 A1360919 H03502 BE208298 R88568 A1350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
127705	966283_2	AJ003322 AJ003324
127728	3398_5	AW404081 R09654 T67160 N50566 N53259
129012	22280_4	R81936 D78695 D78808 D78780 C17009 AA004406 AA122102 R70625 AA148932 H59583 H81148 H80378 H49863 H21162 H46534 H51478 H20702 H46515 H40200 H50046 H23647 H50439 H18383 H21848 H23849 H40182 R21924 H01290 H01283 H42464 W31947 W39660 AA046219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 AA92481 AA088608 R69918 R36334 H80281 N58483 A1075154 A1086754 AA595787 H81051 H01187 A1057251 T96942 H59564 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 R92416 H89486 R36617 R65795 A1088338 A1373324 H66992 R96235 A1494132 R16678 AA088178 AA705358 AA962143 AA148933 R09231 A180937 R70525 T46980 A1200046 H02301 AA367587 R35968 T87106 D78703 N78072 D78666 D63268 R28197 AA085579 R63766 R92415 W00898 R80766 R87875 R27583 R09343 H13646 R27682 T89007
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120934	177521_1	AA226198 AA226513 AA383773
115197	42406_1	R18656 AW968014 AA262288 AW968002 X93079 AJ002788 R51324 A1381600 D80031 AW500520 AW593740 F09382 AA810597 AA282174 AA810595 AA810596
129706	81501_1	AA443241 R23784 R57255 R00047 A457612 R63254 R28645 R27616 H01310 R78829 R76046 R76055 AA369734 N57914 H94864 A1953638 R31669 AW769278 R82398 AA131926 R21776 R79031 A1129553 N70340 A1276116 AA709381 N63734 A1342605
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131170	8113_1	AW303285 AW117398 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW830166 AL041326 AA780690 L40617 U21656 AK93182 AW052487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389464 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 A1673095 AA599106 AW801545 A1539739 A1583730 A1521786 AW386369 AW021010 AA362576 A1289927 AA382582
123532	genbank_AA08733	AA608733
125032	genbank_T74884	T74884
123808	genbank_AA620552	AA620552
102398	entrez_U42359	U42359
118129	genbank_N57493	N57493
109841	genbank_H01052	H01052
118922	220560_1	AW206193 AW137594 A1953685 A1919143 A1424371 AW007668 AW025681 A1954289 R40438 AW070364 A1679653 A1679081 A1623213 A1652310 A1631411 A1565384 A1566734 AA149597 A1538172 A1040831 A1770021 A1914287 AA279311 W73001 A1493117 A1693374 A1802007 A1990845 N29752 R94559 AA806475 AA806828 R09936 R94558 AW300112 W24097 AW003016 N91920 T47910
113119	genbank_T47910	AA029703
104799	genbank_AA029703	T91015
113660	genbank_T91015	AF093097 A1889509 T27070 AA326718 AA024743 W23922 AA478593 A1765668 W23908 U92986 AA081632 N50578 AA085245 AW355046 AW365014 AA981091 AA150231 H53426 AA234651 N50622 T79343 T87389 N91858 H41179 AW009453 AA024744 T27069 A1346379 H88431 AA152289 RA5373 AA477432 A1745607 A1807602 H41152 AA085244 A1242669 A1091032 A1251849 F09857 H88369 A1174488 A1002696 H53427 T87293 N91869 W35270 AA453723 AA453705 AW071829 A1393866 AW071807 W23592 A1342074 D31158 AA833766 A1991896 AA447791 A1864126 AW377239 AA295365 A1887870 R34076 F07607 AA521310 AW499665 R94584 R12183
124250	314220_1	AA350258 H68126
101447	entrez_M21305	M21305
117357	genbank_N24829	N24829
103382	entrez_X94563	X94563
135028	H58818_at	H58818
105225	genbank_AA211777	AA211777
121292	genbank_AA401807	AA401807
105909	82840_1	AA185191 AA190578 A1632307 AA195227 AA743633 A1823408 A1832203 A1653114 AA205307 AW021913 A1687980 A1574198 A1675663 AA17935 AA707350 AA135167 AA34721 A151038 A1098305 R52643 AA780141 AW207645 D19691 A1474970 AA401739 N22905 N70378
100237	entrez_D30715	D30715
114988	genbank_AA251089	AA251089
123423	genbank_AA588484	AA588484

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigene Title for all of the sequences in Table 73.

80	Pkey:	Unique Eas probaset Identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title

Seq ID No: Seq ID number correlation for those sequences in Table 73

Pkey*	ExAcon	UnigeneID	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82932 cyclin D1 (PRAD1: parathyroid adenomas	Seq ID No B1 & B2
	410102	AW248508	Hs.279727 ESTs; homologue of PEM-3 [Clona savignyi	Seq ID No B3 & B4
	101104	AW862258	Hs.169266 neuropeptide Y receptor Y1	Seq ID No B5 & B6
	447761	AF061573	Hs.18492 protocadherin 8	Seq ID No B7 & B8
	428183	AW969726	Hs.58381 ESTs, Weakly similar to serine protease	Seq ID No B9 & B10
10	439221	AA737106	Hs.32250 ESTs, Moderately similar to I7885 serin	Seq ID No B11 & B12
	121619	AA525339	Hs.178062 ESTs, Weakly similar to phosphatidylseri	Seq ID No B13, B14, & B15
	104659	AW969769	Hs.105201 ESTs	Seq ID No B16
	105782	H09748	Hs.57987 B-cell CLL/lymphoma 11B (zinc finger pro	Seq ID No B17 & B18
	129977	NM_000399	Hs.1395 early growth response 2 (Krox-20 (Drosop	Seq ID No B19 & B20
15	100299	D49493	Hs.2171 growth differentiation factor 10	Seq ID No B21 & B22
	116301	AW969706	Hs.293332 ESTs	Seq ID No B23 & B24
	106533	AL134708	Hs.145998 ESTs	Seq ID No B25-B27
	131313	R86290	Hs.76874 ribosomal protein L44	Seq ID No B28 & B29
	105316	AI671245	Hs.24835 hypothetical protein FLJ14584	Seq ID No B30 & B31
20	113003	AW292315	Hs.7215 ESTs	Seq ID No B32
	102838	U94320	Hs.158330 neuropeptide Y receptor Y5	Seq ID No B33 & B34
	102745	AW753865	Hs.74376 osteonectin related ER localized protei	Seq ID No B35-B40
	123308	C14187	Hs.157208 ESTs	Seq ID No B41 & B42
	120147	AI917116	Hs.211869 hemoglobin, beta	Seq ID No B43
25	123049	BE047680	Hs.91546 dkkkopt (Xenopus laevis) homolog 2	Seq ID No B44 & B45
	119082	AF252297	Hs.7457 cytochrome P450 reductase metabolizing pr	Seq ID No B46 & B47
	106301	AW352357	Hs.100343 MAGE1 protein	Seq ID No B48 & B49
	128478	AA708206	Hs.6451 ESTs	Seq ID No B50-B53
	106111	AW875398	Hs.2649 PRO0859 protein	Seq ID No B54 & B55
30	131307	NM_000025	Hs.96886 adrenergic, beta-3-, receptor	Seq ID No B56 & B57
	120830	AI668170	Hs.116602 ESTs	Seq ID No B58 & B59
	127664	AA806164	Hs.159156 ESTs	Seq ID No B60
	102725	AB026187	Hs.50651 protocadherin 11	Seq ID No B61 & B62
35	132520	AA257992	Hs.17109 Janus kinase 1 (a protein tyrosine kinas	Seq ID No B63 & B64
	130637	AA356764	Hs.44685 integral membrane protein 2A	Seq ID No B65 & B66
	117802	N35020	Hs.105827 C3HC4-like zinc finger protein	Seq ID No B67 & B68
	128797	NM_002975	Hs.179999 stem cell growth factor; lymphocyte secr	Seq ID No B69 & B70
	129703	BE388866	Hs.81866 Homo sapiens, clone IMAGE:3457003, mRNA	Seq ID No B71 & B72
	125770	AA143045	Hs.77256 v-kit Hardy-Zuckerman 4 feline sarcoma v	Seq ID No B73 & B74
40	414761	AI077228	Hs.97532 enhancer of zeste (Drosophila) homolog 2	Seq ID No B75 & B76
	420462	AF050147	Hs.61835 chondromodulin 1 precursor	Seq ID No B77 & B78
	410268	AA316181	Hs.37744 six transmembrane epithelial antigen of	Seq ID No B79 & B80
	104681	U29590	Hs.30247 Homo sapiens beta-1 adrenergic receptor	Seq ID No B81 & B82
45	416836	D54745	Hs.30247 cholecystokinin	Seq ID No B83 & B84

Table 72B

Play: Unique Eos probeset identifier number  
 CAT number: Gene cluster number  
 Accession: Genbank accession numbers

Play	CAT Number	Accession
50	131307	NM_000025 X72881 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134
	131313	R06290 H02411 C18327 AA367588 AA367657 H89632 C17954 AA568860 AI752883 AA599451 H04280 AI128118 AW193364 N94503
55		AA029995 T40538 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226
		AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R66818 H73711 R58545 D79189 AW265710
		R77684 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156823 AA368336 H63662
	116301	AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW969697 AA040063 AI807206 AW663917 AA454645
60		AA489238 BE241958 AA743491
	103080	AU077231 AA852219 M74092 X69798 M64349 NM_001758 AA228806 M73554 BE409154 AA160086 BE384352 AA160620 BE382880
		BE261734 AA113821 BE407745 AA156380 BE390267 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077
		W05266 AI824103 AI489061 AA642344 AI042658 AA906539 W60380 AI571777 AL135581 AA112340 W75469 AA582929 AI085348 AI278890
		AA126942 AI023701 AI873252 AA156319 AI180622 W60289 AI274886 R81309 AA100801 AA227161 AI566929 AA160603 AI074344 AI344581
65		AI150778 AA852218 AA158286 N20142 AA622148 AA854225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI669636
		AI674613 AA842544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE060779
		AI918938 BE168117 BE087369 AW955539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H86084
		AI146884 BE075154 AW99247 AI188525 AI752230 AW283140 W03329 N26056 AA948080 AA113073 H98284 AA227101 AA631077
		AA148042 AI740837 BE087278 AA149570 W44495 BE089351 AA376044 N25775 H27771 AA064705 BE091204 R89337 N32676 N27141
70		BE164704 H86049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T08020 W23852 AA082709 BE167894 AA076515 R97329
		BE541980 N42086 AA102307 AA113772 BE276181 H26622 W44436 W67604 W45412 AW771113 AI700678 AA502628 AA133137 BE274186
		BE396080 BE813371 BE612645 W46650 W95203 W92651 AI087288 R76299 AW604781 N56320 AI912334 AA403248 AW189156 H24970
		AW298822 AW080962 AI073747 W24123 AA577586 H27175 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W49531 AA908347
		AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AI151696 T32084 AI689037 AI624182
75		W49709 AW514883 AI100676 AI368087 AAC69474 AA525859 AW771076 AA029402 AA994114 AI351505 AW770816 AI333694 AI289794
		AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI055890 AI660881 AI368117 AA403090 AI272818
		AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079958 AI752231 AA076431 AA113245
		AI168564 AA918995 AI066484 AI123599 AI921518 W94588 AA535600 AA064665 AA705388 AA064623 AA962503 AI824928 AW131205
80		AW275281 AI280632 T29597 W48728 W954336 W38317 W94768 AI084717 W46567 AI245545 AW302501 N72201 AW510563 AW079132
		AA207054 AI143740 AW440672 AA632164 AI280285 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526
		AA487486 R92970 AA934071 AA80448 AA063257 C05786 N99089 R42969 AA887085 AA862686 AA533833 AA682304 H51748 BE539444
		AI382164 AI814595 BE537043 AI168307 BE408935 AA453506 R89428 AA938527 AA936890 AW369618 AW264602 R18074 AI474189
		AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086852 BE406324 AW292848 AI768962 BE540703 BE409478 AA931692



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410102	117657_1	AA730357 AI126690 AA630149 AW241515 AI147003 AI183499 N90923 AI968582 AA354145 AI147297 BE550502 AI085777 AI709087
410268	11897_1	AA773947 AA469192 AI199289 AI127085 H89232 N30719 AK028165 AW029469 AI709314 AA780834 AA778057 H89125 AI654762 T93061
414761	14860_1	N59622 AI360625 AA719982 AI248242 AA233925 AW262512 AW438666 AA010378 AA484010 AW438790 N22875 AA483718 AI185407
		AA736720 AA684587 AA648672 AA503406 AA508123 AA503140 H46638 N75812 AA730938 D60548 AA483039 AA507705 AA480448
		AI768654 AA656955 AA730803 AA330312 AW021127 BE172031 AW961052 AA339070 AA648172 BE172692 AA174175 AA492012 AA491590
		AW118733 AA484130 AA730783 AA730510 D62577 D62828 AI469294 AI801343 N53447 AA740226 AI831983 AA516146 D79799 AI758212
		AA484040 H38039 AI038772 AI039410 AA528387 AA730576 AA527231 AA748111 D62946 U36439 AA721708 H22130 AA559229 H51620
		AA283355 AA730970 R01595 N72450 AA469123 AA579389 AA480477 AA283306 AA347822 AA328013
		AW248508 AI278454 AI369343 AW291235 AI343946 AI347189 AA970152 AI279668 AI971894 AA664359 AI191039 AA084598 AA081641
		AA316181 BE439545 AC005053 AF186249 AW386101 AC004969 AA730199 AA032221 AI666139 AI167942 AA809228 AI184070 AI394674
		AW969977 AA032279 AW079284 AA513174 AA888312 AI453179 AA483363 AA528432 AA578511
		AU077228 U61145 AL044256 AA208185 AL044975 NM_004456 X95653 AW890905 AA332806 AW965453 BE289226 U52865 BE275009
		AA428252 AA769212 AA312778 AA810901 AA461315 AI959285 AI953668 AW295248 AI291422 AA704747 Z44716 BE541235 AW608806
		AA588583 AW403788 AW408386 AA053521 T87571 AA581163 BE183241 T97906 R89149 AI808196 BE618521 AI970278 AI652680 AW130143
		AI970272 AW187254 BE550449 AI628403 AA010143 AW005107 AA251815 AA805836 N53459 AA055309 AA643678 AI345816 AI345618
		AI635728 AI871286 AI018437 AI262614 H75287 AI033155 AI203388 AA205802 AI475265 AW594186 AI696069 AI333312 AW264710 AA876764
		AA864892 AA173158 AI292066 T79837 W93985 AA506427 AA815135 AI376342 AA010144 AI310421 AI223350 AA970576 N33926 T88364
		AI050913 N55088 AA101673 AA626665 AA251840 N88857 AI890053 H05930 AI474199 AI436166 AA628810 N64452 AI205538 AA055310
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		T99430 AI051764 R45991
416836	16233_1	D54745 AU077189 NM_000729 R71188 H87563 R87071 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571
		H19813 AI745597 AI769202 AI205982 AW205841 R64324 AI201975 H46893 C18067 R71189 N29729 AI799838 AI091209 H87455 R82443
		AW970995 AW072136 N40841 H13148 AI219052 N30191 T28007 AI817428 AA503602
420462	18379_1	AF060147 NM_007015 AB006000 AB005989 BE218114 AI703147 AI985891 BE222034 BE549774 BE327618 AI651459 BE549987 AI657194
		BE222414 BE046984 AW470357 AW339338 C02526 AW590220 AI298082 AW286998 AI333135 AI867818 AA730514 BE348513 AA405500
		AW136179 AA327834 BE327350 BE327366
428183	287965_1	AW969728 AA424028 AI266636 AI271571 AA423988 AI266634 AA702780 AA452037 AI424856 AA742931 AA483361
439221	46993_1	AA737106 N35765 N35779 AF086045 N30152 AW374028 AI478237 AA923682 AI382236 AA846668 AI627389 AI371709 H98083 H95983
		H26576 H95984 AA745021 AA639180 H26575
447761	7355_1	AF061573 NM_002590 AA780138 AW135620 AI197884 AA483348 R05468 AW969724 H29216



Table 73: Sequences

Seq ID NO: B1 DNA sequence

Nucleic Acid Accession #: NM\_053056.1

Coding sequence: 210..1097

5	1	11	21	31	41	51	
	CACACGGACT	ACAGGGGAGT	TTTGTGAAG	TTGCAAAGTC	CTGGAGCCTC	CAGAGGGCTG	60
10	TCGCGCAGT	AGCAGCGAGC	AGCAGAGTCC	GCACGCTCCG	GCGAGGGGCA	GAAGAGCGCG	120
	AGGGAGCGCG	GGGCAGCAGA	AGCGAGAGCC	GAGCGCGGAC	CCAGCCAGGA	CCCACAGCCC	180
	TCGCCAGCTG	CCCRAGGAAGA	GCCTCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAAAATG	GTGCABAAGG	360
15	AGGTCTGCCC	GTCCATGCGG	AAGATCGTCG	CCACCTGGAT	GCTGGAGGTC	TGCGAGGAAC	420
	AGAAGTGGCA	GGAGGAGGTC	TTCCCGCTGG	CCATGAACCTA	CTTGGACGCG	TTCTGTGCGC	480
	TGGAGCCCGT	GAATAAGAGC	CGCTGCAGC	TGCTGGGGGC	CACCTGCATG	TTCTGTGCGC	540
	CTAAGATGAA	GGAGACCTTC	CCCTGAAGG	CGAGAGAGCT	GTGCATCTAC	ACCBACRACI	600
	CCATCCGCGC	CGAGGAGCTG	CTGCAATGAG	AGCTGCTCCT	GGTGAACAAG	CTCAAGTGGG	660
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	CAGTGCAGG	CCGTAACCTG	AGGAGCCGCC	ACAATCTCCT	GTCTTACTAC	CGCCTCACAC	900
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25	TGGAAGCCCT	GCTGGAGTCA	AGCCTGCGCC	AGGCCAGCA	GAACATGGAC	CCCAAGGCCG	1020
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50	TCACACCGGA	AGGTTTCTTA	ACACTAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2520
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60	CTGCTACCGT	TGACTTCCAG	GCAAGGTTTG	GAATATTTCA	CATCGCTCTT	GTGTATCTCT	3120
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70	GATGATTTGA	ATAGCTTCTG	GAATTTGTTT	AAGTTTGGGG	TATGTTTAA	CTGTTATGTA	3720
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	CAATCTCTAA	TGAAGCCAGC	TCACAGTGCT	GTGTGCCCCG	GTCACTAGAC	AAGCTGCCGA	3840
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	CAAGTCTGAG	GGTCTGGGCG	GCGGCGGCT	GGGTCTGTGC	ATTTCTGTTT	GCACCGGGC	4200
80	GCTTCCCGAG	ACCAACATGT	AACCGCATG	TTTCCAGCAG	AAGACAAABA	GACAAACATG	4260
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Seq ID NO: B2 Protein sequence

Protein Accession #: NP\_444284.1

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	AEKLCIYTDN	SIRPESBLLQM	EULLVNKLKW	NLAAMTPHDF	IEHFLSRMPE	AEENKQIIRK	180
	HAQTFVALCA	TDVKFISNPP	SNVAAGSVVA	AVQGLNLRSP	NNFLSYTYRLI	RFLSRVIRCD	240
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	CGCCCTTCAG	CTGGCTCTCG	ATCAACTCTG	CCTCTGGGT	TTCGGGGAGC	CCCCCGCCCC	180
	CAGGGGGGGC	GAGGACGGGG	GAGGTGGGGG	GGGCGGGCGC	CCGCGCGAGC	CGACAGCCCC	240
	CCCGCAGCCG	GCGCGCGCGC	CGCGCGCCGC	GGCGCCCCCG	GC CGCCCCGA	CGACGGCCCC	300
20	CGCAGCGCAG	ACGCCCCCAGC	CCCCCACCC	CCCCAAAGGG	CGAGGCGAGC	CCAAGCTCTG	360
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	GCTGTGGTG	GGCCCCAAG	GGGCAACCAT	CAAGCGCATC	CAGCAGCAAA	CCAACACATA	780
	CATTATACA	CCAAGCCGTG	ACCGCGACCC	CGTGTTCGAG	ATCACGGGTG	CCCCAGCCAA	840
	CGTGGAGCGT	GCGCGCGAGG	AGATCGAGAC	GCACATCGCG	GTGCGCACTG	GCAAGATCCT	900
30	CGAGTACAAC	AATGAAAAGC	ACTTCTCTGG	GGGAGGCCCC	GAGCGAGCAA	TGATAGCCG	960
	CTACTCCGAC	GCTGGGGGCG	TGCACCAACC	CGGCTGCAAG	CCCCCTCTCA	CCTTCCGGCA	1020
	GAACAGCCTG	GGCTGCATCG	CGGAGTGCGG	AGTGGACTCT	GGCTTGGAGG	CCCCACGCTT	1080
	GGGTGAGCAG	GGCGGGGACT	TTGGCTACGG	CGGCTACCTC	TTTCCGGGCT	ATGGCGTGGG	1140
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	GCTGTGTGTC	ACTCCACCCC	TTCTTCCGAG	GAGGGGGTGG	GTAAAGGGGA	GAGGGAGAAAT	1980
	TACCACCTGT	ATCGAGAGGT	GCTCTTTGCA	ATCCCTAAGC	CCTCTGGTCC	TGACCTCCGA	2040
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65	GGAGGAGGAT	CACAGCCAGG	AAACCTGCCC	TGTGACGACT	TCCCTCTCTC	CCGCTCTATG	3060
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	CTCCACTCTT	TACCCACAAA	GGCAGAGAGC	TGTTACACTA	GGGGGCTCAG	CAAAATCAAT	3240
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70	AAAATAGAGG	AGAGAAAGAG	AGCATGAGAG	GGAGCGAGAC	AGGCGACCAA	CACAGAGGAG	3360
	AGAAACACAA	AATAGCAAAA	AAAAAATAAA	AAAGCAGTTC	TTTATAATTT	AATATTCTAT	3420
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Seq ID NO: B4 Protein sequence							
Protein Accession #: XP_044166.2							
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	ALYKEAEELR	KSSSNITTECV	PVPTSEHVAE	IVGQGCKIK	ALRAKNTYVI	KTPVRGEEFV	180
	FMVTGRREDV	ATARRBIIISA	AEHFSMIRAS	RNKGGAAPGV	APALPGQVTI	EVRVPYRVVG	240
	LUVGPKGATI	KRIQQQTNTY	IITPSRDRDP	VFEITGAPGN	VERAREEIEI	HLAVRTGKIL	300
80	EYNNENDFLA	GFPDAAIDSR	YSDANRVHQP	GCKPLSTFRQ	NSLGCIGECG	VDSGFAPRL	360
	GEQGQDFGYG	GILFPGYGVG	KQDVYGVVAE	TSPPLWAGQE	NATPTSVLFS	SASSSSSSSA	420

KARAGPPGAH RSPATSAGPE LAGLPRRPPG BPLQSPSKLG GGGLRSPGGG RDCMVCPESE 480  
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5 Seq ID NO: B5 DNA sequence  
Nucleic Acid Accession #: NM\_000909.1  
Coding sequence: 209..1363

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15 TGATGTGAT CTGCCCTGG CCATGATATT TACCTAGCT CTGTCTATG GAGCTGTGAT 360
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   GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
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Seq ID NO: B6 Protein sequence  
Protein Accession #: NP\_000900.1

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   CVSITVSIFS LVLLAVEREQ LIINERGHRE MNRHAYVGLA VIWVLAVASS LEFLIYQVMT 180
65 DEFFQNVITLD AYKDKYVCFD QPFSDSHRLS YTTLLLVLOY FGPLCFIPIC YFKIYIRLKR 240
   RNMMDKMDKED NKYRSSRTKR ININLLSIVV AFVLCWLPIT IFNTVFDNWH QLIATCNHML 300
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70 Seq ID NO: B7 DNA sequence  
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80 TCCCTTTCGA GCTCTTCAAC CTCTGCTGGG TGCTCTCAGT GGCCAGAGC AAAACAGTCT 300
   GATACAGCAC CTTGAGGAG GATGCCCGG GCAOGGTCAT CGGAGCCCTG GCCGAGSACC 360
   TGCAATATGA AGTATCGGT GACACAAGCT TCCGCTGAT GAAGCAATTC AACAGCTCTC 420
   TGCTCCGGGT GCGGGAAGGC GAGGGGAGC TGACGTCGG GAGCGCGCGC CTGACCGCG 480
   AGCGGCTGTG TGGCCAGGCC CCGCAGTGCG TGCTGGCCTT CGATGTGTCT AGCTTCTCGC 540

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5 AGGAGCAGTT CCGGCTGGTG CACGTGGAGG TAGAGGTGAG GGACGTCAAC GACCACGGCG 600  
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 CCGCCGCGCG CGTTCGACTC GGGGAGCGG ACGTAGCTC GCGGCGGGA GCGGGAGCG 1380  
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 CGCGCGCCCC GTGCGGCACA GTGCGGCCCT ACACGTGGCG TGTGGGCGAG GAGAAGGACA 1680  
 20 ACGCGCGCGT CTTCACGCGG CCGGTCTATG AGGTGTGGGT GCGCGAGAAC AACCCGCCAG 1740  
 GCGCTACCTT GCGCACGGTG GCGGCCCGCG ACCGCGACCT GGGCCGCAAC GGGCAGGTCA 1800  
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 CGGTGGACCC AGCTACCGGA GCGATCTAGC CGTTCGCGAG CTTGACTAT GAGACGCTGC 1920  
 25 GCCAACTGCA CGTTCGCTAT CAGCTAGCG ACGCGCGCTC CCGTCAGCTT TCCAGCAGCG 1980  
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 55 AATTTTGTAT ATATGCAAGA TATGCAAGA TATGCAAGA TATGCAAGA TATGCAAGA 3780  
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Seq ID NO: B8 Protein sequence  
 Protein Accession #: NP\_002581.2

65 1 11 21 31 41 51  
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 TSFRLMKQFN SSLLKVRGCD GQLTVGDAGL DRERLCQAP QCVLAFDVVS FSQEQFRLVH 120  
 VEVEVRDVM HAPFPFRAQI PVEVSEGAIV GTRIFLEVTV DEDVGANGLO TVRLAEFHPSP 180  
 FKVELQTRAD GAQCADLVLL QELDRESQAA YSLELVAQDG GRPPRBATAA LSVEVLDAAD 240  
 70 HSPAFPQCAV AEVELAEDAP VGSLLLDLDA ADPDEGPNQD VVFARGATPE PEARRLFRID 300  
 PRSGRLTAG FVDYERQDTY ELDVRAQDRG PGPRAACTCKV IVRLKDVNDN APDIAITPLA 360  
 APGAPATCFP AAAAAAALG GADASEPAGA GTPEAGATSL VPEGAARESL VALVSTSDRD 420  
 SGANGQVACA LYGHEHFRLO PAYAGSYLVV TAASLDREIR AEYNLTIVAE DRGAPPLRTV 480  
 RPYTVRVGDE CTTGCTTCTAT ATAATAAAG CTAAAGTGGG AGTATTGOC AAAGGAACCT 540  
 75 VGRAGGAVST YVSVDPATGA IYALRSFDYE TLRQLDVRIQ ASDGGSPOLS SSALVQVRVL 600  
 DQNDHAPVLV HPAPANGSL E VAVPGTAKD TVVARVQARD ADEGANGELA FELQQQEPRE 660  
 AFAIGERTGE TLLTGDLSEQ PPGRVFRALL VISDGGREPL TTTATVSVFV TAGGGRGPA 720  
 PASAGSPERS RPPGSLGLVS GSVLQMDTFL IVIIVLAGSC TLLLAALIAI ATTCKNRKKE 780  
 80 VRKGALREE RPPGAGGGAS APGSPHEAAR GAGPRPMFMD VLTFFPGTGA PFGSPAADAP 840  
 PPVAAAEEVP GSEGGSATGE SACHFEGQOR LRGAHAEPYG ASFGFGKEPA PPVAVNKGHS 900  
 FWTISGREAE KPSGKDSGKG DEDFNDSDD ISGDALKKDL INHMQSLWA CTAECKILGH 960  
 SDRCNSPSCS GPNAPSPSPR PQMSTFCKS TSLPRDLPRR DNYQAQLPK TVGLQSVYEK 1020  
 VLHRYDRTV TLLSPFRPGR LFDLQEGIVF LYQSPFGRYL SPKCGANENV

Seq ID NO: B9 DNA sequence  
Nucleic Acid Accession #: AL121939.12  
Coding sequence: 185..1426

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GATCTCAGCT GACAGTGGCC TCGGGGACCA AACAGCCTG GCAGGACAAA ATTAGAAGAT 180
CAAAATGGAA AATATGCTGC TTTGGTTGAT ATTTTCACC CTGGGGTGGG CCCTCATGTA 240
TGATCTGAAA ATGGAATGGG ATTTTATGTG GCACCTGAGA AAGGTACCCC GGATTTGTCAG 300
TGAAAGGACT TTCCATCTCA CCAGCCCCGC ATTTGAGGCA GATGCTAAGA TGATGGTAAA 360
TACAGTGTGT GGCATCGAAT GCCAGAAAGA ACTCCCACT CCCAGCCTTT CTGAATTGGA 420
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AGTTCAAGAT TTGGTTCTTG AGCGGACTCA AATATCACC ACAAGGGGAG TATCTGTTAG 540
GAGAAAGAGA CAGGTGTATG GCACCGACAG CAGGTTGAGC ATCTTGGACA AAAGGTTCTT 600
AAACAATTTC CTTTTCAGCA CAGCTGTGAA GCTTTCCAGG GGCTGTAGTG GCATCTCAT 660
TTCCCTCAG CATGTCTTAA CTGTGCCCCA CTGTGTTTAT GATGGAAGG ACTATGTCAA 720
AGGAGTAAAA AAGCTAAGGG TAGGGTTGTT GAAGATGAGG AATAAAGTG GAGGCAAGAA 780
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TCCGAAGGGC TGGGCAAGAG GAGGCATGGG GGAAGCTACC TTGACTATG ACTATGCTCT 1020
TCGGAAGCTG AAGCTGTCTC ACAAAAAGAA ATACATGGAA CTGGAATCA GCCCAACGAT 1080
CAGAAAGATG CCGGTTGAAA TGATCCACTT CTCAGGATTT GATAACGATA GGGCTGATCA 1140
GTGGTCTCAT CGTTTITGCA GTGTGTCTGA CGAATCCAAT GATCTCCTTT ACCCAATATG 1200
CGATGCTGAT TCGGGCTCCA CCGGTTCCGG GGTCTATCTG CGTCTGAAAG ATCCAGACAA 1260
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CGGGTTTCAG AAGGACTACA ACGTTGCTGT TCGCATCACT CCCCTAAAAT ACGCCAGAT 1380
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AGGGCGGTGT ATCATCTAAA TCACAGAGAA AACAGCTCT GCTTACCGTA GTGAGATCAC 1500
TTCATAGATT ATGCTGGAC TTGAATCTGT TCAATAGCAT TTCAACATTT TTCAAAATCA 1560
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CAATGCCAAG TATATACTCT TCTTTACATG GTGATGATT TCATTGTGAG AAAAATTTTG 1680
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GACTCCTTAA TGGACTTATT CTCAGGGTCC TACTCTAAGA AGAATCTAAT AGGATGCTCG 1800
TTGTGATTA AATGTGAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA 1860
ATAGAGACAG AAGATTACAA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGTCTAT 1920
GCCCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGGGA CATTTAGTTT AGTTTTTTTG 1980
AAGAATTACA AATCAGAGAA AARGCANGC ATTATAAACA AAACATATAA CTGTTTACT 2040
GCTTTAAGAA ATAACAATTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTCT 2100
ATGAATAAAA CCTAGTTTAG AAATAGGGA GCTGAGACAT TTAAAGATCT CAAGTTTTTA 2160
TTTAATAAT ACTCAAMTA TGGACTTTTC ATGTATGCAT AGGGAAGACA CTTCACAAAT 2220
TATGAATGAT CATGTGTTGA AAGCCACATT ATTTATGCT ATACATTCTA TGTATGAGT 2280
GCTACATTTT TAGGACAAAG AATCTGTAA TCTTTTCAA GAAAGAGTCT TTTCTCCTT 2340
GACAAATCC AGCTTTTGTG TGAGGACTAT AGGGTGAATT CTCTGATTAG TAATTTTAGA 2400
TATGTCCTTT CTAAAAATG AATAAATTT ATGAATATGA CTTAAAAAAA AAARWOGAGC 2460
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Seq ID NO: B10 Protein sequence  
Protein Accession #: CAC35071.1

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KRQVYGTDSR FSLIDKRLPT NPPFSTAVKL STGCSGLIS PQHVLTAAC VHDGKDYVKG 180
SKLLRVGLLK MRNKSQKKR RQSKRSRREA SGGDQRETER EHLRERAKGG RRRKKSGRGQ 240
RIAEGRPSFQ WTRVKNTHIP KGWARGGMD ATLDYDYALL ELKRAHKKKY MELGISPTIK 300
KMPGGMIHFS GFDNDRADQL VYRFSVSEDE SLDLYQYCD ARSGSTGSGV YLRKLDPKK 360
NWKRKIIAVY SGEQWVDVHG VQKQXNVAVR ITPLKYAQIC LWIHGNDANC AYG

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Seq ID NO: 11 DNA sequence  
Nucleic Acid Accession #: NM\_002035.1  
Coding sequence: 108..1106

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CTGCCGCGCT CTCGCTGGCC TTGCTGCTGC TGCTGTACAT GGTGCTCCG CTCATCAGCC 180
CCAGCGCCCT CGCCCTGCCC GGGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
GGAAGTGCA TGTCTATGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGCAAGAA 300
ATGAGGATAA GCTGCTGCGG GCAAGAGAA AATTTGAAT GCACCTTATT AATGACAAAC 360
AGGTGGTGCT TTGCATATCA GTTGTATGAT CTCAGGACTA TAACCAAGTA GAGATGTCA 420
TAAACACAGC ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAAATTGT GCAGGAATGG 480
CAGTGTGAGG AAAATTGTA GATCTTGAAG TTAGTACCTT TGAAGGTTA ATGAGCATCA 540
ATTACCTGGG CAGCGTGTAC CCCAGCCTGG CGTGATCAC CACCATGAAG GAGCGCGGG 600
TGGGCAGGAT CGTGTGTTG TOCTCCGAG CAGGACAGTT GGGATTAATC GGTTCACAG 660
CCTACTCTGC ATCCAGTTT GCATTAAGGG GATTGGCAGA AGCTTTGAG ATGGAGGTGA 720
AGCATATAA TGTCTACATC ACAGTTGCTT ACCCACCAGA CACAGACACA CCTGGCTTTG 780
CGAAGAAAA CAGACCAAG CTTTGGAGA CTCGACTTAT TTCAGAGGCC ACATCTGTGT 840
GCAACCCAGA ACAGGTGGCC AAACAAATTG TTAAGATGCA CATAACAGGA AATTTCAACA 900

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GTTCCCTTGG CTGAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960  
 CTTCTATTAC TGAGGGGCTC CAGCAGGTGG TCACCATGGG CCTTTTCCGC ACTATTGCTT 1020  
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 CTGAAATGCG AGACAAAAC TCCCTAATCTT CTTACCCCTT GGAAGAAGAC TGTTTCCAAA 1140  
 TAATTTGAAC AGCTTGTCTG TAAATGGGAC CCAATTTTGG GCTTATAGAC ACTTATGTAT 1200  
 TGTTTTCGAA TACGTGAGAT TGGACCATGG CTCTTCAGGA ATGTGGCTGC AAGCAAGGGG 1260  
 CTAGAAGTTC ACCTCCTGAC AGTATTATTA ATACTATGCA AATATGGAAT AGGAGACCAT 1320  
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 AAGTAAAGAA CAGGATTCCT GAATGATCAT TAAATTGTGT TCTATTATTT CTTTTTGGCC 1440  
 CCCCAGAGA TTAAGTCCAG AAATGTACTT TCTGGCAGAT AAAGAAATCT TGAGGACTTT 1500  
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 CCCCATAAGC TACGAGGGGG ACAGGAGAGG GCAGTGCAAT GGAAGTAAA GAGATATTTT 1800  
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 AGCTTAAGAA TTTACAGTTC CTTCAATAAC CATGATGACC TGAAGTTCAC CTATCCCAT 1980  
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 TTAACCTAAC TCATGAATTA ATTAAGCAA ATGAAAAAAT TAAAAAGTGT GACTTTTTCT 2160  
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Seq ID NO: B12 Protein sequence  
 Protein Accession #: NP\_002026.1

1 11 21 31 41 51  
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 CAGMAVSGKF EDLEVTFFER LMSINVLGSV YPSRAVITM KERRVGRIVF VSSQAGQLGL 180  
 PGFTAYSASK FAIRGLAERL QMEVKPYNVY ITVAYPPDID TPGFAEENRT KPLEIRLISE 240  
 TTSVCKPEQV AKQIVKDAIQ GWENSSLSGD GYMLBALTCG MAPVTSITEG LQOVVTWGLF 300  
 RTIALFLYLS FDSIVRRCMQ QREKSENADK TA

Seq ID NO: B13 DNA sequence  
 Nucleic Acid Accession #: CAT Cluster

1 11 21 31 41 51  
 CTGGGATGCG ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTTAA TTTTAAAAAT 60  
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 TTTGGATTGG TTAAGTCCAA TTATTAAATG CTGGGTTTC AAATTCOCAG CTGGAAGGAC 180  
 CACCCATTTA AAAACTTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAATAAT 240  
 CCAGGCATGG GTTTGACATA TTTCCAGAGC TCAATCTGCG AGTGTTCAC ATGCACATAC 300  
 AAGATCCAGG GTCTCATGTT AAAATCACTT ACATACCCAG AAAGACCACC ACITTCAGAG 360  
 TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420  
 AAGAACACAT AAGATGCCCT CTTCCATCAA ATGCACCTGC TTGTGAATTA ATGGACTTGT 480  
 AAATGAAACA ATGCAATCAG TCTTTTATAA TGCACTGTTC AATTTGAGAT TCAAGTATTT 540  
 CTATTTCTTG GAAAAAATTT TAAGAATCAA AAATAAGAA AATAAAAGT GCATACAGTT 600  
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Seq ID NO: B14 DNA sequence  
 Nucleic Acid Accession #: XM\_086767.1  
 Coding sequence: 276..611

1 11 21 31 41 51  
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 TCGGCTGGGT TATCAAGCCA AGCTATTTAA AGGTGTTTAA AAAGAAAGGA TGGAAAGGAG 180  
 ACCCTCTAGG AOCACGTGTG TTTTGGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT 240  
 ATTTTGTCTT CAGTATAATT GTTCCAGATA AAACATGATG GATGAGCTCG TTTTCATTTA 300  
 AATTATTAAA TCAGCTTGGG ATGATTGAAG AGCCAAGGCT TTTTGAAGA AACAAACCAT 360  
 TTTATAAATC TCAGAAGTGC AAGATTCTTG CTCATTTTAA TAATGACTTT GTAAATATTT 420  
 CAGCATTTGG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCACA TGCACATACA 480  
 AGATCCAGAG ACCTCATGTT AAATCACTTA CATACCCAGA AAGACCACCA CTTTGCAGGT 540  
 ATAATATTGT ACTTAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCAA 600  
 AGAACACATA AGATGCCCTC TTCCATCAAA TGCACTTGCT TGTGAATTA TGGACTTGT 660  
 AATGAACAAA TGCATACAGT CTTTATAAT GCACGTGTTCA ATTTGAGATT CAAGTATTT 720  
 TATTTCTTGG AAAAAATTTT AAGAATCAAA AATAAAGAAA ATAAAAATG CATACAGTTA 780  
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Seq ID NO: B15 Protein sequence  
 Protein Accession #: XP\_086767.1

1 11 21 31 41 51  
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 LQCSCTCYKI QRLMLKSLTY PERPPLCRYN IVLKDRBEVF LNPNTCTPEN T

Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

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	ACACAACAGT	AAATAGGCAG	TGTTGTATTT	TCATTTTCAG	ATGTTTGAAT	GGAACAAGAA	120
	AAGTGCTATT	AGCCCAAGCT	TCCTACATTC	ATTAAAGAG	TGACTATCAA	AAACAGCAAC	180
	ATGCACATATG	GTACATATGC	ACAAATGGA	ATTATATCAA	CAATATACA	AAATACCCAA	240
	AATAAAATAT	TTACAGGTTT	AAAAATATAA	ACATTGATTC	CTCTATCCCA	TAAACCAT	300
10	GGAGTGGAGA	AAGGAGGAAA	GACCCATITG	CTATTTAGAA	TCCTTTTAA	AACAAGTTT	360
	TAAACATAG	AATTAGTTCT	AGGAGACAAT	TTTTGATGTT	TTTCAGGGGT	TAAACATTCT	420
	ATTATAAAA	TAACATCTAT	AAACCTACTA	ACAATTTTCC	TCCTGTGCAC	AAAAATAATA	480
	CTGCCAAAC	CTGTCTCTCA	AGACATGCCT	GACITTCAGG	AAAGCTAATT	ATGGAATGG	540
	AGTTTCTCT	TTGGGTTATC	TTTGTTACTA	TTTTCAATA	ACCAGCAACT	CCCTATATTA	600
15	CACGTAGATA	CTTTATATAA	ATAACGTGGG	CGAAACCTGA	AGTTCACAAT	GAGCCTGCTA	660
	GGTAGCTGGT	GTCAAGTAGA	AATGATAGGA	ATTGACTTTG	CCAACCAACT	CAAAAGCATT	720
	TTCCCTGATA	TTCCCTGATA	ACCTACCATT	ATCAGATCCT	CCATATTCAA	TAAGATTAT	780
	CCTGGAAGCA	ATGAAATATG	TAAATATTAC	TTTGCTAGAG	TTTCTCTCC	TTTATTTAGA	840
20	AATAAATG	TAGTGGGAC	CAGTGGTGT	AATGTAGATA	CTTGAGAAGT	TTCAITGATT	900
	CCTTCAGACC	CATGCCG					

Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM\_022898.1

Coding sequence: 268..2739

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	GAAAGAGCAA	AATAAAGAG	AAGAAGAGGA	GGAAGAGAGG	GAAAGAGAGG	AAGGGAAAAA	120
30	AAACACCAAC	CCGGGAGAG	GAGGAGGTGC	GGCGGCGCG	CGCGGCGCG	CAGCGCGCG	180
	AGCGGCGCG	CGCGGCGCG	GACCCCTCC	CCCGGCTCC	CCCATCAGTG	CAGCTCTCCG	240
	GGGATGCCA	GATAGATGC	CGGGGCAATG	TCCCGCCCA	AACAGGCAAA	CCGCGAGCAC	300
	TTGTCCCA	GGGAGCTCAT	CACCCAGAG	GCTGACCATG	TGGAGGCGC	CATCTCGAA	360
	GAAGACAGG	GTCTGGAGAT	AGAGAGGCCA	AGTGGCTTGG	GGCTGATGGT	GGGTGGCCCC	420
35	GACCTGAC	GTCTCACCCT	TGGCCAGTGT	CAAAATGAAT	TCCCTTGGG	GGACATCCTG	480
	GTTTTTATAG	AGCAACAAG	GAAGCAGTGT	GGCGGAGCT	TGGGTGCTG	CTATGACAAG	540
	GCCCTGACA	AGGACAGCC	GCCACCTCC	TCACGCTCC	AGCTCAGGAA	AGTGTCCGAG	600
	CGGTGGAGA	TGGGATGCCA	AGTCACCCC	GACGAAGATG	ACCACCTGCT	CTCACCCACG	660
	AAAGGCATCT	GTCCCAAGCA	GGAGAACATT	GCAGGTAAAG	ATGAGCCCTC	CAGCTACATT	720
40	TGCACAACAT	GCAAGCAGCC	CTTCAACAGC	GGGTGGTTC	TGCTGCAGCA	CGCGCAGAAC	780
	ACGCAACGCT	TCCGCATCTA	CCTGGAGCCC	GGGCGGCGCA	GCAGCTCGCT	CAGCGCGCG	840
	CTCACCATCC	CGCCCGCGCT	CGGCGCGGAG	GCGGTGGGCG	AGTCCCGGCT	CATGAATTTT	900
	CTGGGGACA	GCAACCCCTT	CAACCTGCTG	CGCATGACGG	GCCCCATCCT	CGCGGACAC	960
45	CCGCGCTTC	CGGAGGCGG	CCTGCCGGC	ACGCGGCTC	TCTTCAGTCC	CGCGCGCGC	1020
	CACCACTCG	ACCGCAGCG	CCTCAGTGCC	GAGGAGATGG	GGCTGCTGCG	CCAGCACCCC	1080
	AGTGCCCTTG	ACCGAGTCAT	CGGCTGAAAC	CCCATGGCCA	TGAGCTGCGC	CGCCATGAGC	1140
	TTCTCGCGC	GGCTCGCGA	GCTGGCGGGC	AACAGCTCCA	CGCGCGCGC	CGTGTCCCGG	1200
	GGCGCGGCA	ACCTATGCA	CGGCTCTCT	AACCCCTTCC	AGCCAGCCCG	CAAGTCCCGG	1260
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Seq ID NO: B18 Protein sequence  
 Protein Accession #: NP\_075049.1

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Seq ID NO: B19 DNA sequence

Nucleic Acid Accession #: NM\_000399.2

Coding sequence: 339..1769

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 CTGTGATTT TTTTCTCTG GTGTGTGTGG TGGTGTGTTT TAAGTGTGGA GGGCAAAAGG 240  
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 AGCGAGGAGG TTGGTCTCC TGGTGTGTGG AGGAGCAAT GATGACCGCC AAGGCCGTAG 360  
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Seq ID NO: B20 Protein sequence

Protein Accession #: NP\_000390.2

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Seq ID NO: B21 DNA sequence

Nucleic Acid Accession #: NM\_004962.2

Coding sequence: 457..1893

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40	TAAATGCTCA	GTTTCAGAAC	CTTTGGGCCA	CATAGTGATT	TTGGAAAACA	GGATAATCGT	2340
	GGTGTAATAG	AGTGTTCCTT	TTCAAAGTCC	ACTGCAGAGC	TTTTATCCAT	ATGGTATGCA	2400
	CATGTAGCCA	ATATTGGTTT	CTTTTCTTAA	ATATATATAT	TTTATTTTAA	AACAACAAAA	2460
	AGGGAGGGCG	TTGACACCAT	TCCCCACAGA	GATAGTCATG	CTGAGTGGGG	GTGTTTAAAA	2520
	CATGCATATT	GAAATAACAC	ATATAGTAAC	GTGGGAATAC	TAAAAAATAA	CCAAGATTTT	2580
45	ATATTTTGTG	AAATTAACAT	TCTATACTCG	TAGATTGTGT	ATGTTATGTG	TTTTATGGA	2640
	AACTAATAAA	ATTAAAGGTA	CAGTGGTATC	TTGA			

Seq ID NO: B22 Protein sequence  
Protein Accession #: NP\_004953.1

	1	11	21	31	41	51	
	MAHVPARTSP	GPFGQLLLLL	LPLFLJLLRD	VAGSHRAPAW	SALPAAADGL	QGDRLQHRP	60
	GDAAATLGPS	AQDMVAVBMH	RLYKYSRQG	ARPGGNTVR	SFRARLEVD	QKAVYFFNLT	120
55	SMQDSEMLT	ATHFHYSEPP	RWRPALEVL	KPRAKNAGSR	PLFLGPFTRQ	RLLFRLSQM	180
	TATQGLLRGA	NALAPFPRLG	WQAKDISPIV	KAARRDGELL	LSAQLDSEER	DPGVPRPSFY	240
	APYILVYAND	LAISEPNVA	VTQLRDFPFP	AGDPEPRAP	NNSADPRVRR	AAQATGFLPD	300
	NEPLGLDERP	FRABAGHFHK	EQLNPSPPRA	LKPRFGRKDR	RKKQGEVFMA	ASQVLDYDEK	360
	TMQKARKKQW	DEPRVCSRRY	LKVPFADIGW	NEWIISPKSF	DAYYCAGACE	FEMPKIVRPS	420
60	NHATIQSIVR	AVGIIPGIPE	PCCVPDRMNS	LGVLFLDENR	NVVLKVYPM	SVDTCACR	

Seq ID NO: B23 DNA sequence  
Nucleic Acid Accession #: AK026322.1

	1	11	21	31	41	51	
65	ATTCTTTAAA	TACTTAAACA	TGGTTATAAC	AGCTGTGTTT	TAAGCTCCTT	GTCTGTTAAT	60
	TCCATCATCT	GTCAATTTTG	CATCTGTTTT	TATTGACTAA	CTTCTTCCTT	CATCATGGTC	120
	ACATATCCTT	GCTCTTCCCG	ATATTAGTA	AAGTTAGTTT	GGATGCTGGA	TTGTTTAAAT	180
	TTAGCATTTT	GGTTCGACTT	TGCTTTTAAA	AGTATTGGAC	TTGCTTTTGA		240
70	TAGTGAATTT	ACTTGCRAAT	CAGCTTGATC	ATCTGAGGAC	TTGTTTITAA	CTTTTGTGCA	300
	AAAGGCTATG	CTACTTCAAG	TATAATAAAA	CCTAGTTTAA	GTGTTATCCT	ATAACTAAGG	360
	CATGTGTGTA	ATTGTAATGT	CTCCAACCTT	GTGTGACTTC	TGAAAATTGT	TCAGCTCCCA	420
	ATTTGCGAGT	AAATTTTFTT	GTTCAGCCTT	GCAGTCTCAT	CCTACTCAAG	TGTGGCTCTG	480
	TATCCACAAA	CAGTCTTGGA	GATCTCATGA	AGATTTCIGA	AACTTTTCCT	CTGCAGGATA	540
75	CCTTCCTTTG	TGGTTATGTG	CCCTGAAAAC	TCCAGCCTCC	GTGCTTTCAA	TTCAAGTAAA	600
	CTACTACTCT	GCTTGGATTC	CCCTCTTATA	CAATGGTCTA	CCAAGTGACT	GCAACAGAAA	660
	ATCTAAGGGA	ATTTCAGGAG	TCACCTCAAT	TATTTTCTCT	TTTTTCAGGG	ATTATAGTAG	720
	TACTATACCA	CCTGTGAGCC	AATGTGTGAG	AATGGTGGTT	TCATACATTT	TCTCCAAATC	780
80	TTTCTTCTCA	TTATGTGTTT	ATCTCTGGCA	GTTTGAGCCA	AGAGAGGGCA	CGGAGAAGTA	840
	CAATGACTAG	AGAGCACTTC	TGTTGAGGCT	CATTTCATGA	CCCTACCCCG	AGTGCTTTAT	900
	GAATGTGTGC	TGAGATGTC	ATACAGCATC	ACAGCTTCTT	CTCTAATTTA	TGAGCCATAA	960
	TTTTTTTFTT	TGTATTTTAA	TTGTATTAAC	TGCTTGGTTC	CAAGAGGATG	ATGAGGAGGA	1020
	CTACTATAGG	ATAAATTTGT	TTTTATAGAG	CAATTTCTCA	TGGGTACCGA	GGGATAGTAC	1080

TCCATTTTCC TCACTGATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200  
 TATGGAATCC TTATGCTTT TTCTCAGGCT GCCTCTGTTA CATGAAATAA AGCCAGAGTT 1260  
 GATTGTGAAA AAAAAAAAAA AAAA

5

Seq ID NO: B24 DNA sequence  
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
10	TGTATACATT	CCTTTCAAAT	AAAGACCTTG	AGAAAACAGC	AGAGCCAAGT	GAAGATCACC	60
	TAAAGAACCT	TGTGGCTAAAT	TTATACTTCA	TGTAGTAGCA	GTGGGTACTG	GGCAGGGTCT	120
	CTTCCCACT	CTGATGATTT	GTGCTCTTAT	TTTTCTTAGA	TTTACCTCAT	CTAGGGCATA	180
	TTCTTTTCCC	TCTTCTCTTT	TACCTTTCTT	GGTCTGTATC	CCTCTGTACT	CAGTTCCCTT	240
	AAATTATGGG	ACTACAAACT	AAATYACTAG	AAAAGCATAC	ACTTATTTTA	TTTGAATGCA	300
15	GAAATGCTAT	CTATCAGTAT	ATATACATAA	GAATGTATAT	TACAGTATAT	CTATATATAC	360
	TTAACACTGT	AACCTTCAGT	ATTCCCCAGT	TAGCGTACCT	AACCTCTCTG	TGGGTTATGT	420
	TAATTCCTAT	TAGACTACTA	GAGAAAAACC	AACCTGGCAGT	TTGCTAAGCA	TATCTACTGG	480
	TGTTTCTTCT	CGGCCCCCTT	TTGGCTAATT	GATGTAAATTA	TACTGGCTCT	AAAGATTTC	540
	TGCCCCATAA	GTAAATAGTA	TAGCCACATT	CTGAACATAT	CAAAAGTACA	AACCTAGGAG	600
20	GAGTGTATGT	ACAAAATGT	AAAATTTTAT	GAAATGAAC	ATGTTTTTAT	GATGTTATTT	660
	CTAGTTCATA	AGAATGTGAT	GACTGCTTTG	CTTCATTTAT	GTACGTTCCT	ATTATATCTT	720
	TGCTGTCTAT	CATTCACAAA	TTTATATCAG	ATTAGGATAA	ACTAAGCCAT	TTTATGTATT	780
	TTATTTTAAA	CCTTATTTTG	GCAGAGTAAT	TCCTTAGAAT	TGGAAAAGCT	GTACCTTTGA	840
	AATTACCAAT	TTATTACAAA	ACATAGAAAT	GTATTGTAGC	TACAAAGACA	ACCAAGCATT	900
25	TTCTGTGTTT	TAATGATAT	CTAAAAAAT	ACATTTAGTT	TATTTTACTC	AGTTTGTAAA	960
	TGATTTTTTT	ACTGGCTCTA	TTGCCTTAAA	ATACTAAGA	GATTAAATGAT	TCTTTGTATA	1020
	ATTTCCTTTT	TCTTTGTCTT	TTTTTGTACA	TTTCGCAGAG	TTATATCTAT	AGTTTGTATA	1080
	ACATTTCTTT	ATGTATCTTG	GATAACTGAA	AACAACATAA	GGTGTGCGG	ATTAGAAAAT	1140
	AATTTGTAGC	AGTAGAATTA	CTGATGTAAT	ATGTATGTTG	GACTGAAGTA	TTTCTTTATA	1200
30	AACATCTCAT	TTGATTTTAA	GCAAAATGTA	TGTTAAAGCA	TGTTTTCATA	TCAGTAAAGT	1260
	CATTGTCCGA	CCTTCTGAAA	ATGAAAGGTT	TTTACCTAGA	TACTGTAAAT	TACAACCTCT	1320
	TAACAATCAT	ATTGTGCTAT	GTGTGTTTCT	GCAACCAAAA	ATGTTTATGG	GCCTCATGTA	1380
	GGCTTAAGAT	TGTAGCCAAA	AATGGACTGA	GTTCAGGACC	CTTCAGGAG	TAGGCATTCA	1440
	GTTCAGGAGC	AGTTGGTACT	TTGTAACCCA	GACTTACAGT	TTAAAAATAT	CAAGTTAGCT	1500
35	GATGTTTCAT	TATAATAAAA	ATACTATTTT	GCCTTAGAGT	TGATTTACAA	ATATTTGTGC	1560
	TTAACATTAG	AAATAGCTGT	TTTAAATGTT	AGTTAACATA	TTAATCTTTT	CAGAAAAAAA	1620
	GCATGGTTTA	TTTTTAATAA	TGAAATAGAG	AACATAATAC	GTAATGTTCA	GTATAACAGC	1680
	TGAGTTAAAA	CATCTGCCAG	GATTATACATC	AGTGCCTTTT	TGCCAATGCA	TAGAGGCATT	1740
	TTTCTCTAAG	TATGATGGCT	AATGATAACT	ATTCTTTGTT	ACACATTCAA	GTCACTCCCA	1800
40	TACAAGTAAC	TAGTGGGTGA	TATGTTTCAC	TCCAAAGGGT	GTATTAATCT	TGAATGCTAA	1860
	TCATGAAGAC	TTAAGTTAGG	ACAACACTTC	AAACCAGGAA	GTGTGAACCT	ATTTA	

Seq ID NO: B25 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..1144

45

	1	11	21	31	41	51	
50	ATGGAGCGCG	GGATGCACCT	CGGTGCAGCG	GCCGCCGCGG	AGGACGACCT	CTTCTGCAC	60
	AAGAGCCTGA	GCOCCTCCAC	CTCCAAGCGG	TTGGAAGCGG	CTTCCGCTC	CACGCCCCCG	120
	GGCATGACCC	TGTCCCTGGC	GCOCGCCGCT	CGGGAAGCGC	CGGCGTCTC	CTCCTGCTCG	180
	CCCTCGGCT	GCCTCGAGCC	GGCTGACCCC	GAGGGGGCAG	GGCTGCTGTT	GCCCGCCGCT	240
	GGAGGAGCGG	GCGGCGGCGG	CGCGGGAAGT	GGCGGCGGCG	GCGGCGGCGG	GGTGGGGTTC	300
	CCCGGGCTGC	TAGTAGGTTT	AGCCGGGCTT	GGGGGGGACC	CTAGCCTAAG	CAGCCTGCGG	360
55	GCGGGGGCGG	CCCTTTGCTT	CAGTAGCGGC	GAAAGCGCGA	GCGGGGGCTC	GGTGGCCGAG	420
	AGCAGCGCGG	GCGAGCAGAG	CCCGGAGGAC	GACAGGCGAG	GTGCTGCGGA	GCTCCTGCTG	480
	CGGGCGGAG	TAGCCGACCC	CGGGGCTCTC	CCGGGAGCGG	GAGGTGGTGG	CGCGAAGGCA	540
	GCGAGGGGCT	GCTCCATGCT	CCACCTCCAC	GGCGGCGCCA	GGTCCCTCC	GGGGGGGCTG	600
	GGCGGGCGCG	GCGGCGGGGG	TAGCAGCAGC	GGTAGCAGTG	GCGGCGGTGG	CGGTAGCGGT	660
60	AGCGGCAGCG	GCGGCAGCAG	CAGCAGCAGC	AGCAGCAGCA	GCAAGAAATC	CAAGAGCACA	720
	AAGGCGCTGC	GGCTTAACAT	CAATGCCCGA	GAGCGCCGCG	GGATGCACGA	CCTGAACGAC	780
	GCGCTGGACG	AGCTGCGCGC	GGTGAATCCC	TACGCGCACA	GCCCTCGGTT	GCGAAAGCTC	840
	TCCAGATGCG	CCACGCTGCT	GCTCGCCAA	AACATACATC	TCATGCAGGC	GAGGCGGCTG	900
	GAGGAGATGC	GCGCCTTAGT	CGCCTACCTC	AACGAGGCGC	AGGCCATCTC	GGCTGCTCTC	960
65	CTGCCGAGCT	GCGCGGCTGC	AGCGGCAGCA	GCTGCTGCCC	TGCACCCGCG	GCTCGGCGCC	1020
	TACGAGCAGG	CAGCGGCTGA	CCCGTTGAGC	GCGGAGCTGC	CCCGGCTGTC	CTCCTGCGCG	1080
	GAGAAGTGGG	CCCTGTTTAA	CAGCGTCTCC	TCCAGGCTCT	GCAACAGATG	CACGAGAGAG	1140
	CCTT						

70

Seq ID NO: B26 Protein sequence  
 Protein Accession #: FGENESH predicted

	1	11	21	31	41	51	
75	MERGMHLGAA	NAGEDDLFLK	KSLSASTSKR	LEAAFRSTPP	GMGLSLAPPP	RERPASSSSS	60
	PLGCFEPADP	EGAGLLLPFP	GGGGGGGAGS	GGGGGGGVGV	EGLLVGSAGV	GGDPSLSSLP	120
	AGALCLKYU	ESASRGSVAE	SSGGGQSPDD	DSGRCCLVL	RAGVADPRAS	PGAGGGGAKA	180
	AECSNAHLH	GGASVPPGGL	GGGGGGGSSS	GSGGGGGGSG	SGSGSSSSSS	SSSSKKSKEQ	240
	KALRLINAR	ERRRMEDLMD	ALDELRAVIP	YAESPSVRKL	SKLATLLAK	NYILMQAAL	300
80	ERNRLVAYL	NQGQALSAAS	LPSSAAAAAA	AAALHPALGA	YEQAAGYPPS	AGLPPAASCP	360
	EKCALFNSVS	SSLCTQCTEK	P				

Seq ID NO: B27 DNA sequence  
 Nucleic Acid Accession #: cat cluster

Seq ID NO: B28 DNA sequence  
Nucleic Acid Accession #: NM\_002581.2  
Coding sequence: 368..5251

808

GTACCACTAT TGGGTCATAA CTATTTTCAGG AACTGAAGAG AGTGAGCCAT CACCTGCTGT 3180  
 CACATACATC CATGGACGTG GGTACTGTGG CGATGGCATT ATACAAAAG ACCAAGGTGA 3240  
 ACAATGCGAC GACATGAATA AGATCAATGG TGATGGCTGC TCCCTTTCT CCGGACAGA 3300  
 AGTCTCCTTC AATTGTATTG ATGAACCCAG CCGGTGCTAT TTCCATGATG GTGATGGGT 3360  
 ATGTGAGGAG TTGGAACAAA AAACCCAGCAT TAAGGACTGT GGTGTCTACA CGCCCCAGG 3420  
 ATTCTGGAT CAGTGGGCAT CCAATGCTTC AGTATCTCAT CAAGACCAGC AATGCCAGG 3480  
 CTGGGTCAIC ATCGGACAGC CAGCAGCATC CCAGGTGTGT CGAACCAAGG TGATAGATCT 3540  
 CAGTGAAGGC ATTTCCAGC ATGCTTGTGA CCCTTGCAAC ATCAGCTACC CATATTCCTCA 3600  
 GCTGGCTCAG ACCACTTTT GGCTCCGGGC GTATTTTCT CAACCAATGG TTGCCGAGC 3660  
 TGTCATTGTC CACCTGGTGA CGGATGGGAC ATATTATGGG GACCAAAAGC AGGAGACCAT 3720  
 CAGCGTCGAG CTGCTTGATA CCAAGATCA GAGCCACGAT CTAGGCCTCC ATGTCTCTAG 3780  
 CTGGAGGAAC AATCCCTGA TTATCCCTGT GGTCCATGAC CTCAGCCAGC CTTCTACCA 3840  
 CAGCCAGGCG GTACGTGTGA GCTTCAGTTC GCCCTGGTC GGCATCTCGG GGTGGCCCT 3900  
 CCGTTCCTTC GACAACTTTC ACCCGCTCAC CCTGAGCAGC TGCCAGAGAG GGGAGACCTA 3960  
 CAGCCCTGCC GAGCAGAGCT GCGTGCATT CGCATGTGAG AAAACTGACT GTCCAGAGCT 4020  
 GGTCTGGAG AATGCTTCTC TCAATTCCTC CAGCAGCAGC CGCTACCAAG GTGCCAGTG 4080  
 TACTGTGAGT TGCCGACAG GCTACGTGCT CCAGATACGG CGGATGATG AGCTGATCAA 4140  
 GAGCCAGAGC GGACCCAGC TCACAGTGAC CTGTACAGAG GGCAAGTGA ATAAGCAGGT 4200  
 GGCCTGTGAG CCAGTCGACT GCAGCATCCC AGATCACCAT CAAGTCTATG CTGCTCTCTT 4260  
 CTCTGCTTCT GAGGCGACCA CCTTTGGCAG TCAATGTTC TTCCAGTGCC GTCACTCTGC 4320  
 ACAATTGAAA GGCACACAA GCCTCCTGAC CTGCATGGAG GATGGGCTGT GGTCTCTCCC 4380  
 AGAGGCCCTG TGCCGACAG TGTGCTCTGC TCCACCCCT GTGCCCAAGT CAGACCTCCA 4440  
 GACCGCCCGG TGCCGAGAGA ATAAGCACAA GGTGGGCTCC TTCTGCATAT ACAATGCAA 4500  
 GCGTGGATAC CATGTGCTTG GATCTCTCTG GAAGTCAAAG AAACGGGCTT TCAAGACTCA 4560  
 GTGTACCCAG GATGGCAGCT GCGAGGAGG AGCTTGTGTT CCTGTGACT GTGACCCACC 4620  
 TCCACCAAAA TTCCATGGGC TCTACCATG TACTAATGGC TTCCAGTCA ACAGTGAGTG 4680  
 TAGATCAAG TTGGAAGACA GTGATGCTTC CCAGGACTT GGGAGCAAT TCATTCAATG 4740  
 CCGGAAAGAT GGCACCTGGA ACGGCTCCTT CCATGTCTGC CAGGAGATGC AAGGCCAGTG 4800  
 CTGCTTCCA AACGAGCTCA ACAGCAACT CAACTGCGAG TGCCCTGATG GCTATGCCAT 4860  
 AGGTCTGAG TGTGCCACTT CGTCTCTGGA CCAACACAGC GAGTCTATCA TCTGCTCAAT 4920  
 GAGCGTGAAC GTGGCTGAG TCCGCCACTG GCTGAACCCC ACACGGGTAG AGAGAGTTGT 4980  
 CTGCACTGCT GGTCTCAAGT GGTATCTCTA CCTGCTCTG ATTCACTGT TCAAGGCTG 5040  
 TGAGCCCTTC ATGGGAGACA ATTATGTGA TGCCATCAAC AACCGAGCTT TTGCAACTA 5100  
 TGACGCTGGG GATGTCTGCA CTCTCCAGT GAAGACCAAA AAGGTCAACC CATTCCTAT 5160  
 TCTCTGTGAC CTACAGGCTG ACTGTGCTTG TCGGAGCCCC CAGGCCCAAG AACACAGCG 5220  
 GAAAGACTCT CGGGATACA GCCATGGCTA AGGAAGCACA AGAAGTGTG AAGAATTCC 5280  
 CAGCGCAGG CAGCAGCATC CTTGTGATT GATTTCACAG TCAGCTGCTC AACGGAATG 5340  
 CCTCTCCACA CAGGGATCC TTAGCACCCA ACGGTCTGC CTTAATTTT ACCCAGGAAG 5400  
 GACTCACATT GGGCGAATG AACCAAGTTT CGCCATGCTG GATGATGAAA TGGATTCCTA 5460  
 TCCCAAGTCT TGAGATGGAT TGCATATACA GTGTGCAGTC CCAGAGCTTC CTAAATTTCT 5520  
 AGCCATTGT CACACACCA CAGCAAAAA AAA

Seq ID NO: B29 Protein sequence  
 Protein Accession #: NP\_002572.1

1 11 21 31 41 51  
 MRLWSVLHL GLLSAALGCG LAERPRRARR DPRAGRPRP AAGPATCATR GPRPPRLAAA 60  
 AAAAGRAWFA VRVRRRRQQR BARGATEEPS PPSRALYFSG RGBQLRVIRA DLELPDRAFT 120  
 LQVLRLEGG QRSFVITGL YDKCSYISRD RGVVVGIIHTI SDQDNKDPRY FFLKTDRLAR 180  
 QVTINAHRS YLPGQVYVLA ATYDQGFML YVNGAQVATS GBQVGGIFSP LTQCKKVLML 240  
 GGSALNNHNR GYIEFSLWK VARTOREILS DMSTHGAHTA LPQLLLQENW DNVKHAWSPM 300  
 KDGSFPKVEF SNAHGLFLLT SLEPFLCQQT LCNTEKVIAS YKQLSSFRQP KVVRYRVVNL 360  
 YEDHKNPTV TREQVDFQHH QLAERFKQYN ISWELDVLEV SNSSLRRRLI LANCDISKIG 420  
 DENCDPBCNH TLTGSDGGDC RHLRHPAFVK KQHNGVCDMD CHYERFNFDD GBCDDPEITN 480  
 VTQCTFDPDS PRHAYLDVNE LKNILKLDGS TELNIFPAKS SEELAGVAT WPDKEALMH 540  
 LGGLVLPSPF YGMPFHYTHM IBEIGHSLGL YHVFEGISEI QSCBDPCMET EPSFETGDLG 600  
 NDMPAPKKH SCGDGPGGMD TCGEHSFENT PVNFMSTAD DDCTDSFTPN QVARMHCYLD 660  
 LVYQGWQPSF KPAFVALAPQ VIGHTDSVT LEWFPPIDGH FFERELGSAC HLCLEGRILV 720  
 QYASNASSPM PCSPSGHNSP REARGHPDVE QPCKSSVRTW SPNSAVNPHV VPPACPEPQG 780  
 CYLELEFLYE LVPESLTINV TFVSTWDSS GAVNDIKLLA VSGKNISLGP QNVFCDVPLT 840  
 IRLNDVGBEV YGIQYITLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVVV DPFLQMDVAS 900  
 ILHLNRKFVD MDLNLGSSVYQ YWVITLSTGE ESEFSPAVTY IHGRGYCGDG IIOKDQGEQC 960  
 DDMNKINGDG CSLFCRQEVF FNCIDPSSRC YFHDGQVCE EPEQKTSID CGVYTPQGF 1020  
 DQNASNAEVS HQDQCQPGWV IIGQPAASQV CRTKVIDLSE GISQAWYPC TISYPYSQLA 1080  
 QTTFWLRATF SQPMVAANVI VHLVTDGTYI GDQKQETISV QLLDTKQSH DLGLHVLSCR 1140  
 NNPLIIPVVH DLSQPFYELSQ AVRSFSEPL VAISGVALRS FDNFDPVTL SQRGETYSP 1200  
 AEQSCVEFAC EKTDCRELAV EASLNCSSS DRYHGAQCTV SCRTGYVLQI RRDDELISQ 1260  
 TGPSTVTCT EGKWNQVAC EPVDCSIDPH HQVYASFSFC PEGTTFGSQC SFQCRHPAQL 1320  
 KGNNSLLTCM EDGLNSFPFA LCELMCLAPP FVPNADLQTA RCERNKHVKG SPCKYKCKPG 1380  
 YVEGSSRSKS KKAFAKTQCT QDGSQWQEGAC VPVTCDFPPP KPEGLYQCTN GFQFNSCRI 1440  
 KCRDSDASQ LGSNVTLCRK DGTWNGSFHV CQEMQGCSCV PNELSNLKL QCPDGYAIGS 1500  
 ECATSCLDEN SSGIILEPMV TVRDIPHNLN PTRVERVCT AGLKWEHPA LIRCVKGECP 1560  
 PMGDNYCDAI NNRAFCNYDG GDCCSTSTVKI KKVTFPMSC DLQSDCACRD PQAQESRKD 1620  
 LRYSSE

Seq ID NO: B30 DNA sequence  
 Nucleic Acid Accession #: NM\_032808.1  
 Coding sequence: 61..1008

1 11 21 31 41 51  
 CTAGTCTATC TCGCTTCTT CAACTCTCC TACAACCCA TCAGCACCAT TGAGGCTCC 60  
 ATGTTGCATG AGCTGCTCC GCTGCAGGAG ATCCAGCTGG TGGCGGGCA GCTGGCGTG 120

5 GTGGAGCCCT ATGCGCTCCG CGGCTCAAC TACCTGCGOG TGCTCAATGT CTCTGGCAAC 180  
 CAGCTGACCA CACTGGAGGA ATTAGTCTTC CACTGCGTGG GCAACCTGGA GACACTCATC 240  
 CTGGACTCCA ACCCGCTGGC CTGGGACTGT CGGCTCCTGT GGGTGTTCGG GCGCGGCTGG 300  
 CGGCTCAACT TCAACCGGCA GCAGCCCAAG TGGGCGACGC CGAGTTTGT CCAGGGCAAG 360  
 GAGTTCAAG ACTTCCCTGA TGTGCTACTG CCAACTACT TCACCTGCGG CGCGCGCCGC 420  
 ATCCGGGACC GCAAGGCCCA GCAGGTGTTT GTGGAAGAGG GGCACACGAT GCAGTTTGTG 480  
 TGCCGGGCGG ATGGCGACCC GCGCGCCGCC ATCTCTGGC TCTCACCCCG AAGCACCTG 540  
 GTCTCAGCCA AGAGCAATGG GCGGCTCACA GTCTTCCCTG AAGGCAOGCT GAGGTTGCGC 600  
 TACGCCAGG TACAGGACAA CGGCACGTAC CTGTGCTCG CGGCCAACGC GGGCGGCAAC 660  
 GACTCCATCG CGCGCCAGCT GCATGTGCGC AGCTACTGCG CGGACTGGCC CCATCAGCCC 720  
 AACAGACCT TCGCTTTCAT CTCCAACCA CGGGCGAGG GAGAGGCCAA CAGCACCCGC 780  
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 AAGGGCAACA CAAGACACAA CATGAGATC GAGTATGTGC CCGAAAGTTC GGAAGCAGGC 960  
 15 ATCAGTCTCG CGCGCGAGC CGGCAAGTTC AACATGAAGA TGATATGAGG CCGGGGCGGG 1020  
 GGGCAGGAGC CCGCGGCGCG CGGGCAGGG GAGGGGGCTT GGGCGCCACC TGCTCACTCT 1080  
 CCAGTCTCTC CACTCTCTCT CTAACCTTTC TACACAGTT CTCTTCTCTC CTCCGCTCTC 1140  
 CGTCCCTGTC TGCCCCCGCG CAGCCCTCAC CACCTGCCCT CTTTCTACCA GACCTCAGA 1200  
 AGCCCGAGAC TGGGGACCCC ACCTACACAG GGGCATGAC AGACTGGAGT TGAAAGCCGA 1260  
 20 CGAACCGACA CGCGCGAGG TCAATAATTC AATAAAAAAG TTACGAACTT TCTCTGTAA 1320  
 TTGGTTTCA ATAAATATGG ATTTTATGA AAATTTGAAA TAATAAAAAG AGAAAAAAC 1380  
 TATTTCCTAT AGCTAGTCCG AATGCAAACT TTTGACGTCC TGATGTCTCC AGGGCCCTCT 1440  
 TCCAACTCAG TTTCTTGTTC TTCTCTTCTT CTTCTCTCTT TTTCTCTCTT TTTCTCTCTT 1500  
 25 CTTCCCACTG GGGGAGGGAT CACTCAGGAA AACAGGAAG GAGGTTCAG CCCCACTCTC 1560  
 CTGCCCCACC CGGCCGAGC ACCATCAGGA GCAGGCTAGG GGGCAGGCTT GGGCCAGCT 1620  
 CCGGGCTGGC TTTTTCAGC GCGCAGGTGG AGGGGACAGG TCTGCGGATG GGGGTGGGAG 1680  
 CCTGTCTGCT GGGCTGCTCG GCGGCACAC TGCAAGGGGT GGGAGCCTGG CTTGGGTGTG 1740  
 GCTGAGACTC TGGACAGAGG CTGGGGTCTT CTTGGGGGAC AGCAGGTCA GTGGAGAGAG 1800  
 30 CCAGGGCTCG GAGGTGGGGC CCACCTCAGC CTCTGCTCCC AGCTCTGCTG CTCACTTGCT 1860  
 GTGTGGCTTC AAGCAGGTCA CTGGCTCTCT TGGGCTCAG TCTCCACATC TGTACAAATG 1920  
 GGAACATTAC CCCTGCGCTT GCTACCTCA CAGGGCTGTT GTGAGGAATT GATGAGATGA 1980  
 TGTATGTGAA ACCTTTGTA ACCTGTAAAG CGCTGTGCAC ACGTG

Seq ID NO: B31 Protein sequence  
 Protein Accession #: NP\_116197.1

1 11 21 31 41 51  
 40 MLHRLRLQEQ IQLVGGQLAV VEPYAFRGLN YLRVLNVSGN QLTTLLELVF HSVGNLLETLI 60  
 LDSNPLACDC RLNVVFERRE RLNFNRQOPT CATPEFVQVK RFDKDFPDVLL PNYFTCRRAR 120  
 IEDRAQGVF VDEGHTVQFV CRADGDPFPA ILWLSPRKEL VSAKSNRGLT VFFDGTLEVR 180  
 YAQVQDNQTY LCIAANAGGN DMPAHLFVR SYSPDWPHQP NKTFAFISNQ PGEGBANSTR 240  
 ATVPFFFDIK TLIATWTMGP ISFLGVVLFPC LVLLPLNSRG KGNTKHNIRI EYVPRKSDAG 300  
 ISSADAPRRF NMKMI

Seq ID NO: B32 DNA sequence  
 Nucleic Acid Accession #: CM1 cluster

1 11 21 31 41 51  
 50 CAGCACATAC AAGAAACATA CAGTGTACCT CAAAAGGGGC CTTTGAATG TCATCAAAGG 60  
 GTATATACCT AGTGAGTGGG TTGATGATGC ATCTGGAACA TAGGAATGG GGTCTTTAGC 120  
 GTATTCGGTA CGAAGGAAGC CAGGCTGGTC CTGGCAGGAA GTAAATGATA ATCTTTGGGA 180  
 55 AACCAGGACC CTGCTCCCA GCGCAGAGGT GGAGGAGGGC GGTCAAGGTG GGTCTTACAG 240  
 TGGCACAGCA CTGACAAAGG TAGAGGGAAA TGTATATAGCA CATCTACGCT GCAGTCTGGT 300  
 GAAAGTGGCC GGGGTGGTCC TTGAAAACA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC 360  
 AGCCTTTCGG TCACGGGCGG GGACGCTTGT ATTTAAATAA AATAAATAAA TAAACGTCT 420  
 GGGTATAGAA A

Seq ID NO: B33 DNA sequence  
 Nucleic Acid Accession #: NM\_006174.1  
 Coding sequence: 71..1408

1 11 21 31 41 51  
 65 GAAAGGCTAT CGGTAACAAC TGACCTGCCA CAAAGTTAGA AGAAAGGATT GATTCAAGAA 60  
 AGACTATAAT ATGGATTTAG AGCTCGAAGA GTATTATAC AAGACACTTG CACACAGAGAA 120  
 TAATACTGCT GGCACCTCGA ATTCTGATTT CCCAGTCTGG GATGACTATA AAGCAGTGT 180  
 70 AGATGACTTA CAGTATTTTC TGATTTGGCT CTATACATTT GTAAGTCTTC TTGGCTTTAT 240  
 GGGGAATCTA CTTATTTTAA TGGCTCTCAT GAAAAGCGT AATCAGAGGA CTACGGTAAA 300  
 CTCTCTCATA GGCATCTCG CTTTCTCTGA TATCTTGGTT GTGCTGTTT GCTCACCCTT 360  
 CACATGACG TCTGTCTTGC TGGATCAGTG GAGTTTGGC AAGTCAATGT GCCATATTAT 420  
 GCTTTTCTT CAATGTGTGT CAGTTTGGT TTCACTTTA ATTTAATAT CAATTGCCAT 480  
 75 TGTCAAGTAT CATATGATAA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540  
 CTTCTGATA GCTACTGTCT GGACACTAGG TTTTCCATC TGTCTCCCC TTCCAGTGT 600  
 TCACAGTCTT GTGGAATCTC AAGAAACATT TGGTTCAGCA TTGCTGAGCA CGAGGTATTT 660  
 ATGTTTGGG TCAATGGCAT CTGATTCATA CAGAATTGCC TTTACTATCT CTTTATTGCT 720  
 AGTTCAGTAT ATTCTGCGCT TAGTTTGTCT TACTGTAGT CATACAAGTG TCTGCAAGAG 780  
 80 TATAAGCTGT GGAATGTCCA ACAAAGAAA CAGACTTGAA GAAAATGAGA TGATCAACTT 840  
 AACTCTTCAT CCTATCCAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG 900  
 GAGTATATCA TTATCAAAA AACACAGAG AAGATATAGC AAGAGACAG CATGTGTGTT 960  
 ACCTGTCCA GAAGAGCTT CTCAAGAGAA CCACTCCAGA ATACTTCCAG AAAACTTTGG 1020  
 CTCTGTAGA AGTCAGTCTT CTTATCCAG TAAGTTTATA CCAGGGGTCC CCACTGTCTT 1080  
 TGAGATAAAA CCTGAGAAA ATTCAATGT TCATGAATG AGAGTAAAC GTTCTGTATC 1140

AAGAATAAAA AAGAGATCTC GAAGTGTTTT CTACAGACTG ACCATACTGA TATTAGTATT 1200  
 TGCTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAATCT 1260  
 TATTTCAAAT AGGCATTTCA AGTTGGTGTA TTGCATTTGT CATTGTGTGG GCATGATGTC 1320  
 CTGTTGCTTT AATCCAAATC TATATGGGTT TCTTAATAAT GGGATTAAAG CTGATTTAGT 1380  
 GTCCCTTATA CACTGCTTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence  
 Protein Accession #: NP\_006165.1

1 11 21 31 41 51  
 MOLELDEYYN KTLATENNTA ATRNSDFPVH DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60  
 LILMALMKRR NQKTTVNFLI GNLAFSIDL VLFCSPTFLT SVLLDQWMPG KVMCHIMPFL 120  
 QCVSVLVSTL ILISIAIVRY HMIKHPISNM LTANEGYFLI ATVNTLGFAL CSPLFVFFHSL 180  
 VELQETFGSA LLSSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240  
 GLSNKENRLE ENEMINLTLH PCKKSGPQVK LSGSHKWSYS FIKGHRRRYS KTKACVLPAP 300  
 ERPSQENHSR ILLENFGSVR SGLSSSSKFI PGVPTCFEIK PEENSVDVHEL RVKRSVTRIK 360  
 KRSRSVFYRL TLLILVFAVS WMPLHLFHVV TDFNDNLISN RHFKLVYICIC HLLGMMSCCL 420  
 NPILYGLFNM GIRADLVSLI HCLHM

Seq ID NO: B35 DNA sequence  
 Nucleic Acid Accession #: NM\_014279.1  
 Coding sequence: 286..1689

1 11 21 31 41 51  
 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCCC CCAGCCGAGC 60  
 CCTGCCGAGC CTTGCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120  
 CGGAGGCTTC GCBACAGACA GCGCGCGCGC CGCCGCTCC GGGTGTGAA TCCAGCCGTG 180  
 GGGACACBAG CAGAGCGCGG CCGCGGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240  
 TCCGCGTCCA CCGAGCCGCG CCGCGGCCAG CACCCAGGGC CCTGCATGCC AGGTGCTTGG 300  
 AGGTGGCAGC GAGACATGCA CCGCGCCCGG AAGCTCTCTA GCTCTCTCTT CCTCATCTTG 360  
 ATGGGCACTG AACTCACTCA AGTGTGCCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420  
 AGCTCTGCCC AGGACAGCGA GGCAGGTGT ATCTGCACAG TGGTGCCTCC ACACAGAGCC 480  
 ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540  
 ATGTCTCAAT CCTAGAGAGT CTGAGCAGG CCGACCCAGA GAGACTTCCA GTACGTGGAG 600  
 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAAGTTCA AACAGGTGGA GGAGAGTCAT 660  
 AAGCAACACC TGGCCAGGCA GTTAAAGGCG ATAAAGCGA AAATGGATGA ACTTAGGCCT 720  
 TTSATACCTG TGTTGGAGA GTACAAGGCC GATGCCAAT TGGTATTGCA GTTAAAGAG 780  
 GAGGTCCAGA ATCTGACGTC AGTGTCTAAC GAGCTGCAG AGGAAATTGG CGCCTATGAC 840  
 TACGATGAAC TTCCAGAGCAG AGTGTCCAT CTGGAAGAAA GGCTCCGTGC ATGCATCCAA 900  
 AAACATAGCTT GAGGGAAGTT GACGGGCATC AGTGAACCCG TGACTGTCAA GACCTCCGGC 960  
 TCGAGGTTCG GATCTCGGAT GACAGACCTT CTCGCCCTCG AAGGCGATAA CCGGGTGTGG 1020  
 TACATGGACG GCTATCAACA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGACTTTC 1080  
 ATGAACACGG ACAATTTTAC CTCCACCGT CTCCCCACC CCTGTCGGG CAGGGGCGAG 1140  
 GTGGTCTACA ACGGTTCTAT CTACTTCAAC AAGTTCAGG GCCACATCAT CATCAGGTTT 1200  
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCCGG TTACAACAAC 1260  
 ATGTACCACT ACGCTCGGG TGGCCACTCG GACATCGACC TCATGGTGGG CAGAGAGCGG 1320  
 CTGTGGGCGG CTGTCCCGG CAACCGACAC CTTGGCAACA TCGTGGTCAG TAGGCTGGAC 1380  
 CCGCTGTCCC TGCAGACCTT GCAGACCTGG AACACBAGCT ACCCAAGCG CAGCGCCGGG 1440  
 GAGGCTTCA TCACTGTCGG CACGCTGTAC GTCAACCAAG GCTACTCAGG GGTATCCAG 1500  
 GTCCACTATG CATACAGAC CAATGCTTCC ACCTATGAAT ACATCGACAT CCTATCCAG 1560  
 AACAAATACT CCCACATCTC CATGCTGGAC TACAACCCCA AGGACCGGGC CCTGTATGCC 1620  
 TGGAAACAAG GCGACCATCT CTTCTACAC GTGACCTCTT TCCAGTCAAT CCGCTCCGAC 1680  
 GAGTGTGAGC TCCCTCTCTC TGGAAAGCAA GGGCCCAAGT CCTCACCAAC AAGGACTTCC 1740  
 TGTGAAACTG CTGCGCAAAA GATACCAATA ACTATAACAA TACCATCTT GAAAAATCAT 1800  
 CAGCAGTTCG GATCTGACA TCGAGGGATG GCATTACCTC CGTGTCTTTC CTTTCCAGT 1860  
 CGCGCGGGCA CAGACGTGCG AAGAACTTCC CGTATTGCA GCTGGAACAG CAGGCCAGG 1920  
 CGCCCGGGTT TTCTCCCGG CCGTCTCCT CTCTGGTCAA ACAACATACT AAGAGGCGGA 1980  
 GGCATGACT GTTGCCAGT TCTCACCGGG GAAAAACCA CTGTTAGGAT GGCATGAACA 2040  
 TTTCTTAGA TGTGTGTAG CTCCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG 2100  
 GCTGCACCGG GCGTAGGCT AGTGTAACTC GCATCCCAT GCAAGTCCGT TTCTTGACTG 2160  
 TGTGCTGTC TCTTAGATTA ACCGTGCTGA GGCTCCCAT AGCTCCTGGA CCTGTGCTTA 2220  
 GTACATCTG AAGCGATGGT CAGAGTGTGT AGAGTGAAGT TGCTGTGCCC ACATTGTGTG 2280  
 AACTGCGGTA CCGGTAGAT ACATTGTGCA ACGTCTCTCT GTTATTCCTT TGAGGTGATA 2340  
 ACTTGTATG TTCACTTTAT GCGATGATT TTGTAAATGC AATGCCGTAG TTTGGATTAA 2400  
 TAAGTGGATG GTTTTGTGTT CTAAAAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2460  
 CATAGTCAAG TTCACTGTTA TAATAATCAA AGGAATTAAT CTCTCTTGT TAAATTAGCT 2520  
 AATCATGTA ACCGCAATA GGAAGGGCTC ACTTGGTTT CCGATGGGAC 2580  
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTTAAAGTAA AAAACAAAGG 2640  
 CAAACTTTGT ACTATCCAGT TATCTAAGGA ACRATAAAAA CATTAGGAGA AAAAAAATAA 2700  
 AAAAAAATAA AAAAAAATAA AAAAAAATAA A

Seq ID NO: B36 Protein sequence  
 Protein Accession #: NP\_055094.1

1 11 21 31 41 51  
 MPGRNRWORD MHPARKLLSL LFLILMSTEL TVLPTNPEE SWQVYSSAQD SEGRICITVV 60  
 APQQTMCSSD ARTKQLRQLL EKVQMSQSI EVLDRRTQED LQYVEKMEHQ MKGLESKPKQ 120  
 VEEGHQQLA RQFKAIKAKM DELRLPIPLV KEYKADAKLV LQFKKEVQNL TSVLNLQEE 180  
 IGAIDYDELQ SRVENLEERL RACMQMLACG KLTGISDFVT VKTSGSRFGS WMTDFLAPEG 240  
 DNRVVMYMDG HNRFPVREYK SMVDPMWTDN FTSERLPHPW SGTGQVYVNG SIYFNKFSH 300  
 IIRFDLKTG TILKTRSLDY AGYNWYHYA WGHSDIDLDM VDESGLWAVY ATNQNAGNIV 360

VSRLLDPVSLQ TLQTNWTSYP KRBAGEAFII CGTLYVTNGY SGGTKVHYAY QTNASTYSEI 420  
 DIPFQNKYSH ISMLDYNFKD RALYANNNGH QILYNVTLFH VIRSDEL

Seq ID NO: B37 DNA sequence  
 Nucleic Acid Accession #: NM\_006334.1  
 Coding sequence: 286..693

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1      11      21      31      41      51
|      |      |      |      |      |
10  GCCTGGGGGA GCCATTAGGA GGCAGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
    CCTGCCCAGC CCTGCCCGGA GGCAGAGCGG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
    CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTGAA TCCAGGCGTG 180
    GGGACACGAG CCAGGCGCGG CGCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
    TCCGCTCCA GCGAGCGCGC GCGCGGCGAG CACCCAGGGC CCTGCATGCC AGGTCTGTGG 300
15  AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCTCTCT CCTCATCTCT 360
    ATGGGCACTG AACTCACTCA AGTGTCTGCC ACCAACCTTG AGGAGAGCTG GCAGGTGTAC 420
    AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTGGCCCC ACAGCAGAAC 480
    ATGTGTTCAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
    ATGTCTCAAT CCATAGAGGT CTTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
20  AAGATGGAGA ACCAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GAGAGTCAAT 660
    AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACTTAAAA GAGTTTTCCT AATGCTGCAG 720
    TGACTGAAGA AGCATTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTGTGA 780
    CCATGCAATT TTAATTATAT TTTCCAATAC TTAGCACCAT TTCCTAAGG AACCTTGAAT 840
    ACAACAGAGA TCCCTCTTTG CATCGCACTG TAGCTGCATT TCATGAATAG TTTGAACCTT 900
25  TGTCAATGCA TTTTITGAAA AAGAAAGAAA AAAAAAATT CTTGTATGTG ACTCAAAGCA 960
    TGTAACTTA AGATGTGTGA TTCTAAACTG ACAATAAAGA CCTTCCCC
  
```

Seq ID NO: B38 Protein sequence  
 Protein Accession #: NP\_006325.1

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1      11      21      31      41      51
|      |      |      |      |      |
30  MPGRWRWRD MHPARKLLSL LFLILMGTEL TQVLPTNPRE SQVYSSAQD SEGRICITVV 60
    APQQTMCSDR ARTKQLRQLL EKQNMSSQSI SVLDRRTQRD LQYVERMENQ MKGLSEKFRQ 120
35  VESHHKQHLA RQFKG
  
```

Seq ID NO: B39 DNA sequence  
 Nucleic Acid Accession #: NM\_058199.1  
 Coding sequence: 286..795

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1      11      21      31      41      51
|      |      |      |      |      |
40  GCCTGGGGGA GCCATTAGGA GGCAGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
    CCTGCCCAGC CCTGCCCGGA GGCAGAGCGG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
    CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGTGAA TCCAGGCGTG 180
    GGGACACGAG CCAGGCGCGG CGCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
    TCCGCTCCA GCGAGCGCGC GCGCGGCGAG CACCCAGGGC CCTGCATGCC AGGTCTGTGG 300
    AGGTGGCAGC GAGACATGCA CCCGGCCCGG AAGCTCCTCA GCCTCTCTCT CCTCATCTCT 360
    ATGGCACTG AACTCACTCA AAATAAAGA GAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
50  GAGAGCAGAG GGAAGACCAC AGGAGAGAAG AACTGAAAG AGCTTCCCTT GTTTTGCCTG 480
    GAAGCCCAAG CTGGCTCCTT GGCATCTGCC AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
    GTGGGTATAT GTGCTCCCGC TTACCTTCAG AGCCCTTCTC CTGGTGTCTG CCAGACGATC 600
    AGCCAGTCCC TCCTGAGAGG GTTCTGCAAG GCCTCTAGGA GAGAAATTTT CTGGGCCCCA 660
    GGAAGGCGTG GTGGAGGGTG GTGGTGTGTC ACTGTTGCTG GACAGATGCA TTCACTCATG 720
55  TGCACACACA CACACACACA TGCACACACA GGGAGACAGA TACCTGAGA GAAGAGCCAA 780
    CCAGGTCTCT ATTAGTGGCA AGCTGCCCCA CAAAGGGCTA TGCTGTGTCT TTATTGAGAC 840
    ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTCTGAC ATGGCCGAC CCAAGGGCCC 900
    TCCAGCCTT AATGGCACCC TGAAGCCTCC ATGCCAGGC CAAAGATGC TTTTCTCTCC 960
60  TAAAAA AAAA
  
```

Seq ID NO: B40 Protein sequence  
 Protein Accession #: NP\_478106.1

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1      11      21      31      41      51
|      |      |      |      |      |
65  MPGRWRWRD MHPARKLLSL LFLILMGTEL TQNKRENKAE RMGGPESERK TTGEKTLNEL 60
    PLPCLBAHAG SLALPRMCSP NPNPAVGLCR PAYPQSPSPG AAQTISQSL ERFCMASRRE 120
    VFLAPGRPGG GWNLCITVAGQ MHSFMCETHH THAHTGRQIP AEKSQPGPD
  
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Seq ID NO: B41 DNA sequence  
 Nucleic Acid Accession #: AY038071.1  
 Coding sequence: 1..1686

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1      11      21      31      41      51
|      |      |      |      |      |
75  ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT 60
    CCAACTTTGC TCTCCTCCTA CTGCATCGAC AGCATCCTGG GCGGAGGAG CCGGTGCAA 120
    ATGCGGTTGC TGGGAGCGCG GCAGAGCTTG CTTGCTCCGC TGACCAAGCG CGCGAGCCCG 180
    GAAAGAGCGG TGCAAGGCTC CCTTAAGAGC AGCAGCGCCC CGTTGAGGGC CAGCTGACAC 240
    CTGCGGCCCA AGCTGCGGCG CTTGTACGCG CCGGGGCGGG GCGGCTCCTT TCAGGGTGGT 300
    GCAGCGCGCG CGCGCGCGCG GCGCGCGCGG GCGGCGAGCG CCGCCACGCG CACGGCGGGT 360
    CCAAGCGGGG AGGCGCCCTC GCGGCGACCG CCAACCGCGC GCGCGGGGGA ACGGCGGAGC 420
    GCGCGAGGGG CCGCGCGGCG AGCGCGCGGC GCGCGCGCG CCGCTTGGGA CACGCTCAAG 480
    ATCAGCCAGG CGCGCGAGGT GAGCATCAGC GCGAGCAAGT CGTACCGGGA GAACGGGGCG 540
  
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5  
 10  
 15  
 20

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CCCTTCGTGC CCGCGCGGCC CGCGCTGGAC GAGCTGGGCG GCGCGGGGGG CGTCACGCAC 600
CCGGAGGAGC GCTTCGGCGT GCGCGGCGGC CCGGGCAGCG CCGCGGCTGC GGTGGGTGGC 660
ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAGATGA GGACGAGGAA 720
GAGGAACTGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACGACGCCCG CGCGCTGCTC 780
AAGGAGCCTCC GCGCTGTCTC TGTGGCGGCC ACTGGGCGCG TGGCCCGCAG AGCTGCCGCT 840
GCACTGGCCA CAGAGGGCGG GAGAGCTGCA CCGAAGGAGG AGCTGCTGCT GCACCCGGAA 900
GACGCTGAGG GCAAGGACGG CGAGGACAGC GTGTGCTCT CTGCGGCAG CGACTCGGAG 960
GAGGGGCTGC TGAAACGCAA ACAGAGGCGC TACCGACCCA CGTTCACCAG CTACCAGCTG 1020
GAGGAACTGC AGCGGCGCTT CCAGAGAGCG CACTACCCGG ACCTCTTCAC CAGGGAGGAA 1080
CTGGCCATGA GGTCTGACTT GACCGAGGCC CGAGTCCAGG TCTGGTTCCA GAACCGTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGCAGGC GCGCAGACCC ACCCCCTTGG GCTGCCCTTC 1200
CCGGGGCCCG TCTCCGCCAC CCACCCGCTC AGCCCTTACC TGGACGCCAG CCCCTTCCCT 1260
CCGCAACACC CGCGCTCGA CTCCGCTTGG ACTGCCCTG CCGCGCGCGC CGCGCGCGCC 1320
TTCCCGAGCC TACCTTCGCG TCCGGGCTCG GCCAGCTCC CCGCCAGCGG GCGCGCGCTG 1380
GGCTTGAGCA CTTCCTCGG AGCGGCGAGT TCCGACACC CAGCTTTCAT CAGCCCGGCA 1440
TTCCGCGAGC TCTTTTCAC AATGCGCCCC CTGACACCG CGTCGACCGC GCGCGCGCTC 1500
CTGAGACACC GCAACCCGCG CGTGGAGGGC GCACTGGCAT CCGCGCGCTC GCGCGAGCCG 1560
GCCACGCGCG CCGCAGACAG ACGCGCTCT AGCATAGCGC CGCTGAGGCT CAAGGCCAAG 1620
GAGCACGCGG CGCAGCTCAC GCAGCTCAAC ATCCTGCCGG GCACCAGCAC GGGCAAGGAG 1680
GTGTGC
  
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Seq ID NO: B42 Protein sequence  
Protein Accession #: AAK93901.1

25  
 30  
 35

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1 11 21 31 41 51
M9NQYEEGC SERPECKSKS PTLSSYCID SILGRRSPCK MRLLGAAQSL PAPLTSRADP 60
EKAVQGSFKS SSAPFEAEHL LPPKLRLRYG PGGRLQLQA AAAAAAATAA AAAAAATATG 120
PRGEAFPPFP PTARPERPD GAGAAAAAAA AAAAAMDTLK ISQAPQVSIS RSKSYREXGA 180
PFVPPPPALD ELGGPGGVTH PEERLGVAGG FGSAPAAAGG TGTEDDEREL LEDEEDERDE 240
BELEEDDEEE LLEEDARALL KEPRRCPVAA TGAVAAAAAA AVATEGGELS PKEELLHPE 300
DAEKDGEDS VCLSGSDSE BGLLKRQRJR YRTTFTSYQL EELERAFQRT HYPLVFTREE 360
LAMRLDITEA RVQVWFQNR AKNRKREKAG AQTHPPGLPF PGELSATHEPL SPYLDASFPF 420
PHEPALDSAW TAAAAAATAA FESLPPPPGS ASLPPPGAPL GLSTPLGAAV FEHPAFISPA 480
FGRLEFSTMAP LTSASTAAL LRQPTPAVEG AVASGALADP ATAAADRRAA SIAALRLKAK 540
EHAALQLQLN ILPGTSTGKE VC
  
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Seq ID NO: B43 DNA sequence  
Nucleic Acid Accession #: CAT cluster

40  
 45  
 50  
 55

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1 11 21 31 41 51
CGCTGCCCC CCGTGTGCTT CTCTCTCTTC CTTCTGCTCT GCGTGCTGCG CGGTCTTTGG 60
TTCCGCGCGT TCCGTGCGCC CTCTCTGCGC TTCCGCTTCA CCTCCGCTCT GCGCTGTGCT 120
CTGCTCTCTT CCGCTCTCAT GCGCTCTTCA CCTCCGCTCT TCGTGCTGCT CCGCTCTGCT 180
GCTCGTTTCT CTGTGCTCTT TCTCTCCCGG TCGTGCTGCT GCTCTCTGCT GTTCTCTCTT 240
GTCTGTGTTT GTGGGTCCTC CTCTGCGTCC TGCTCTTTTC TCTTGCGTTT CCGCGGCTTT 300
CCTGTTTGGG TCCCTCTGCT TCTCGCGCGG TCTGTGTGTC GCGGGCGCGC CCGTCTTTTC 360
TTGGTGCTTT GCTCTGCTC TCTGTCTGCT GTTCTCGGCT GTCTGTGCTT TCTCTCTTTT 420
ATCTCTGTTT TTCTCTTTT CTGTCTTTT CTGTCTTTT TTGTCTTTT TTTCTCTTTT 480
GCTGAGGTTG GGGAGAGATA ACGCTGTAAA CTTTATTTT TCGGAAATC TGGAAACCTA 540
CACTCTGCTG CCGCTCTTCA CCAAGAAAGA GCTCACTGTG GGCACCAAGG ACAGGAGACC 600
AATGTGGAGA CTTGTGAGCC TGTGTCCGCG CCGTAATCTT CAGCAGAGG GCAGGCTTCC 660
TGAGCATTGA AGAGAAATAT TGGAGAAACA AAACAGAAAC TGAAAGATA TGCAGGTGT 720
CTTTCTTGGG TGTATTCCA TGATAGATAG TAGGGGCGAG AGTGAGAGAG GCTGACTAGG 780
TCTGGACATG GAGGCTGAAA GAGTCAGGGT GTGATTCCGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GCGTGGAAAT CTGAGGCTCA GTGGTCCAAAG TCACTCAGAG ACAGAAATCAC 900
AGCATAGCCC TTGCTGATGG CAA
  
```

Seq ID NO: B44 DNA sequence  
Nucleic Acid Accession #: NM\_014421.1  
Coding sequence: 718..1497

65  
 70  
 75  
 80

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1 11 21 31 41 51
CCACGCGTCC GCGCGGAGCC CGCGCGAGC GTAGCGCAAG TCCGCTCCCT AGGCATCGCT 60
GCGCTGGCAG CGATTGCTG TCTCTTGTGA GTCAAGGGAC AACGCTTCGG GGCAACTGTG 120
AGTGGCGCTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTGCGTC CCGGGACGTC 180
TCTGATCCG CTACTAAAGC GCTGCTAAC TTTGAAAGG AGCACTGTGT CCGCAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTTGA AGGAGAGGA 300
GCTGATGCGG GCTTCTGAT CAATTAAGAG GAGAGTTAAA CCGCGGAGAT CCGGGCGGGA 360
CAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTCTT 420
TGCACTTGGG GTCAAGCTTC CTGTGGGAGA AAGCGGCTCG CATTTGATTG CTTCCAGTTA 480
TTGCAAGACT TCTGTCTCTG GTGGAGAAGC GGGTCTGCT TGGGTTCCGC TAATTTCTGT 540
CCTGAGGCGT GAGACTGAGT TCATAGGGTC CTGGGTCCCG GAACAGGAA GGGTTGAGGG 600
AACCAATCT GCAAGCCGCC GCGACCCAG TGAGGGGCC CGTGTGTTGG TCTTCTCTCC 660
CTTGTCAATC CCAACCCCTC GGGCTTTGCG TCTTCTGCG GACCCCTCG CCGGGAGATG 720
CGCGGCTTGA TCGGAGCAA GGATTGCTCC TGCTGCTGCT TCTTCTGCG CCGGGTCTG 780
ATGTTGGGCA GCTCAAGAT CGGCAGTTC GCGGCCAAG TCACTCCAT CAAGTCTCT 840
CTGGGCGGGG AGACGCTCG TCAGGCCGCC AATCGATCT CCGGCATGTA CCAAGGACTG 900
GCATTGCGCG GAGTAAGAA GGGCAAAAC CTGGGCGAGG CTAACCTTGT TAGCAGTGT 960
AAGGAGTGT AAGTTGGGAG GTATTGCGAC AGTCCGAC CAGGATCATC GCGCTGCATG 1020
GTGTGTCGGA GAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCC CAGTACCGGC 1080
TGCAATAATG GCATCTGTAT CCCAGTTACT GAAAGCATCT TAACCCCTCA CATCCGCGCT 1140
  
```

CTGGATGGTA CTCGGCACAG AGATCGAAGC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200  
 TGGCAGAATC TAGGAAGACC ACACACTAAG ATGTACACATA TAAAGGGGCA TGAAGGAGAC 1260  
 CCCTTGCCTAC GATCATCAGA CTGCATTGAA GGGTTTTCCT GTGCTCGTCA TTTCTGGACC 1320  
 5 AAAATCTGCA AACCACTGCT CCATCAGGGG GAAGTCTGTA CCAACAACG CAAGAAGGAT 1380  
 TCTCATGGGC TGGAAATTTT CCAGCGTTBC GACTGTGCGA AGGGCTCTGC TTGCAAGATA 1440  
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTCAAAA AATTTGATCA 1500  
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560  
 GGTGGAATAA AAGGTTTACA TGCAGAAGAA TGGCTAAAT AAGAAACGTG ATAGAATAT 1620  
 10 AGATGATCAC AAAAAGGGAG AAAGAAACA TGAAGTGAAT AGATTAGAAT GCGTGACAAA 1680  
 TGCAGTGCAG CCAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 1740  
 GGAAATGTCT ATTATTAAGA GAACAAGCAC ACAGTGGAAA TTAAGTATGA GTAGCATGTG 1800  
 ACTTTCCAAG AGTTTAGGTT TGTCTGGAGG AGAGGTTTCC TTGAGATTGC TGATTGCTTA 1860  
 TACAATAAAC CTACATGCCA GATTTCTATT CACGTTAGA GTTAAACAA ATACTCCTAG 1920  
 15 AATAACTTGT TATACAATAG GTTCTAAAAA TAAAAATGCT AAACAAGAAA TGAAGACATG 1980  
 GAGCATTTGC CAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 2040  
 CAATCAGAGG TCTTGTAGA TAAGAAAAAA ATCAGTCAAT ATTTCCAAAT AATTGCAAAA 2100  
 TAATGGCCAG TTGTTTAGGA AGGCCITTAG GAAGACAAAT AAATAACAA CAAACAGCCA 2160  
 CAAATACITT TTTTCAAAA TTTTAGTTT ACCTGTAAT AATAAGAACT GATACAGAC 2220  
 20 AAAACAGTT CCTTCAGATT CTACGGAAAG ACAGTATATC TCTCTTATC CTATGTGATT 2280  
 CCTGCTCGA ATGCTATATA TTTTCCAAAG TATACCCATA AATTGTGACT AGTAAATATC 2340  
 TTACACAGAG CAGAATTTTC ACAGATGGCA AAAAAATTTA AAGATGTCCA ATATATGTGG 2400  
 GAAAGAGCT AACAGAGAGA TCATTATTTC TTAAGATTG GCCATAACCT GTATTTGAT 2460  
 AGAATTAGAT TGGTAAATAC ATGTATTTCAT ACATCTCTG TGGTAAATGA GACTTGAGCT 2520  
 25 GATCTGTAC TGCACTGGAG TAAGCAAGAA AATTGGGAAA ACTTTTTCGT TTGTTCAAGT 2580  
 TTTGGCAACA CATAGATCAT ATGTCTGAGG CACAGTTGG CTGTTTCATC TTGAAACCTAG 2640  
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 30 GAGTATGAGG GTTTCATGCT CCTCTATAAG CTTCGACTA GCCAATGGCA TCATCCAAAT 2880  
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 35 TTTAAACTTT TGTAGACCAC AATTCACCTT TTAGTTTCT TTTACTTAAA TCCCATCTGC 3180  
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 40 TTATATTTAC AATTTGGTTT CTGCAATATT TTCTTTATGT CCAOCCCTTT AAAAATATT 3480  
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 AAAAAAATA A

Seq ID NO: B45 Protein sequence  
 Protein Accession #: NP\_055236.1

1 11 21 31 41 51  
 50 MAALMRKDS SCCLLLLAAY LMVSSQIGS BRKLNSIKS SLGGETPGQA ANRSAGMYQS 60  
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 RCNNGICIPV TBSILTPHIP ALDGTNRDR NHGHSNHD L GWONLGRPT KMSHIKSHES 180  
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Seq ID NO: 46 DNA sequence  
 Nucleic Acid Accession #: NM\_019885.1  
 Coding sequence: 1..1539

1 11 21 31 41 51  
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Seq ID NO: B47 Protein sequence  
 Protein Accession #: NP\_063938.1

1 11 21 31 41 51  
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 TRMLLGPNV SNSIGDIHRM KRKVFSKIFP HEALESYLPK IQLVIQDTLR AWSGHPEAIN 180  
 VYQEAQKLTF RMAIRVLLGF SIPEEDLGHF FEVYQQFVDN VPSLPVDLPF SGYRRGIQAR 240  
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 TABASTSLIM QLLKPTVLE KLRDELRAEG ILHSGGCPCE GTLRDLTLEG LRYLDCVIKE 360  
 VMLRLETPISG GYRTVLQTFE LDGFQIPKSW SVMYSIRDTH DTAPEVFKDYN VFDPEDFRQA 420  
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Seq ID NO: B48 DNA sequence  
 Nucleic Acid Accession #: AB040527.1; AL136582.1  
 Coding sequence: 94..2319

1 11 21 31 41 51  
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5 CGAGGCTCCG GCAACCTCCG CACAGTCCCA GACAGGCTCC CGGCCCCAGG AGGCTGCTAC 660  
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 10 GAGAGAGACT CCGCGGGTCC CACCCACCTG GAGAGCATCA CAGCCCTCAT TGACGGTGGC 1200  
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 15 GGAAAGAAG TTGGGATCC ACCTGAAGGA GATCGACAAG GAAGAACACC TGTATATPCT 1500  
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 20 GAAGATCCCC AACAGCAACC CACCTGAGTA TGAATTCCTC TGGGGCTGCG GAGCCCGCCA 1800  
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 30 ACAGCACCCT AGCGGCTTC TTCTGTGAG TCGGAGGTGG CATGCAAGAT GAAGCTCTCT 2400  
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Seq ID NO: B49 Protein sequence  
 Protein Accession #: BAB33378.1; CAB66517.1

35 1 11 21 31 41 51  
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 40 SLGPGRLRLS NEEWELNPNV LAQTLVEALQ LDPETLANET AARARNVARA AASNRARAA 120  
 AAAARTAFSQ VVASHRVATE QVSGEDTQPT TYAAEAQGF PEPPLASQPT SQMLVTSKMA 180  
 APEAPATSAQ SQTGSFAQEA ATEGESSACA FSQAPCAREV DANKPSTAFI GQNDVDFDTQ 240  
 PAGVSWAFPP RFRPPAPQZ AATEGESSAS GVPQTGPERE VAATRPKTKK SKKALAKTRN 300  
 45 VEPQNVAA AAKAKMATEI PEPBGAAAT AQBSAEPNAR MGGKRTKSK HLDDYEESSE 360  
 EERETPAVPP TWASQPSLT VRAQLAPREP MAPRSQIPSR HVLCLPFRNV TLLOERANKL 420  
 VKYLMIKDYK KIPKIRADML KIVIREYDEH FFEIIRATY TLEKKPGIHL KEIDKREHLY 480  
 ILVCTRDSIA RLIGKTKDTP RLILLVLILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540  
 FLGDLRLKLT DDFVQKYLE YKIPNENFP EYEFNLGLRA RHETSKMRVL RFIQMNQND 600  
 PREWKAHFLE AVDDAFKTMV VDMAEESHARA QMRAGMNIGD EALLGRWSND DIQVELLTWD 660  
 50 EDGDFGDWA RIFPAFWARY HQYILNENRA NRRATWRAGV SSGTNGGAST SVLDGPSTSS 720  
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Seq ID NO: B50 DNA sequence  
 Nucleic Acid Accession #: XM\_084965.1  
 Coding sequence: 356..2014

55 1 11 21 31 41 51  
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Seq ID NO: B51 Protein sequence  
 Protein Accession #: XP\_084965.1

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KEPRGGGDSG GCGGGRPNPG PFRAAGPGGG SLASSSVAKS HSFFSLKKKN GRSENGKEGP 180
VDASAGAGKQ KRLRLGLFSG MRWHRKDKRA KAFAAEGRAP GGGILILPGSL TASLECVKEE 240
TPRAAREPEE PSQDAPFDPA GCGDIIADQK EEAGPSCKKH VFGPGKPLS KKNPGVVAVQ 300
GGGEEMASGD EVDITLYQEF WDMLSQTEBQ GEPEQJGAOK VAAALETKVY PETPKDTRCV 360
BAKNDASVRK RRLNRLPIE PHPKKEPKHP EKEQJEGVEN SDEGYNDSTT PGEEDSSSS 420
GKKAGIFRDS YSGDALYDLY ADPDGSPATL PGKDNBEETS SLRLKPVSP GTITCPLRTP 480
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Seq ID NO: B52 DNA sequence  
 Nucleic Acid Accession #: FGENESH predicted  
 Coding sequence: 1..2016

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GGGAAGATTA ATAAAGCTGC CTTCAAATTA TTCAAGAAGA GGAATCGGG TGGCACCATG 240
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ATGCGCTGGC ACAGGAAAGA CAAGCGGGCC AAGCGGAGG CCGCGAGGG GCGCGCGCCC 660
GGGGCGGGCT TGATCTTACC CGCTCTGCTC ACCGCCAGC TGAGTGTGCT CAAGGAGGAG 720
ACGCGCAGAG CCGCGCGCGA GCGGAGGAG CCCAGCCAGG ACGCCCGCGG AGACCCAGCA 780
GATGAGCCCG CAGGGGAGAG GAGGATGCCG GCGCCCGCGG ACCGCGCGCC AGCGCGGAGC 840
TGCCGAGAGG CAGAGCGGCT CGCGCACCCC GCGCACACCG GCGCGCGGGG AGAGGAGCGC 900
GCGGGGCATC GCGCGCGCGA GCGCGGGCCC GGGGAGGTCC GCAJCGGCAG GACGCTTCC 960
AGGAGCGGGG CGGTTCCTGT AAAGACGGTC CCGCTTGTGG ACTCGGAAGG CGGCGAGGTC 1020
CGGGCGCGCG CGGTCCTGTA CCTGCGCTCT GTGATGCCAC CCGCAGACCC GTCCGCGATG 1080
CGTATTGTGT TATGTTTTC TGAGGTGACT TCACTGAAAA GCTTTGACTC TCTTACAGGC 1140
TGAGGAGATA TTATTGCGGA CCAAGAGGAA GAGGAGGTC CAGCTGTGGA CAGCATGTC 1200
CCCGGGCCAG GCAAGCGGCG TCTGTCTAAA AAGAACCCTG GGTGGTGGC CTACCAAGGA 1260
GGCGGGGAAG AGATGGCCAG CCGGACGAG GTGAGCAGCA CCTATCTACA GGAGTTCTGG 1320
GACATGCTCT CCCAGACCGA GAGCAGGGA CCGGAGCCCC AGGAGGGGCG GGTAAAGTGG 1380
GCAGCTGCGC TGGAAACCAA GGTGGTGGCC GAGACCCCCA AAGACACCGG GTGTGTGGA 1440
GCGGCCAAGG ACGCTGCTC GTCTAAGCGC AGGAGGCTCA ACCGATTCC CATCGAGCCC 1500
CATCTAAGG AGGAGCCCAA GCACCGGAG AAGGAGCAGC AGGAAGGCGT CCCCACAGC 1560
GACGAGGGCT ACTGGGACTC CACCACGCCA GGCACAGAG AAGACAGCTC GAGCAGGGG 1620
AAGAGGCGCG GCATCCCGCG GATAGCTAC AGCGGGGACG CGCTCTATGA TCTCTATGCT 1680
GACCGGAGCG GAAGTCCAGC AACCTTCTCT GGAGGGGAGG ACAACAGGGA GAOGTCTCTC 1740
CTGTCCCGGT TAAAGCGCGT ATCTCCAGGC ACCATCACCT GTCCACTGCG AACACAGGC 1800
AGCTTGTGTA AGGACTCTAA GATCCCTATT AGCATCAGC ACCTGACCAA CCTTCCATCT 1860
AGCCATCCCG TGGTGACADA GCAACCTCC AGGAGTGAGA TGCCAGAAC AAAATCCCG 1920
GTTTCCAAAG TGCCTGCTCG CAGAGTCAGC AACCGGGGCT TGCTGCGGAC CACCATCAGA 1980
GCAACGGCCT GCCACGACAG TGCCAAAAG TTGTGA
  
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Seq ID NO: B53 Protein sequence  
 Protein Accession #: FGENESH predicted

80

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1 11 21 31 41 51
| | | | |
METSRSRGGG GAVSERGGAG ASVGVCRKKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
KEPRGGGDSG GCGGGRPNPG PFRAAGPGGG SLASSSVAKS HSFFSLKKKN GRSENGKEGP 180
VDASAGAGKQ KRLRLGLFSG MRWHRKDKRA KAFAAEGRAP GGGILILPGSL TASLECVKEE 240
TPRAAREPEE PSQDAPFDPA GEPAGGEFVP APADRAPARS CREABGLAHP GTGARGEDA 300
  
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AGHRAEPGP GEVRAEDAS RTGAVPVKTV FLVDSBGGSG RAPAPDFAS VDPFSDPSAD 360  
 RICLMPSDVT SLKSDSLTG CGDILADQEE EAGPSCDKHV PGPFGKALSK KNPGVVAYQG 420  
 GGEEMASPE VDDTYLQEFW DMLSQTEEQG FEPQEGAAKV AALETKVVP ETPKIDTRCUE 480  
 AAKDASSVKR RLNRIPFEP HPKEEPKHPE KEQEGVPHS DEGYWDSTTP GPEDSSSSSG 540  
 KKAGIPRDSY SGDALYDLVA DFDGSPATLF GSKDNEETSS LSRLKPVSPG TITCPLRTFG 600  
 SLKDSKSPI SIKHLTNLFS SRPVVHQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660  
 ATACHDSAKK L

Seq ID NO: B54 DNA sequence  
 Nucleic Acid Accession #: NM\_014138.1  
 Coding sequence: 60..854

1 11 21 31 41 51  
 CTGCAGAGAC TTCCACAGGAA GGTCCAGGCG CCTCTCAGCC TTGCTACTCA GAACAGCOGA 60  
 TGATGGGCTT CAGTAACCTG AGCCCCGGTC CTGGCCCCAG CCAGGCCGTG CCTCTCCAG 120  
 AGGGGCTGTG CCGCCAGCGG TACAGAGAGG AGAAGACCCT GGAAGAGCGG CGGTGGGAGA 180  
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240  
 ATCACAATGC CCCTATGCT GTTGGGAGSG AAGCCAGAAT CTCCTCATTA GGTGACAGAA 300  
 CTCAGAAATG ATTCCGATGT GAATGTCGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360  
 GGATCCCTGG GAGAGATAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGACGG 420  
 GCCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACAGGCC CGGCGCTCTG CCTGAAGCGG 480  
 CACTCCAGCC ACAGGAGACA GAGGAGAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540  
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTS CACCCCATG 600  
 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGGTGTGGGC 660  
 CCATTTTGGG GACCAACAG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG 720  
 ACAGGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCG AGGAAGGTCC TCATGTTTCG 780  
 TGCTGTCTC TCCTCGATGT CTGTGAGGCA TTCTTTGGCA AEGGACGCTG CBTACACCGG 840  
 GTCTCACCG CATCTCATAT GGTCTCTGTG ATGCATGTTG TCGCTTTCC ACOCGGGATC 900  
 TCCATCTCTC TTCCCTTCTT GCTGTCACTA AGAGATCACA TGCTCTGTGA GTGTGAATGC 960  
 CTGTGTGCTG TCCTGTGCTT TTGCACCAAT GAGTTGACTG CCTCTGAGAA GCAGCACTAG 1020  
 GCCTGTTGAA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAATGGGC AGGTAAACGC 1080  
 AGTGTGGGAA AGGAATGTGG AATGAGAACT TGGTGTCTCA CGCTGTACT ATTGTGTAA 1140  
 ATGTTTACT ATGTGATAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG 1200  
 TAGTAGTCTC CCTTACAGGA ATTTTGTAGC GGGTTCTCA TCATCAATAC CAATAAATA 1260  
 TATGTAGGAA TGGAAAAAAA AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA 1320  
 AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA 1380  
 AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA

Seq ID NO: B55 Protein sequence  
 Protein Accession #: NP\_054857.1

1 11 21 31 41 51  
 MMGLSNLSPG PGPQAVPLP EGLLRQRYRE EKTLEERRNE RLEFLQKKKA FLRHVRRRHR 60  
 DNMAYAVGR EARISPLGDR SQNRFRCSER YCQSHRPNLS GIPGESNRAP EPSSWETLVQ 120  
 GLSGLLSLSG TNQPSPLPEA ALQPOETEER QRERQCESK IMFORLLKQW LEEN

Seq ID NO: B56 DNA sequence  
 Nucleic Acid Accession #: NM\_000025.1  
 Coding sequence: 198..1424

1 11 21 31 41 51  
 GCTACTCTTC CCCCAGAGAC GGTGCAACCG AGGGAGTTGG GGTGGGGGGA GGCTGAGCGC 60  
 TCTGGCTGGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTCGCTCTC ATGCTTGTCT 120  
 GTCCCTCTCC CTGAGGCGAGG TGATTTGGGA GACCCCTCTC TTCTCTCTTT CCTACCGCC 180  
 CCAGCGCGGA CCGGGGATG GCTCCGTGGC CTCAGAGAA CAGCTCTCTT GCCCATGGC 240  
 CGGACCTTCC CACCTTGGG CCAATAACG CCAACACGAG TGGGCTGCCA GGGGTTCGT 300  
 GGGAGGCGGC CCTAGCCGCG GCCCTGCTGG GCTGGCGGT GCTGGCCAC GTGGGAGGCA 360  
 ACCTGTGTT CATGTGGCC ATCGCCTGGA CTCGAGACT CAGACCATG ACCAAGCTGT 420  
 TCGTGAATTC GCTGGGCGCA GCGGACCTGG TGATGGGACT CTGGGTGGTG CCGCCGGCGG 480  
 CCACCTTGGC GCTGACTGGC CACTGGCCCT TGGGCGCCAC TGGCTGCGAG CTGTGACCT 540  
 CGGTGGAGCT GCTGTGTGTG ACCGCCAGCA TCBAACCCCT GTGCGCCCTG GCGGTGGACC 600  
 GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GGTCAACAG CGCTGCGCCC 660  
 GGAAGCTGT GGTCTGGTG TGGGTGCTGT CGGCGCGGT GTCTTTGCG CCTATCATGA 720  
 GCCAGTGTG GCGGTAGGG GCGGAGCGG AGGCGCAGG CTGCACTCC AACCCGCGCT 780  
 GCTGTGCTT CCGCTCAAC ATGCCCTACG TGCTGCTGTC CTCTCTGCT TCTTCTTACC 840  
 TTCTCTCTT CGTGAATGCT TTGCTTACG CGCGGTCTT GTGTGTGGCT ACGCGCCAGC 900  
 TGCGCTTGT CCGCGGGAG CTGGGCGCT TTCCGCGGA GAGTCTCTG CCGGCGCGT 960  
 CGGCTCTCT GCGCCGCGC CCGGTGGGA CGTGGCTTCC GCGCGAGGG GTGCGCGCT 1020  
 GCGGCGCGG GCGGCGCGC CTCTGCTCT CTGCGGAGCA CCGGCGCTG TGCACCTTGG 1080  
 GTCTCATCAT GGGCACTTC ACTCTCTGT GGTTCGCTT CTCTTGGCC AACGTGCTGC 1140  
 GCGGCTTGG GCGGCTCTCT CTAGTCCGG GCGCGGCTT CTTTGGCTG AACTGCTAG 1200  
 GTTAGGCAA TTCTGCTTC AACCGCTCA TCTACTGCG CAGCGCGGCT TTTCGAGCG 1260  
 CCTTCCGCG TCTTCTGTG CCGTGGCGC GTCGCTTGG TCCGAGGCC TGGCGCGCG 1320  
 CCGGCGCGC CCTCTTCCC TCGGGCGTTC CTGCGGCGG GAGCAGCCA GCGCAGCCA 1380  
 GGCTTGGCA AGGCTCGAC GGGGCTCTT GGGGAGTTTC TTAGGCTTGA AGGACAAGAA 1440  
 GCAACACTC TGTGATCCG AACCTGTGA AAACCTTGG CCTCTGTCA GAATGAGTCC 1500  
 CATGGATTC CCGGCTGTG AACTCTACC CTCAGAAC TGACGACTG GCAATGTGAC 1560  
 CCAAGGAGG ATCCTTACCA AGTGGGTTT CACCTCTCT TTGCTCTCTG TCTGAGAGAT 1620  
 GTTTCTAAA CCGCAGCCT GAACCTACT CCTCCCTAG TGGTAGTGT CAGGTGCCGT 1680  
 GGAGCAGCAG CCGGCTTGT GTAGGGCAC CCATCAACG GCTTGCCTGT GCACTCAGT 1740  
 AGTGTCTAGG GCAAGAGAG CTCCCTGTG TCCATCTCT CTGCAACCA AACCTGATG 1800

5  
10  
15

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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
AAGATTTCGG GTTTTATCTC TGTTTCCCTT ATTACTGCTC TCAGGCAGTG GCCTCTCTCA 1920
CITTAGGCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAGGAGC TTCGCCAGGG 1980
TTTGGGGAGC TCAGGGGTTT ATAAGARGGT GAAACCATTAG AACAGATCCC TTCTTTCTCT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTGGGCCCA CTTCCTCTCC 2100
GTTGTGTTTC TTTTCATAAT CCACCTACTC CTTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTCTCTC CTAATCTTCA TCAAAACAAA 2220
AATGAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCTTCTCTG AAATCTCTGA AATCCAGTTG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGGCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGGG 2400
GCATTGTGTC CCTTCATGCT ATAATCCAGT GGTGCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGCGTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTT CTGGGTTTGG 2520
TCAAAATGCT TGTGTCTGAA ATATATTCTG ATGTTTCCCA GCTTTTCCAC AACCTCTACC 2580
TTCCACTCA CCTTCCCCAG CTACAAAAT CTGTATTATC CTCTTAAAGT AAAACTGGAG 2640
TTAC

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Seq ID NO: B57 Protein sequence  
Protein Accession #: NP\_000016.1

20  
25  
30

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1 11 21 31 41 51
MAPWPHENSS LAPWFDLPTL APNTANTSGE PGVPWEAALA GALLALAVLA TVGNNLJLVIV 60
AIANTPELQT MINVFTSLA AADLVMLLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120
VTASIELCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VWVVSAAVSF APIMSQWWEV 180
GADABAQRCH SNPRCCAFAS NMPVLLSSS VSFYLLPLVM LEVYARVFWV ATRQLRLLRG 240
ELGRFPPEBS PFAPSRSLAP APVGTCAFFE GVPACGRRA RLLPLREHRA LCTGLGLWGT 300
FTLCMLPPFL ANVLRALGGP SLVPGPAFLA LNWLGYSANSA FNPPLYCRSP DFRSAFRRLL 360
CRGRRLPFE PCAARPALF PSVPEAARS PAQPRLCQRL DGASWGV8

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Seq ID NO: B58 DNA sequence  
Nucleic Acid Accession #: NM\_032553.1  
Coding sequence: 37..1038

35  
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50  
55

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1 11 21 31 41 51
CACCATTAGG CAAAGATAGT TTCTCTAGAG AGAATCATGC CTGCTAATTA CACGTGTACC 60
AGGCCAGATG GAGACAATAC AGATTTTCGA TACTTTATTT ATGCAGTGAC ATACACTGTC 120
ATTCTGTGTC CAGGCTCATG AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG 180
AAGAAACAA AACGAGCTGT GATATTTATG ATAAACTTAG CCATTGCTGA CTTACTACAA 240
GTCTTTCTCT TGCCACTGAG GATCTTCTAC TACTTGATTC ATGACTGGCC ATTTGGGCCT 300
GGTCTCTGCA TGTCTGTGTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGCTCTGCA TCAGTGTGCG ACGATTTTGG TTTCTCATGT ACCCCTTTGG CTTCCATGAC 420
TGCAAAACAG AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCTTGGCC 480
TGTGTACTCT TTCCACTCCT CAGAACCACT GATGATACCT CTGGCAATAG GACCAATGTC 540
TTTGTGATC TTCCATACCAG GAATGTCAAC CTGGCCCACT CGTTTGTAT GATGACCAAT 600
GGCGAGTTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAGAGCG 660
GTTTATACAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
TIGAGATGTA TTCTAACCTG TGCAAGGGTA TTCTTAATTT GCTTTGCACC TTATCATTTT 780
AGTTTCTCTT TTGATTTCTT GGTGAAGTCC AATGAAATTA AAGCTGCGCT AGCCAGAAAG 840
GIGATTCTAA TATTTCTATC TGTGGCATGT TGTCTTGCTA GTCTGAATTC ATGTCTTGAC 900
CCAGTCATAT ACTACTTTTC CACTAATGAG TTCCGAAGAC GGCCTTCAAG ACAAGATTTC 960
CATGACAGCA TCCAACCTCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020
ACACCTGAAT TATGCTAATA CAAAAACCA AACTGAATGT GACCTGAAAT GCAAGTACAT 1080
CAGAACATAT TATGCTAATA CAAAGCCAG GGAAGAACTT GCAAAACAA ACAGCTTTTC 1140
AGTTCTGCTC TATCTTACTG CTAATGGGAA TTCACTTCTT CAAAGCAGGA CCTATTTGA 1200
GCATTACGAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTTT CTTCAGT

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Seq ID NO: B59 Protein sequence  
Protein Accession #: NP\_115942.1

60  
65  
70

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1 11 21 31 41 51
MPANYCTFRP DGDNTDFRYF IYAVTYTVIL VPGLIGNILA LNVFYGYMKE TKRAVIFMIN 60
LAIDLQLVL SLPLRIFFYL NHDWPFPGPL CMFCFYLYV NMYASTYFLV CISVREFWFL 120
MYPRFHDCK QKDYLYSLA GWLIICLACV LEPFLRTSDT TSGNRTKCFV DLETRFVILA 180
QSVMMTIGE LIGFVTPALI VLYCTWKTIV SLQDKYPMAG DLGERQKALK MLITCAGVFL 240
ICFAPYHBSF PLDFLVKSNK IKSLARKVI LIFESVALCL ASLNSCLDPV IYFSTNEFR 300
RLSRQDLWD SIQLHAKSFV SNHTASTMT ELC

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Seq ID NO: B60 DNA sequence  
Nucleic Acid Accession #: CAT cluster

75  
80

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1 11 21 31 41 51
GATTGGGATT TTAATCCGAC TCACTATAGG GAATTTGGCC CCTCGAGGCC AAGAATTCGG 60
CCCGAGGGTT AGACATTAA CTGAGTCTT TTCATATCAC GGTATGCTTT TATTTTACC 120
TCATATATAA TTAATTTTCA TCTGGGCATA TATTCCAGA TTAGAAATCA TTTCTTTCA 180
TACATTTTAA GGAATTTATA CATTGTCATC TGAATTTGTA TTCTATTCT TCTAGAAAC 240
AAGAGTGGAC TTGATATCCG TCTGATATA TTTCTTTGTT TGGTAAAGAG CCTCTTTT 300
CCCTTTTAT TTTCACTTC TCTTCTCTA GTGTTTATA TCTTATTTT ATGAATGTAG 360
TCTAATTAT TAGAACCTG TCTCCAGTA TGTGTTTATT TGGGTTTGTG TTTGAAAT 420
TGCTCCAGG TCGAGTTTA TGTGTGTTA TGTTCCTAT TTGAGGTTG ACACCTAGAA 480
AATTTTCTCA ATTCGAAAC TATTTTCTT CAGCACTCAG AAATTTTAT CAAAGATTAT 540
TTCCACGATT ATTTCTCTCT CTGCTTTT CTGTTCTTA ACCTAGATT CAATTGTTA 600

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ATGTTAGACC TTACACATCT TCAATGTATC ATATATATTT CACTCATATT ATTTATGTCT 660  
 ATATCTTTTG GACTATTGTG TGAAGGCAAT AAATGTATAT TACTTTAAAA AAAAAAATAA 720  
 AAAACTECAT TTTCAAATTT AATACACACA AATTGTGCAT ACCACACAC ATATACCACA 780  
 GATATATCCA TTTTCAGGAT TTCTTTAAGT GTTATTTTAA AATAATCAT ATTCCTATTT 840  
 TGTGAAGTGT GGGATTCTCT GAAACTTTTT GAAAACCTCT ATTAGTCTGT GTTGTGTGGT 900  
 TTCTTTTAAA TTATCTCTTC CTTCAGAAAT ACTTTGTGTG TTTGAATTGT AGTCTTTGCC 960  
 ATTCAATAAG CGGGCTTTCC TTGAATACCA GATAACTCTG AGTTTCCTGT TCATATTTAA 1020  
 GAATAAATAA CCTAATTTGA AAAAAAATAA AAAAA

Seq ID NO: B61 DNA sequence  
 Nucleic Acid Accession #: NM\_014522.1  
 Coding sequence: 846..3911

1 11 21 31 41 51  
 15 CTGGTGGTCC AGTACCTCCA AAGATATGGA ATACACTCCT GAAATATCCT GAAAACTTTT 60  
 TTTTTCAGA ATCCTTTAAT AAGCAGTTAT GTCAATCTGA AAGTTGCCTA CTGTACTTTT 120  
 ATATTAATAG CTATTCCTGT TTTTCTTATC CAAAGAAAAA TCCTCTAATC CCTTTTTCAC 180  
 ATGATAGTGT TTACCATGTT TAGGCATTAG TCACATCAAC CCTCTCCTTC TCCCAAACTT 240  
 20 CTCTCTCTCA AATCAAACTT TATTAGTCCC TCCCTTATAA TGATTCCTTG CCTCGTTTAA 300  
 TCCAGATCAA TTTTTCCTCA CTTTGATGCC CAGACCTGAA GAATGAGCT ACTGTATAAA 360  
 TTATTCATGT CCAAGAGAAAT AATTGCATTT TAAACCCATA TTATAACAAA GAATAATGAT 420  
 TATATTTTGT GATTTGTAAC AAATACCCCT TATTTTCCCT TAACATTTGA ATTAATATTT 480  
 TTAATTATTT GTATTCCTCT TAACATCTCT GGTATATTA AATATTATCT TTATATATTT 540  
 25 TATCATGGGT GGCACCTTTT ATAGGTACTC TGTGTCTATT TTGATCTGT AGGTATCTTA 600  
 TTTCTATTAT CTTTATCTTT AATGTACGAA TTCATAATAT TTGATTCAGA ACAAATTTAT 660  
 CACATAATTA CAGAGGTGCA ATTATGCTAA CATCTCATTT ACTGATTTTA ATTTAAAAA 720  
 GTTTTGTGTA ACATGCAATG TTAGGGTTGG CTCTTAATA ATTTCTCTCT CCTCTCTCT 780  
 CTCTCTCTCT CTTTGTGCTA GTTGTGTGCG GGTATATTA ACAAACCTGA ACAAGTGTAC 840  
 30 CTGATATGGA CTGTGTGTCC GGCAGGTACA TTTTCGCGGT CCTGCTAGCA TGCCTGGTGT 900  
 TCCCTCTCGG CGCCAGGAG AAAAACTACA CCATCCGAGA AGAATGCCA GAAAACGCTC 960  
 TGATAGGCGA CTGTGTGAAA GACCTTAAC TGTCTCTGAT TCCAAACAAG TCCTTGACAA 1020  
 CTGCTATGCA GTTCAAGCTA GTGTACAGA CCGGAGATGT GCCACTGATT CGAATTGAAG 1080  
 AGGATACGGT TGAGATCTTC ACTACTGGCG CTCGCAATGA TCGTGAGAAA TTATGTGCTG 1140  
 35 GTATCCCAAG GATGTAGCAT TGCTTTATG AAGTGGAGGT TGCCATTTTG CCGGATGAAA 1200  
 TATTTAGACT GGTAAAGATA CGTTTCTGTA TAGAAGATAT AATGTATAT GCACCATTTG 1260  
 TCCAGCAAC AGTTATCAAC ATATCAATTC CAGAGAACTC GGTATTAAC TCTAATATA 1320  
 CTCTCCCGC GGCCTGTGAT CCTGACGTAG GAATAAACGG AATTCAAAAC TACGAATTA 1380  
 TTAAGAGTCA AATCATTTT GGCCTCGATG TCATTGAAC ACCAGAAGGA GACAAGATGC 1440  
 40 CACACTGAT TGTTCAAAAG GAGTTAGATA GGGAGAGAAA GGATACCTAC GTGATGAAAG 1500  
 TAAAGTTGA AGTGTGTGCC TTTCTCTCAA GATCCAGTAC TGCTATTTTG CAAATGAGTG 1560  
 TTACTGATAC AATGACAAAC CACCCAGTCT TTAAGGAGAC AGAGATTGAA GTGAGTATAC 1620  
 CAGAAATGCT TCCGTGAGCG ACTTCAGTGA CACAGCTCCA TGCCACAGAT GCTGACATAG 1680  
 GTGAAATGCT CAGAGATCAC TTCTCTTICA GCAATCTAGT CTCCAAACAT GCCAGGAGAT 1740  
 45 TATTTCACTT CAATGCCACC ACTGGACTTA TCACATCAA AGAACCCTG GATAGGGAAG 1800  
 AAACACCAA CCACAGTTA CTGGTTTGG CAAATGATGG TGGATTGATG CCAGCAAGAG 1860  
 CAAATGATCT GGTAAATGTT ACAGATGTCA ATGATTAATG CCCATCCATT GACATAAGAT 1920  
 ACATCTCTAA TCCGTCTAAT GACACAGTTG TTCTTTTCAA AATATTTCCA CTCAACACCA 1980  
 50 AATGTCTCT CATACTGTG ACGGATAAGG ATGCGGACCA TAATGGCAGG GTGACATGCT 2040  
 TCACAGATCA TGAATCCCT TTCAGATTAA GGCCAGTATT CAGTAATCAG TTCTCTCTGG 2100  
 AGACTGCAAC ATATCTTGAC TATGATCTCA CAAAGAATA TGCCATTAAT TTACTGGCTG 2160  
 CAGATGCTGG CAACCTCTCT TTGAATCAGT CAGCAATGCT CTTCATCAA GTGAAGATG 2220  
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 55 ACTCTCTGG CATCTCAGTT ACGAAGTAA GTGCAATGGA TGCAGACAGT GGCCTTAATG 2340  
 CTAGATCAA TTACTGTCTA GGCCTGATG CTCCACCTGA ATTCAGCCTG GATGTGTGTA 2400  
 CAGGATGCT GACTGTAGTG AAGAACTAG ATAGAGAAA AGAGGATAAA ATTTATTCA 2460  
 CAATCTGGC AAAAGATAAC GGGGTACCC CCTTAACCG CAAATGTCAC GTCTTTGTAA 2520  
 GATTTATGA TCAGATGAC AATAGCCGAC TTCTCTCTCA CAATGAATAC AACTTCTATG 2580  
 60 TCCAGAAAAC CCTTCCAGG CATGGTACAG TAGGACTAAT CACTGTAACT GATCTGATT 2640  
 ATGAGACAA TTTCTGAGTT ACGCTCTCCA TTTTAGATGA GAATGATGAC TTCACATTG 2700  
 ATTCACAAAC TGTGTCTATC CGACCAATA TTTGATTTGA TAGAGAAAAC CAGAAATCTT 2760  
 ACATCTCTTA TGTAAAGGCT GAGGATGGTG GTAGATATC ACGTTCTTCA AGTGCCAAAG 2820  
 TAACTATAAA TGTGGTTGAT GTCAATGACA ACAAACAGT TTTCTATTG CCTCTTCCA 2880  
 65 ACTGTTCTTA TGAATGGTT CTACCTCCA CTAATCCAG CACAGTGGTC TTTCAAGTAA 2940  
 TTGCTGTTGA CAATGACACT GGCATGAATG CAGAGGTTCT TTACAGCAT GTAGGAGGAA 3000  
 ACACAGAGA TCTGTTTGA ATCGACCAAG AACAGGCAA CATAACATTG ATGAGAAAT 3060  
 GTGATGTTAC AGACCTTGGT TTACACAGAG TGTGCTTCAA AGCTAATGAC TTAGGACAGC 3120  
 CTGATCTCT CTTCAGTGT GTAAATGTCA ATCTGTCTGT GAATGAGTGT GTGACCAATG 3180  
 70 CTACACTGAT TAATGAACGT GTGCGCAAAA GCACTGAAGC ACCAGTGACC CCAATACAGT 3240  
 AGATAGCTGA TGTATCTCTA CCAACTAGTG ACTATGTCAA GATCTGTGTT GCAGCTGTTG 3300  
 CTGGCACCAT AACTGTCTGT GTAGTTATTT TCATCACTGC TGTAGTAAGA TGTGCGCAGG 3360  
 CACCAACCTT TAAGGCTGCT CAGAAAACA AGCAGAAATC TGAATGGGCT ACCCAAAC 3420  
 CAGAAACAG GCAAGTGATA ATGATGAGA AAAAGAAAAA GAGAGAGAG CATCCCCCTA 3480  
 75 AGAATCTGCT GCTTAATTTT GTCACTATTG AAGAACTAA GGCAGATGAT GTTGACAGT 3540  
 ATGGAACAG AGTCACACTA GACCTTCTTA TTTGATCAGA AGAGCAACA ATGGGAAAGT 3600  
 ACAATGSGT AACTACACTT ACTACTTTCA AGCCCGACAG CCTGATTTG GCCCAACACT 3660  
 ACAAATCTG CTCTCCACAG CCTGCCCTTC AAATTCAGCC TGAACCTCCC CTGAATGCA 3720  
 AGCACCACAT CATCCAAGAA CTGCCCTCTG ATAAACACTT TGTGGCTCTG GACTCTATCT 3780  
 80 CCAAGTGTTC CTCAGAGAGT TCAGATCCCT ACAGCGTTTC TGACTGTGGC TATCCAGTGA 3840  
 CGACCTTGA GGTACCTGTG TCGGTACACA CCAGACCGGT AGGTATCCAA GTTCTCAACA 3900  
 CAATCTCTA ACTATTTTAT TATTATTTAT TTTAGTTGAT GTAGAACTTT ACAAATCTA 3960  
 TTGACTTCAA AGAGGGATCA AACAATCAT ATTCACAGA TGTACCCAAT AGATATATGG 4020  
 ATTCATTAAG GTTTGGTAGA AGATGAGAAC AAAATAACTA CTGATTTAGG AAAATGGAT 4080  
 GCAGATAAAT AATTATAGTA GGGCAATT TGTCTGTAGA TGCAGTATG AACTCTCTG 4140



5 CTAGAGATA TATTGAAAAA AACTTCAACA CAAAGGGTTG TAGCAGTGTG CTCAGTACCA 4200  
 TTGGTGTGAT GAGGATCAGA ATAGTCTGGG CTAGATACAT CACATTAAAG CTTTTCAGAA 4260  
 TCTGATATAA AGCTCTATAA ACTAATGATA TTGAGAAGCC TAGCTTCACT TGGGAAAAATC 4320  
 TGTGCTGTGT CACAGAAATT CAGCACCAAG TTATTCCGCC CACTCTCTAC CAGGCCCTTCA 4380  
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 GCATATTAT GCAAGGTATT TTGAGCCCTT CAGAAGACAT TCT

10 Seq ID NO: B62 Protein sequence  
 Protein Accession #: NP\_055337.1

15 1 11 21 31 41 51  
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 EQNIPGLDVI ETPFGDMFQ LIVQKELDRE EKDITVVMKV VEDGGPPQRS STAILQVSVT 240  
 DINDNHFVK ETEIEVSIPE NAPVGTSTQ LHATDADIGE NAKIRFSSFN LVSNIRRLP 300  
 20 HLNATTGLIT IKSPLOREET FNRKLLVLAS DOGLMPARAM VLNVNVDVND NVPSIDIRYI 360  
 VNPVNDTVVL SENIPLNTKI ALITVTDKDA DNRGRVCTF DEEIPFRLRP VFSNQFLLET 420  
 AAYLDYESTK EYATKLAAD AGKEPLNQSA MLFIKVDEN DNAPVFTQSP VTVISIPENNS 480  
 PQIQLTKVSA MDADSGPMK INYLLGPDAP PFSLDCRTG MLTVVKLDR EKEDKYLFTI 540  
 LAKDNGVPEL TSNVTVFVSI IDQNDNSPVE THNEYNFYVP RNLPRHGTVG LITVTDEDVG 600  
 25 DNSAVILSIL DENDDFTIDS QTGVLRPNIS FDREKQESYT FYVKAEDGGR VSRSSSAKVT 660  
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 RDLFALDQST GNITLMKCD VTDGLHRLV VKANDLGQPD SLFSVVIUNL FVNESVTNAT 780  
 LLENEVRKST BAPVTFTTEI ADVSSPTSDY VKILVAAVAG TITVVVIFFI TAVVRCRQAP 840  
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 30 NRVTLDLPID LEEQTMGKYN WVTTPITTEK DSPDLARHYK SASPOAPQI QPBTPLNSKH 960  
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35 Seq ID NO: B63 DNA sequence  
 Nucleic Acid Accession #: XM\_059180.2  
 Coding sequence: 276..3740

40 1 11 21 31 41 51  
 GCGGCGGCCG CCGAGTATCC TGGAGCTGCA GACAGTGGG GCTTGGGCCC AGTCCCGGCT 60  
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 GCGGCTTAGC GAGCCTGGCG GTGCGACCCA GCCACGCGAG CGACGGGGCG CTGCTCTGGC 180  
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 45 ACTGCAATGC CATGGCTTTC TGTGCTAAA TGGAGAGCTC CAAGAAGACT GAGGTGAACC 360  
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 GCCTGGCTCC TATTGAGAG CCGAAGACCG AGCGGGATGG ACATGATATT GAGAACGAGT 840  
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 55 CAGAACGCGC CAGGACATC AGCTACAAGC GATATATTCC AGAACATTTG AATAAGTCCA 960  
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 AATACTTGGC TACCTTGGAA ACTTTGACAA AACATTACGG TGCTGAATAA TTGAGACTT 1140  
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 60 ACGTCTCTTA CTACGAGAG ATGGTGACTG GGAATCTTGG AATCCAGTGG AGGCATAAAC 1260  
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 AACACAAGAA GGATGAGGAG AAAACAAGA TCXGGGAAGA GTGGAACAAT TTTCTTACT 1380  
 TCCCTGAAAT CACTCACATT GTAATAAAGG AGTCTGTGGT CAGCATTAAC AAGCAGGACA 1440  
 65 ACAAGAAAAT GGAACGTGAAG CTCTCTTCCC ACAGGAGGAC CTGTGCTTTT GTGTCCCTGG 1500  
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 CCCCGTGTAT CGTCCACAAC ATACAGAATG GCTGTCTATG TCCAATCTGT ACAGATATCG 1620  
 CCATCAATAA ATTGCGGCAA GAAGGAAGCG AGGAGGGGAT GTACGTGCTG AGGTGGAGCT 1680  
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 TGCAGGTTTC GGAACGAGC TTCCCGAGCT TGGGAGACCT CATGAGCCAC CTCAGAGGC 1860  
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 75 TTGGGAGAGG CACGAGACCA CACATCTATT CTGGGACCTT GATGGATTAC AAGGATGACA 2100  
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	GGTGCAGGCC	AGTGACACCA	TCATGTAAGG	AGCTGGCTGA	CCTCATGACC	CGCTGCATGA	2760
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	AAGAGCAGAA	TCCAGATATT	GTTTCAGAAA	AAAAACCAGC	AACTGAAGTG	GACCCACAC	2880
5	ATTTTGA AAA	GCGCTTCTTA	AAGAGGATCC	GTGACTTGGG	AGAGGSCCAG	TTTGGGAGG	2940
	TTGAGCTCTG	CAGGTATGAC	CCCGAAGGGG	ACAATACAGG	GGAGCAGGTG	GCTGTTAAAT	3000
	CTCTGAAGCC	TGAGAGTGGG	GGTAACACCA	TAGCTBACT	GAAAAAGGAA	ATCGAGATCT	3060
	TAAGGAACCT	CTATCATGAG	AACATTTGTA	AGTACAAAGG	AATCTGCACA	GAAGACGGAG	3120
	GAAATGGTAT	TAAGCTCATC	ATGGAATTTT	TGCCCTCGGG	AAGCCTTAAG	GAATATCTTC	3180
10	CAAGAATAAA	GAACAAAATA	AACCTCAAAC	AGCAGCTAAA	ATATGCCGTT	CAGATTGTGA	3240
	AGGGGATGGA	CTATTGGGT	TCTCGGCAAT	ACGTTACCGG	GGACTTGGCA	GCAAGAAATG	3300
	TCCTTGTGTA	GAGTGAAAC	CAAGTGAAAA	TTGGAGACTT	CGGTTTAACC	AAAGCAATTG	3360
	AAACCGATAA	GGAGATATTAC	ACCGTCAAGG	ATGACCGGGA	CAGCCCTGTG	TTTTGGTATG	3420
	CTCCAGAAATG	TTTAATGCAA	TCTAAATTTT	ATATTGCCCTC	TGACGCTCTG	TCTTTTGGAG	3480
15	TCACTCTGCA	TGAGCTGCTG	ACTTACTGTG	ATTTCAGATT	TAGTCCCATG	GCTTTGTTC	3540
	TGAAATGTAT	AGGCCCAAC	CATGGCCAGA	TGACAGTCAC	AAGACTTGTG	AATACGTTAA	3600
	AAGAAAGAAA	AGCCCTGCGG	TGCCCAACCTA	ACTGTCCAGA	TGAGGTTTAT	CAACTATGAA	3660
	GGAAATGTGT	CGAATATCAA	CCATCCAATC	GGACAAGCTT	TCAGAACCTT	ATTGAAGGAT	3720
	TTGAAGCACT	TTTAAATATA	GAAGCAGTAA	TAACATTTAA	ATTCCACAGA	TTATCAAGTC	3780
20	CTTCTCCTGC	AACAAATGCC	CAAGTCAATT	TTTAAAAATT	TCTAATGAAA	GAAGTTTGTG	3840
	TTCTGTCCAA	AAAGTCACTG	AACCTACACT	TCAGTACATA	TACATGTATA	AGGCACACTG	3900
	TAGTGCTTAA	TATGTGTAAG	GACTTCTCT	TTAAATTGGG	TACCAAGTAA	TGATGACAC	3960
	ATAATGACAA	CGAATATCAA	AATGACACT	TAGCACTCC	TCCTTGTGGA	AAGAATATAC	4020
	CACCAATTCA	TCTGGCTAGT	TCACCATCAC	AACCTGATTA	CCAAAAGGGG	ATTTTGTAAA	4080
25	ACGAGGAGTT	GAACAAAATA	ATATCTGAAG	ATGATTGCTT	TTCCCTGCTG	CCAGCTGATC	4140
	TGAAATGTAT	TGCTGGCACA	TTAATCATAG	ATAAAGAAAG	ATTGATGGAC	TTAGCCCTCA	4200
	AATTTGAGTA	TCATATACAT	ACTAGACCAT	GCATCTCTAA	AATATTAGAT	ACCAGGTAGT	4260
	ATATATTGTT	TCGTATCAAA	AATGACTGTA	TTCTCTCACC	AGTAGGACTT	AAACTTTGTT	4320
	TCCTCAGTGG	CTTAGCTCTT	GTCTCTTGGG	GTGATCATA	GCACCCATTT	TTGAGAAAGC	4380
30	TGGTCTTACA	TGGGGGGGAT	GCTGTGGAAT	AGATAATTG	CTGCATGTTA	ATTCTCAAGA	4440
	ACTAAGCCTG	TGCCAGTGCT	TTCTTAAGCA	GTATACCTTT	AATCAGAACT	CATTCCCGAA	4500
	ACCTGGAATG	TATTAACATC	GCCTTTAAGA	AACGTCAATG	TATATCTCTT	TATAACTCTA	4560
	CCACTTTGGG	GCAGCTTATT	CCAGCACTGG	TTTTGAATGC	TGTATGCAAC	CAGTCAGAA	4620
	ACCACATAGG	CTGCACTGTT	CTTAGAGGGT	TTCCATACCT	ACCACCGATC	TACAGGGGTT	4680
35	GATCCCTGTT	TTTACCATCA	ATCATCACCC	TGTGTGCAA	CACCTTGAAG	ACCCGGCTAG	4740
	AGGCACATAG	GACTTACAGG	TCCACTAGAC	AGTTTTCAGT	TTGCTTGGAG	GTAGCTGGGT	4800
	AATCAAAAT	GTTTAGTCT	TGATTCAATG	TGAACGATTA	CGGCTTTTAT	GACCAAGAGT	4860
	CTGAAATCT	TTTGTGTTAT	CTGTTTAGTA	TTCGTTTGT	ATTGTTACTT	TTCACTGTT	4920
40	GAGCCCAAT	TCAGGATTTG	TTCACTGGCA	GCAATGAAGT	TGCCATTTAA	ATTGTTTCT	4980
	AGCTTACATC	ACCAAGGTCT	CTGTGTCAA	CCTGTGGCCA	CTCTATATGC	ACTTTGTTTA	5040
	CTCTTTATAC	AAATAAATAT	ACTAAGACT	TT			

Seq ID NO: B64 Protein sequence  
Protein Accession #: A39577

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	CIRAAQACRI	SPLCHNLFAL	YDENTKLWYA	PNRTITVDOK	MSLRHLHYMR	FYPFNWHGTM	120
50	DNEQSVWRHS	PEKQKNGYEK	KKIPDATPLL	DASSLEYLFA	QGGYDLVKCL	APIRDPKTEQ	180
	DGHDIENFCL	GMAYLAISEY	AMMKMQLPFE	LPKDISYKRY	IPETLANKSIR	QRNLLTRMRI	240
	NNVFDFPLKE	SNKTIICDSS	VSTHDLKVYK	LATLETLMKH	YGASIPFETM	LLISSSENMN	300
	WFHSNDGGHV	LYYEVMTIGN	LGIQWRHKPN	VVSVEKERNK	LKRKILENKO	KKDEERNKIR	360
	ESWNNFSFPF	EITHIVIKES	VVSINKQDNK	KMELKLSHBE	EALSFVSLVD	GYFRLTADAH	420
55	HYLCTDVAFP	LIVHNIQNGC	HGPICTEYAI	NKLREQGSEE	GMVYLRWSCT	DFDNILATVI	480
	CFKBSQVQG	AQKQPKNFQI	EVQKGRYSLE	GSDRSFPPLG	DLMSHLKKQI	LRTDNISFML	540
	KRCCQPKPRE	ISNLLVATKK	AQWQPVYPYM	SQLSFDRIK	KDLVQGEHLG	RGRTRTHYSB	600
	TLMDYKDDBG	TSESEKIKIVI	LKVLDPSHRD	ISLAFPERAS	MMRQVSHKHI	VYLYGVCVRD	660
	VENINVEEFV	BGGPLDLFME	RKSDVLTTPN	KFKVAKOLAS	ALSYLEDKOL	VHGNVCTKNL	720
60	LLARESIDSE	CGPFIKLEDP	GIPITVLGRQ	ECIERIFNLA	PECVEDSKML	SVAADKNSFG	780
	TTLWEICYNG	EIPLDKTLIA	EKERFYKSRG	RPVTPSCKBL	ADLMTRCMNY	DPNQRPFFRA	840
	IMRDINKLEE	QNPDIYSRKK	NQPTVDPTTH	FEKRFILKRI	DLGSEHFGKV	ELCRYDPEDN	900
	TGEQVAVKSL	KPEBGGNHLA	DLKKEIELLR	NLYHENIVKY	KGICTEDGGN	GIKLIMEFLP	960
	BGSLKEYLPE	NKNKINLQQL	LKYAVQICKG	MDYLGSEQTV	HRDIAARNVL	VESEHQVKIG	1020
65	DFGLTKALET	DKEYYTVKDD	RDSPVFWYAP	ECLMQSKFYI	ASDVNSFGVT	LHELLTYCDS	1080
	DSSPMALFLK	MIGPTHGQMT	VTRLVNLTKE	GKRLPCPPNC	FDEVYQLMRK	CWEPQPSNRT	1140
	SPQNLEGGFE	ALLK					

Seq ID NO: B65 DNA sequence  
Nucleic Acid Accession #: NM\_004867.1  
Coding sequence: 140..931

75	1	11	21	31	41	51	
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	TAAACAGGATC	TCCTCTTGCA	GTCTGCAGCC	CAGGACGCTG	ATTCCAGCAG	CGCCTTACCG	120
	CGCAGCCCGA	AGATTCACTA	TGGTGAAAAA	CGCCTTCAAT	ACCCCTACCG	CGGTGCAAAA	180
	GGAGGAGGGG	CGGAGAGAGG	TGGAGGCCCT	CCTGAGCGCG	ACGGTCAGAA	CTCAGATACT	240
	GACCGGCAAG	GAGCTCCGAG	TTGCCACCCA	GGAAAAAGAG	GGCTCTCTCT	GGAGATGTAT	300
	GCTTACTCTC	TTAGGCCTTT	CATTCTCTTT	GGCAGGACTT	ATGTTTGGTG	GAGCCTGCAT	360
80	TTACAAGTAC	TTACATGCCA	AGAGCACCAT	TTACCGTGGG	GAGATGTGCT	TTTTTGATTC	420
	TGAGGATCTT	GCATAATCCC	TTCTGTGGAG	AGAGCCTAAC	TTCTGTGCTG	TGACTGAGGA	480
	GGCTGACATT	CGTGAAGATG	ACAACATTGC	AATCATTTGAT	GTGCTGTGCC	CCAGTTTCTC	540
	TGATAGTGAC	CTTGACAGCA	TTATTATCAT	CTTTGAAAAG	GGAAATGACT	CTTACTCTGA	600
	CTTGTGTGCT	GGGAAGTGCT	ATCTGATGCC	CCTCAATACT	TCTATTGTGA	TGCCTCCAAA	660

AAATCTGGTA GAGCTCTTGG GCAAACCTGGC GAGTGGCAGA TATCTGCCCTC AAACCTATGT 720  
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 TATTACCAA CTTTGCATA ACAGAAAGTC CTTCGCCCTT CGTCGCAGAG ACCTCTTGCT 840  
 GGGTTTCAAC AAACGTGCCA TTGATAAATG CTGGAAGATT AGACACTTCC CCAACGAATT 900  
 TATTGTTGAG ACCAAGATCT GTCAAGAGTA AGAGGCAACA GATAGAGTGT CCTTGCTAAT 960  
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 TTACTCATGC ATTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAA AAAA 1080  
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Seq ID NO: B66 Protein sequence  
 Protein Accession #: NP\_004858.1

1 11 21 31 41 51  
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 15 MVKIAFNFTT AVQKEEARQD VEALLSRTVR TQILTGKELR VATQKEKGGSS GRCLMLLLGL 60  
 SFILAGLIVG GACIYKYFME KSTIYRGEMC FFDSEDPANS LRQGEFNFLEP VTEADIREF 120  
 DNIAIIDVFP PSFSDSDPAA IHDPEKGMT AYLDLLGNC YLMLPLTSIV MPFKNLVELF 180  
 GKLAGRYLP QTVVREDLV AVVEIRDVSN LGIFIQLCN NRKSPRLRRR DLLLGFNKRA 240  
 IDKWKIRHF PNEFIVETKI CQE

Seq ID NO: B67 DNA sequence  
 Nucleic Acid Accession #: XM\_083862.1  
 Coding sequence: 121..813

1 11 21 31 41 51  
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 25 ACBGGGAGG TCTGAGCTGT GGGCTGAGGC AGCGCAGCCG CTGCGCCAGG GTGCGGATG 60  
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 30 GCAAAACATG TTACGTGGT TCGAGAGAGT GGCTCCTTAA CTTATGAAGA ATTTCTCGGG 240  
 AGAGTAGCTG AGCTTAATGA TGTAAACGGCT AAAGTGGCTT CTGCGCCAGG AAAACATCTT 300  
 CTCTTTGAGG TACAACCTGG GTCTGATTCC TCTGCTTTT GGAAAGTGGT TGTACGGGTG 360  
 GTCTGTACCA AGATTACAA AAGCAGTGGC ATTGTGGAGG CATCAGCGAT CATGAATTTA 420  
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 35 AGCTCCACCT CTGAAGAAC TGATGAAAC TCATCCTCTG TAACATCTTG TCAGGCTAGT 540  
 CTTTGGATGG GAAGGGTGAA GCAGCTGACC GATGAGGAGG AGTGTGTAT CTGTATGGAT 600  
 GGGCGGCTG ACCTCATCTT GCCTTGTGCT CACAGCTTTT GTCAGAGTGT TATTGATAAA 660  
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 40 TCTTGGGTGG TATCAGATGC ACCCACTGAA GATGATATGG CTAACATAT TCTTAACATG 780  
 GCTGATGAGG CAGGCGAGCC CCACAGGCCA TGACCTTGAA GTGAAAGTCT TCTGTGCTA 840  
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 ACAGGAAAT CCAATTTGCC CACTCTTTTA TTTTGTCTAT TCTGATCAT TGTCCCCCTT 960  
 TTAATAATAA ACTTCCCATG TCTTCCAAAA AAAAAA AAAAA

Seq ID NO: B68 Protein sequence  
 Protein Accession #: XP\_083862.1

1 11 21 31 41 51  
 | | | | |  
 50 MGQIQSDQTQ LVINKLPERV AKHVILVRES GSILTYEFLG KVAELNDVTA KVASGQEKHL 60  
 LFEVQPGSDS SAFKVVVVRV VCTKLNXSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ 120  
 SSTSEEDFN SSVTSQDAS LMMGRVKQLT DEEBCCICND GRADLILPCA HSPQKCIDK 180  
 WSDRRHRCPI CRLQMTGANE SWVVSADPTE DDMANYILNM ADEAGQPHRP

Seq ID NO: B69 DNA sequence  
 Nucleic Acid Accession #: NM\_002975.1  
 Coding sequence: 180..1151

1 11 21 31 41 51  
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 60 CGACCAACCG ACCGGACAGA GACGAGGAGA GGAACAGHAA GAGAGAAGCT GGGAGAATCG 60  
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 ACCCTCCCA CCACAGCAT CCAGACATCT GGAACCTTGG GTGCCAAGAG TCCAGCTTAA 180  
 65 TGCAGGCAAC CTGGCTTTTG GGGCTTTTGG TGGTCCCCCA GCTCTTGGGC TTTGGCCATG 240  
 GGGCTGGGG AGCAGAGAGG GAGTGGGAGG GAGGCTGGGG AGGTGCCAG GAGGAGGAGC 300  
 GGGAGAGGGA GGCCTGATG CTGAAGCATC TGCAGGAAGC CTTAGGACTG CTTGCTGGGA 360  
 GGGGGGATGA GAATCTGTCC GGAACCTTGG AGGGAAAGA GGAACCTGGG ATGAGGAGG 420  
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 70 CTCCACCCC TGAGGACATC GTCACTTACA TCTGGGCGG CTTGGCCGCG CTGGACGCG 540  
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 AGGAGGGGCA GGCTCGCGCC GAGCGCGAGC ACGGCGGCTT GAGGGCTGCG CTGAAGGGGC 720  
 TGCCTCTGGG CCACAGTGC TTCTTGTCTT CCGCGGACTT CGAAGCTCAG GCGCGGGCGC 780  
 75 AGGCGCGGTG CACGCGCGCG GCGCGGAGCC TGGCGCAGCC GCGAGACCGC CAGCAGATGG 840  
 AGGCGCTCAC TGGTACCTG CCGCGGCGCG TCGCTCCCTA CAACCTGCCCC GTGTGGCTGG 900  
 GCGTGCACGA TCGCGCGCGC GAGGCGCTCT ACCTCTTCCA AAACGGCCAG CGCTGTCTCT 960  
 80 TCTTGGCTCG GCATGCTCA CCGCGCCCGG AGCTCGGCGC CCGAGCCAGC GCTCGCGCG 1020  
 ATCGGCTCAG CCGGACAG CCAACAGGTC GCACGCTCGA GAACCTGCGT GCGCAGGCTT 1080  
 TCCCTTCTTA GCGGGGCGCG TACCCGCGCT CCTTGGCCAT CCCACACCC GGCCTTTCCT 1200  
 TCGCGCGTGC CACCCCTCTT CCGGAATCCT CCTTCCCTTC CTGCGCACGA ATGGCAGGCT 1260  
 CTTCCCGGAC CCGCAGTCTG GCGGGGCTCT TCGGCTGCGG GCACTCTCTC 1320  
 TTGTTAGTGT CTTTCTTGA AGGGGCGGGC ACCAGGCTAG GTCCGGTGCC AATAATCTCT 1380  
 TGTGGAATCT GAAAAA AAAAAA

Seq ID NO: B70 Protein sequence  
Protein Accession #: NP\_002966.1

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      RGDENPAGTV EGKEDWEMEE DQGESEEEEA TPTPSSGFSP SPTPEDIVTY ILGRLAGLDA 120
10     GLHQLHVRLE ALDTRVVVELT QQLRQLRNAA GUTRDAVOAL QEAQGRABRE HGRLEGCCLKG 180
      LRLGHKCPFL SRDFEAQAAA QARCTARGGS LAQPADRQOM EALTRYLRAA LAPYNWFVWL 240
      GVHRRRAEGL YLFENGQRVS FFAWHRSPRP ELGAQPSASP HPLSPDQPNG GTLENCVAQA 300
      SDDGSWRDHD CQRRLLYYVCE PFP
  
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Seq ID NO: B71 DNA sequence  
Nucleic Acid Accession #: BC000839.1

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20     TGGGCTTTB TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGGTCCCCC TTCCTATGAT 120
      GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AGTTAACTCT GAGGAGATGG 180
      GCGCTGCAAG CCTCCTCTCT AGCCGTCTGT TCAGAAATA GCGTTTTTGA AATGCCCTGA 240
      GTTGACCTAA TGTCTTATTG GGTCTCTGTC TGCAGGATTT ACGGCGACGT TGAAGCCGAA 300
      GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAGG AATGGGACAA 360
25     GACCCATCTT TATGCAAAAGC CAGCGTTACA GTAAATGTTCC AGCATCTCAT AATCTATCCT 420
      GGGGAATTCG GCTGCCCTCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCTCTAT 480
      CTTACAGAGC AGCTTGTGTC TATATACCAT TGAAGAGCCT TCAGAGCTBA GAGGTACTAC 540
      TAACCAATAA CCTGCTTGGC TCAAGGGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT 600
      TTGAGGAAAA CTAGCTGTCT GTGTTCACTC CAGGCTGAAG TTACAGGTCT GAGCAATAAA 660
30     GGTGTATAAA AATAGGAATC TGTCTTGGAG GACATCAGAA GGTGAATTTT CCAAGTTCTT 720
      GGACAACTTA GCTGTTGAAG AGCTTCTGCG GTTTGGGGGG TATTTCAGAT GTACCTTAAA 780
      GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTGCT 840
      GTGTATCA CA TTTCTGTATT TTATCACCCC CTCTCTGCAA CATTAATTAT CTGGAATCTA 900
      CCTGCCCCCT TGTCTTTTAA ATACAGGGCC TTGGTFTTGT TACCCAGGCT GGTTCACAG 960
35     CCATAGCTTT AAGAGATCCT CTCACACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA 1020
      TTCATGGCAC CCAGACTTTG CTGCTTCTCT TACATGATCC AGGCCAGAA CCCAACTCA 1080
      GGCATGAT AGATGACAC TTTGTAAAC TACTGACCTA GCTTGTGTC AATGTTGTAT 1140
      TGAACCTCC ATAACCTCAC TTGCTGCTG TTCTCTGTA TACAGCCACC TTCGTGTC 1200
40     GTCATGAGCC TTTAGGTCTC CATTTGCATA TTGCAATATC TATGTTCCAT GTAGGTAGCT 1260
      CATTCAGGCG CTGTCTCTTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCAATTTG 1320
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Seq ID NO: B72 DNA sequence  
Nucleic Acid Accession #: CAT cluster

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45     1      11      21      31      41      51
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50     CTTTGTACTT GTCTTTTCTT TTTATTTTCT TTTGAGCGAT TGTGGAACA TAGCATAGCA 120
      CGCACTATGG CACGAGGCTC GTGCTGCTTG GCGAGGGGGA CTGGCGGATA AGGTCTTGTG 180
      CGTGGGCTCG AGGCTTAAAA GTAGCAGTGG GGTCTTGTGA AGGACAAAT GGCGATGGCG 240
      GGCGGTGTAG GTCCCTCTTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG 300
      TGAGGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC CGTCTGTTCA 360
55     GAAAAATAGG TTTTGGAAAT GCGCTGAGTT GACCTAATGT CTATTTGGGC TCCTGCTGTC 420
      AGGATTTAAG CACACGTTGG AACCGAAGAG AGCTCTGTTG TTGCAATGTT CAGGCCACAA 480
      GAGCTTACTG GTGAAGGAAT GGGACAAAGC CCATCTTTAT GCAGAGCCAG GGTACAGTA 540
      ATGTTCCAGC ATCTCATAT CTATCTGCGG GAATTCAGCT GCTTCCAGG GTGAATACAG 600
      GTATCTCTGA TGACAGTCTG CTTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCATGA 660
60     AAAGCCCTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGCCAGC 720
      ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGTCTGTG TTCCTCCAG 780
      GCTGAAGTTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGAATCTGT CTGGAGGAC 840
      ATCAGAGGAT GAATTTTCCA AGTCTTGGG CAACCTAGCT GTTGAAGAGC TTTCTGGGTT 900
      TGGGGGGGAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAAGA CACTGGGAGC 960
65     CAAAGABACA GCAGTTGAGG GTTTGCTGTG TATCACATTT CTGTATTTTA TCACCCCTT 1020
      CCTGCAACAT TATTTATCTG GAATCTACCT GCGCTTTTGT TTTTLAGATA CAGGGCTTGT 1080
      GTTTTGTATC CAGGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT 1140
      TCCAAAGTGG TGGGATTGCA GGTGTGATTC ATGGCACCCA GACTTTGCTG CCTTCTTAC 1200
70     ATGATCAGG CCGCAGAACCC AAATCAAGGC ACTGTATAGA TGACCACTTT GGTAAACTAC 1260
      TGACCTAGCT TGTGGCAAT TGTGATTTGA ACTTCCATA ACTCCACTTC GTGTCTGTT 1320
      CTCTGTATAC AGCCACCTTC TGTTCCTGTC ATGAGCCTTT AGGTCTCCAT TTGCATATT 1380
      CAAATACATAT GTTCCATGTA GGTAGCTCAT TCAGGGCTTT GCTCTTCACT TCAAAAAAGG 1440
      TTCCCTTGAG GACTGGCTGT CAATTTGTGT TGCCTGTGTT GTTGTGATG AAAATAATAA 1500
75     AATGATTGAT TACATAAAAA AAAAAAATAA AAAAAACAAA CAAAAAAC 1560
      CGCGGCGCTT TTTCCCGGGC GCACAAAGTT ATAAACGCC GTCCATC
  
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Seq ID NO: B73 sequence  
Nucleic Acid Accession #: NM\_000222.1  
Coding sequence: 22..2952

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      CTGCTCTTAC TGTCTGCGGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120
  
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	CCGTCCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCGCGT	GGGCGACGAG	180
	ATTAGGCTGT	TATGCACTGA	TCCGGGCTTT	GTCAAAATGGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACACGT	GCACCAACAA	ACACGGCCTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCCCAAGC	TTTTCCCTGT	TGACCGCTCC	TTGTATGGGA	AGAAGACAA	CGACACGCTG	420
	GTCCGCTGTG	CTCTCACAGA	CCCAGAAATG	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGCGGGCAT	CATGATCAAA	540
	AGTGTGAAC	GGCCTTACCA	TCGGCTCTGT	CTGCAATTGT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGTGCT	CGGAAAAATT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAAGC	TGTGCTGT	660
	GTGTCTGTGT	CCAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTAC	AGTGACGTGC	720
	ACAATAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAACGTGGA	AAAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGGTGACT	TCAATTATGA	ACGTACAGCA	840
	ACGTGTACTA	TCAGTTCAGC	GAGAGTTAAT	GATTCTGGAG	TGTTTATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCACAACA	ACCTTGGAG	TAGTAGATAA	AGGATTTCATT	960
	AATATCTTCC	CCATGATAAA	CACCTACGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTG	1020
	ATTGTGTAAT	ATGAAGCAAT	CCCCAAACCT	GAACACGAGC	AGTGGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAGATGA	TATCAGATAC	1140
	GTAAGTGAACT	TTCACTTAAC	GAGATTAAAA	GGCACCAGAG	GAGGCACTTA	CACATTCTCTA	1200
20	GTGTCCAAAT	CTGACGTCAA	TGCTGCCATA	GCATTTAATG	TTTATGTGAA	TACAAAACCA	1260
	GAAATCTCTGA	CTTACGACAG	GCTCGTGAAT	GGCATGCTCC	AATGTGTGGC	AGCAGGATTC	1320
	CCAGAGCCCA	CAATAGATTG	GTATTTTGTG	CCAGGAACTG	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGATGTGCA	GACACTAAAC	TCATCTGGGC	CACCGTTTGG	AAAGCTAGTG	1440
	GTTCAGAGTT	CTATAGATTG	TAGTGCAATC	AAGCACAAATG	GCACGGTTGA	ATGTAGGCT	1500
25	TACAAAGATC	TGGCAGACAG	TTCTGCCAT	TTTAACTTTG	CATTAAAGG	TAAACACAAA	1560
	GAGCAAAATCC	ATCCCCACAC	CCGTTCACCT	CCTTTGCTGA	TTGGTTTGGT	AATCGTAGCT	1620
	GGCATGTATGT	GCATTATTGT	GATGATTTCTG	ACCTACAAAT	ATTACAGAA	ACCCATGTAT	1680
	GAAGTACAGT	GGAAAGTGTG	TGAGGAGATA	AATGGAAACA	ATTATGTTTA	CATAGACCCA	1740
	ACACAACTTC	CTATGATCA	CAAAATGGAG	TTTCCAGAA	ACAGGCTGAG	TTTGGGAAA	1800
30	ACCTTGGGTG	CTGAGCTTTT	CGGGAAGGTT	GTGAGGCCAA	CTGCTTATGG	CTTAATTAAG	1860
	TCAGATGGGG	CCATGACTGT	CGCTGTAAAG	ATGCTCAAGC	CGAGTGCCCA	TTTGACAGAA	1920
	CGGGAGGCC	TCATGTCTGA	ACTCAAAGTC	CTGAGTTACC	TTGGTATCA	CATGAATATT	1980
	GTGAATCTAC	TTGAGGCTCG	CACCAATTGA	GGGCCCAACC	TGGTCATTAC	AGAAATTTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTGAGA	AGAAAACGTC	ATTCATTAT	TTGTTCAAAG	2100
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	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGGCGG	ACAAAAGGAG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCCGCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
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40	GCAGCCAGAA	ATATCTCTCT	TACTCATGGT	CGGATCACAA	AGATTGTGTA	TTTGTGCTA	2460
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	AAATGGATGG	CACCTGAAAG	CATTTFCAAC	TGTTATACAA	CGTTTGAAGG	TGACGTCTGG	2580
	TGCTATGGGA	TTTTCTTTTG	GGAGCTGTTT	TCITTAGGAA	GCAGCCCTCA	TCTTGAATG	2640
	CGGTGTGATT	CTAGATTCTA	CAAGATGATC	AAGGAAGGCT	TCCGGATGCT	CAGCCCTGAA	2700
45	CACGCACTTG	CTGAAATGTA	TGACATAATG	AAGACTTGCT	GGATGTCAGA	TCCCTTAAAA	2760
	AGACCAACAT	TCAAGCAAAAT	TGTTACGCTA	ATTGAGAAAG	AGATTTCAGA	GAGCACCAT	2820
	CATATTACT	CCAACCTTAGC	AAACTGCGAG	CCCAACCGAC	AGAGGCGCGT	GGTAGACCAT	2880
	TCTGTGCGGA	TCAATCTGCT	GGCAGCACCC	GCTTCTCTCT	CCAGGCTCTG	GCTTGTGCTC	2940
	GACGATGTCT	GAGCAGAATC	AGTGTGTTGG	TCACCCCTCC	AGGAATGATC	TCTTCTTTTG	3000
50	GCCTCATGTA	TGGTATTTT	CTTTCTTTT	AACCTTGATC	CAACFCCAGG	ATAGTGGGCA	3060
	CCCCACTGCA	ATCCGTGCTT	TCTGAGCACA	CTTTAGTGGC	CGATGATTTT	TGTCATCAGC	3120
	CACCATCTCTA	TTCGAAAGGT	TCCAACTGTA	TATATTCCCA	ATAGCAACGT	AGCTTCTTACC	3180
	ATGAACAGAA	AACATCTGTA	TTTGGAAAAA	GAGAGGGAGG	TATGGACTGG	GGGCTAGAGT	3240
	CCTTTCCAGG	GCTTCTCCAA	TTCTGCCCCA	AAATATGGTT	GATAGTTTAC	CTGAATAAAT	3300
55	GGTAGTAATC	ACAGATTGGC	TTCAAGACCA	TCCATAGTAG	TATGATGATA	CAGATTAGA	3360
	AGCTGAAAAC	CTAAGTCTCT	TATGTGGAAA	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACCT	GGGCTTAAAG	AATCTAGTAT	TTCATGCTGG	GAATGAGACA	TAGGCCATGA	3480
	AAAAATGAT	CCCCAAGTGT	GAACAAAAGA	TGCTCTTCTG	TGGACCACTG	CATGAGCTTT	3540
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60	GCCTCCCTAG	CCAGCACTTG	TATATACGCA	TCTATAAAT	GTCCGTGTTT	ATACATTGTA	3660
	GGGGAACAA	CCATAGAGTT	TGTTTTCTGT	ATACAAACCT	GGCATTTATG	CCACTGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAACAGG	TTAATACCAT	TTTTTAAGGA	3780
	AACAATATAA	CCACAAAGCA	CAGTTTGAAC	AAAATCTCCT	CTTTAGCTG	ATGAACCTTAT	3840
	TCTGTAGATT	CTGTGGAACA	AGGCTTACG	CTTCAGAAATG	GCAATGFACT	CAATGGATTT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCACT	GCAATGGCTCC	CACAGGAGTG	GGAAAAACAT	3960
	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAATAAAGT	ATAGGTTTAG	CCTCTCTCGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTAGCTTT	GTATGTGTGT	4080
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70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGCAGTTC	ACCTGCACCT	AAGGCACCTT	GTTATTTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATATATG	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTTAGACT	4380
	TAGGCTTGGG	TATTATTCTT	GTAGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
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75	TTGCTGTGAA	AGATTACAGT	ATGTTGCCCT	TATGGTTTCC	CCCTTCTACA	TTTCTTAGAG	4560
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	CTGACACCTT	TCCAAAGTTA	ACAGATTTTG	GGGTGTGTGT	GTCAACCAAG	AGATTGTGTG	4680
	TGCGCATACT	TTGTCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTGC	4800
80	TTGCGCATCT	TTGTCTGAAA	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
	AAGTGGTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTGC	4920
	AATGCTTTTT	GAATATTTCC	AAGCCCATGA	GTCCCTGAAA	ATATTTTTTA	TATATACAGT	4980
	AACITTAGTG	GTAAATACAT	AAGCGGCGTA	AGTTTAAAGG	ATGTTGTGTG	TCCAGTGTG	5040
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Seq ID NO: B74 protein sequence  
Protein Accession #: NP\_000213.1

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PGFVKQTFEI LDETENENKQW EWIKEAEAT NTGKYTCTNK HGLNSIYVF VRDPAKFLV 120
DRSLYGGKEDN DTLVRCLPLTD PEVTNYSLEKQ CQKRLPKDL RFIEDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSSEKF ILKVRPAFKA VPVSVSKAS YLLREGESFT VTCTIKDVSS 240
SVYSTWKREN SQTKLQEKYN SWHGDENYE RQATLTSSA RVNDSGVFMC YANNTFGSAN 300
VTTTLEVVDK GFNIFPMIN TTVFVNDGEN VDLIVEVEAF PKPEHQWYIY MNRITFDKWE 360
DYPKSENEEN IRYVSELHIL RLKGTGGTY TFLVNSSDVN AALAPNVYVN TKPEILLYDR 420
LVNGLMLQVCA AGFPEPTIDH YFCPGTEQRC SASVLPVDVQ TINSSGPFPG KLVVQSSIDS 480
SAPKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIHPT LFTPLLIGFV IVAGMMCIIV 540
MILTYKYLQK PMYEVQWKVV EEINGNNYVY IDPTQLPYDH XWEFFRNRLS FGKTLGAGAF 600
GKVVVEATYV LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLSYLGNH MNIVNLLGAC 660
TIGGPFLVIT FYCCYGLLLN FLRRKRDSFI CSKQEDHAEA ALVKNLLESK EBSGSDSTNE 720
YMDMKPGVSU VVPTKADKRR SVRIGSYIER DVTPAIMEED ELALDLEDLL SFSYQVAKGM 780
APLASKNCTH RDLAARNILL THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAPE 840
IFNCVYTFES DVWYQGIFLW ELFSLGSSPY PGMVDSKPY KMKEGFRML SPEHAFARMY 900
DLMKTCNDAD PLKRPFTQI VQLIEKQISE STNHIYSNLA NCSFNRQKPV VDHSVRINSV 960
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Seq ID NO: B75 DNA sequence  
Nucleic Acid Accession #: NM\_004456  
Coding sequence: 58..2298

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CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCGTGTA GCTCATTCGG CGGGACTAGG 300
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GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAAGTACA CGGGGATAGA 540
GAATGTGGGT TTATAAATGA TGAAATTTTT GTGGAGTTGG TGAATGCCCT TGGTCATAT 600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAGAGAGAAGA AAAGCAGAAA 660
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CCACAGTATC ACCAGCTTTC GGAGGAGAGA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
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Seq ID NO: B76 Protein sequence  
Protein Accession #: NP\_004447

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MVDETVLHN IPYMGDEVD QDGTFLLELI KNYDGKVGSD RECGFINDEI FVELVNALGQ 180
YNDDDDDDG DDFERBEKQ KLEDRHDDK ESRPERKFTS DKILEAISM FPDKGTAEL 240
KECYKELTQ QLPALPPEC TPNIDGNAX SVORBSLHS FTLEFCRCP KYDCFLHPH 300
ATPNTYKRW TETALDNKPC GPQCYOHLG AKEFAAALTA BRIKTPPRP GRRRGRLFN 360

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NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEBEEK KDETSSSSSEA NSRCQTPFKM 420  
 KPNIEPPENV EWGGAEMSMF RVLISTYYDN FCAIARLIGT KTCRQVYEFK VKESSIIAPA 480  
 PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDEPRQPC DSSCPCVIAQ 540  
 NFCEKFCQCS SECQNRFFGC RCKAQCNTKQ CPCYLAUREC DPDLCLTCGA ADHWDKKNVS 600  
 CKNCSLQRGS KKHLLAPSD VAGWGIKID PVQKNEFISE YCETLISQDE ADDRKGKVDK 660  
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Seq ID NO: B77 DNA sequence  
 Nucleic Acid Accession #: NM\_007015  
 Coding sequence: 1..1005

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 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240  
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 GACAACAGCT TCTGTAGTTC TAAGGTGTTA GAACCTCTCG GTGACCTTCC TATTTTCTGG 600  
 25 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGRAAGAA GAGAAGTGGT AAGAAAAATT 660  
 GTTCCAACTA CCAACAAAAG ACCACACAGT GGACCCAGGA GCACCCAGG CGCTGGGAAGA 720  
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 ATCTGTGTGA TAGAATGAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900  
 30 GGGGCTATT ACCCATGACC TTATAATTAT CAAGGCTGCC GTTCGGCTCG CAGAGTCATC 960  
 ATGCCATGTA GCTGGTGGGT GGCCTGTATC TTGGGCTATG TGTGAAATCA CTTTATATAT 1020  
 CACGTGCTGT AAATATGAAA CTAGCTGAAG AGACACCAA AGAAGCATT AGGCAGGTTC 1080  
 ATGCTGATGG GACCATATAA TATTTTACA CGCAGCCTGA GCGGTATTC TTGACACTCT 1140  
 35 TAACAGAATT TTTTAAATCG TTTTCCAGAA CTTTATATTA TGCAAATCCA CTGAAAGGGT 1200  
 AGTTCAAGTC TAAATATGCA TAACCCCGTT ATTTGTTATT TTTTATTCG ATTGATTTC 1260  
 CATAAGTCTT CCCTGCTGTG CATCTTCCA AGCTATTTG AAATAACAC GAAATTTAC 1320  
 AGTTTCCC

Seq ID NO: B7B Protein sequence  
 Protein Accession #: NP\_008946

1 11 21 31 41 51  
 | | | | |  
 45 MTESDKVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISS AVLLLFGAIG 60  
 AFYFWKGSDB HYNVHYHMS INKGLQDGSB BIDAGNNLET FFMGSGABEA IAVNDFQNGI 120  
 TGRFAGGSEK CYIKAQVKAR IPEVGAVTKQ SISSKLEBKI MEVKYERNBL IWVAVDQPVK 180  
 DNGFLSSKVL ELCSGLPIYW LKPTYPKEIQ RERREVRVKI VPTTKRPHS GPRSNFGAGR 240  
 50 IANNETRESVQ EDSQAFNFDN PYHQOEGESM TFDPRLDHEG ICCIECRSY THCQKICEPL 300  
 GGYYPWPYNY QGCRSACRVI MPCSNWVARI LGMV

Seq ID NO: B79 DNA sequence  
 Nucleic Acid Accession #: NM\_012449.1  
 Coding sequence: 66..1085

1 11 21 31 41 51  
 | | | | |  
 55 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60  
 AATTAAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAG ATGAAGCCTA 120  
 60 GGAGAAATTT AGAAGAAGAC GATTATTTCG ATAAGGACAC GGGAGAGACC AGCATGCTAA 180  
 AAGAGACCTGT GCTTTTGCAT TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240  
 CAGAACTTCA GCACACACAG GAACCTTTTC CACAGTGGCA CTTGCCAAAT AAAATAGCTG 300  
 CTATTATAGC ATCTCTGACT TTCTTTACA CTCTCTGAG GGAAGTAATT CACCCTTAG 360  
 CAACCTTCCA TCAACATAT TTTTATAAAA TTCCAATCCT GGTCATCAAC AAGTCTTTC 420  
 65 CAATGGTTC TACACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATG 480  
 TCCAACCTCA TAATGGAACC AAGTATAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540  
 TAACAAGAAA GCAGTTTGGG CTCTCAGTT TCTTTTTCG TGACTGCAT GCATTTTATA 600  
 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC 660  
 AGGTCCACAA AAATAAGAAA GATGCCCTGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720  
 70 ATGTGTCTCT GGGAAATGTG GGAATGGCAA TACTGGCTCT GTTGGCIGTG ACATCTATTC 780  
 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACCA TATTCAGAGC AAGCTAGGAA 840  
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCCCTGGAT AAGTGGATAG 900  
 ATATAAACA ATTGTATGG TATACACCTC CAACITTTAT GATAGCTGTT TTCCTTCAA 960  
 TTGTGTCTCT GATATTAAAA AGCATACTAT TCCTGCCATG CTTGAGGAG AAGTACTGTA 1020  
 75 AGATTAGACA TGGTTGGGAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCCTAGT 1080  
 TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATGA TATATTTTAT CACCAACATT 1140  
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAGGAAA AAAAAAAAAA AAAAA

Seq ID NO: B80 Protein sequence  
 Protein Accession #: NP\_036581.1

1 11 21 31 41 51  
 | | | | |  
 80 MRSRKDITNQ EELWQMKPRR NLEEDDYLRK DTGETSMLEK FVLLHLHQTA HADEFDPCSE 60  
 LQHTQELFFQ NMLPIKIAAI IASLTFLYTL LREVIPLAT SHQYFYKIP ILVINKVLPM 120

VSITLLALVY LPGVIAAIVQ LHNQTKYKCF PHWLKRWMLT RKQFGLLSFF FAVLHAIYSL 180  
 SYPMRRSYRY KILNWAYQQV QONKEDAMIE HDVVRMEIYV SLGIVGLAIL ALLAVTSIPS 240  
 VSDSLWREF HYIQSKLQIV SLLLGTHIAL IFAWNKWIDI KQFVWYTPPT FMLAVFLPTV 300  
 VLIFKSILFL PCLRRKILKI RHGWNEDVTIKI NKTRICSQL

Seq ID NO: B81 DNA sequence  
 Nucleic Acid Accession #: NM\_000684  
 Coding sequence: 87..1520

10 1 11 21 31 41 51  
 TGCTACCCCG GCGGCGGCTT CTGGGGTGTG CCCCAACCAC GGCCAGCCCG TGCCACACCC 60  
 CCGCCCCCGG GCGCTCCGCG CTCGGCATGG GCGCGGGGGT GCTCGTCCCG GCGCGCTCCG 120  
 AGCCCGGTAA CCGTGTCTCG GCGCGACCGC TCCCGGACCG CGCGGCCACC GCGCGCGCGC 180  
 TGCTGGTGCC GCGCTCGCGG CCGGCTCGCT TGCTGCTCTC CGCAGCGAA AGCCCGGAGC 240  
 CGCTGTCTCA GCGGTGACA GCGGCGATGG GTCTGTCTGAT GCGCTCATC GTGCTGCTCA 300  
 TCGTGGCGGG CAATGTCTCG GTGATCGTGG CCATCGCCAA GACGCGCGCG CTGCAGAGCG 360  
 TCACCAACCT CTCATCARG TCCCTGGCCA GCGCGACCT GGTATGGGG CTGCTGGTGG 420  
 TGCGTTTCGG GCGCACATC GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGCG 480  
 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGCCAG CATCGAGACC CTGTGTCTCA 540  
 TTGCGCTGGA CCGCTACCTC GCGCATCACT CCGCTTCCG CTACCGAGC CTGCTGAGCG 600  
 GCGCGCGGGG GCGGCGGCTC GTGTGACCGG TGTGGGCCAT CTCGCGCTCG GTGTCTCTCC 660  
 TGCCCATCTC CATGCACTGG TGGCGGGCGG AGAGCGACGA GCGCGCGCGC TGCTACAAGC 720  
 ACCCCAGTGG CTGCGACTTC GTCAACCAAC GCGGCTACGC CATCGCTCCG TCCGTAGTCT 780  
 CCTCTACGCT CTCAGTGGAC ATCATGGGCT TGCTGTACCT GCGGGTGTTC GCGAGGCGCC 840  
 AGAAGCAGGT GAAGAAGATC GACAGCTGGG AGCGCGCTTT CCTCGCGCGC CCAGCGCGCG 900  
 CCGCTCGCGC CTGCGCTCGC CCGCTCCCGG GCGCGCGCGC GCGCGCGCGA CCGCGCGCGC 960  
 CCGCGCGCGC CCGCGCGCGC GCGCGCGCTG CCGCGCGCGC TGCGGGTAAG CCGCGCGCGC 1020  
 CCGCGCTGCT GCGCGCTACG GAGCAGAAAG CGCTCAAGAC GCTGGGCATC ATCATGGCGG 1080  
 TCTTCAAGCT CTGCTGGCTG CCTTCTTCC TGCGCAACGT GGTGAAGGCC TTCCACCGCG 1140  
 AGCTGGTGGC CAGCGCGCTC TTCTGTCTCT TCACTGGCT GGGCTACGCC AACTCGGCT 1200  
 TCAACCCCAT CATCTACTGC CCGAGCCCGG ACTTCGCAA GCGCTTCCAG GGACTGCTCT 1260  
 GCTGCGCGCG CAGGCTGCGC CCGCGCGCGC AGCGACCTCA CCGAGACCGG CCGCGCGCTC 1320  
 CGGGCTGTCT GCGCGCGCGC GAGCCCGCGC CATCGCGCGG GCGCGCGCTC GAGCGCGCGC 1380  
 ACGACGATGT CBTGCGGGCG CCGCGCGCGC CCGCGCTGCT GAGCGCGCTG GCGCGCTGCA 1440  
 ACGCGCGGGC GCGCGCGCGC AGCGACTCGA GCTTGGACGA CCGGTGCGCG CCGCGCTTCC 1500  
 CTTGCGATC CAGGTGTGAG GCGCGCGCGC GCGCGCGCGA CTCGCGCGAC GCGCTTCCAG 1560  
 GCGAACGAGG AGATCTGTGT TTAATTAGAA CCGATAGCAG GTGAATCTGA AGCCCAAT 1620  
 CTTGCTGTA ATCATCGAG GCAAGAGAA AAGCCAGGA CCGTTCGACA AAAAGGAAAG 1680  
 TTTGGGAAGG GATGGGAGG TGGCTTCTG TTG

Seq ID NO: B82 Protein sequence  
 Protein Accession #: NP\_000675.1

45 1 11 21 31 41 51  
 MGAGVLVLGA SEPGNLSAA PLPDGAATAA RLIVPASPEA SLLPPASESP EPLSQQWTAG 60  
 MELLMALIVL LIVAGNVLVI VAIKTPRLQ TLNLFIMS L ASADLVMLL VVPPGATIVV 120  
 WGRWEYGSFF CELWTSVDVL CVTASISTLC VIALDRYLAI TSPFRYQSL TRARARGLVC 180  
 TVWALISALVS FPIIMBMWNR AEDDEARRCY NDEKCCDFVT NKAYAIASSV VSFYVPLCIM 240  
 AFVYLVVFRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP EPAAAATAP 300  
 LANRAGKRR PSRLVALREQ KALKTLGLIM GVFTLCWLPF FLANVVKAEH RELVDELFLV 360  
 FFMWLYAMS AFNPITYCRS EDRKAFQGL LCCARAAAR RHATGDRFR ASGCLARPGP 420  
 PPSPGAASOD DDDVDVVGATP PARLLEPWAG CNGGAARDSD SGLDEPCRP G PASESKV

Seq ID NO: B83 DNA sequence  
 Nucleic Acid Accession #: NM\_000729.2  
 Coding sequence: 2..421

60 1 11 21 31 41 51  
 GGCTCAGCTG CCGGCTGCTT CCGGTTGGAA ACGCCAAGCC AGCTGCGGTC CTAATCCAAA 60  
 AGCCATGAAC AGCGCGGTGT GCGCTGTGCT GCTGATGGCG GTACTGGCGG CTGGCGCCCT 120  
 GACGCGCGCG GTGCTCTCCG CAGATCCCGC GGGCTCCGGG CTGCGACGGG CAGAGGAGGC 180  
 GCGCGCTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240  
 CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAGACT CTTCTGGAC GAATGTCCAT 300  
 CGPTAAGAAC CTGCAGAAC TGGACCCGAG CCACAGGATA AGTGACCGGG ACTACATGGG 360  
 CTGGATGGAT TTTGGCGGTC GCGATGCCGA GGAGTATGAG TACCCCTCTC AGAGGACCCA 420  
 GCGCGCATCA GCGCAACCGA AGCAACCTCC CACCCAGAG GAGGCAGAA TACACAACAA 480  
 TCACACTCAT AACTCATTTG CTGTGAGTGT TGACATTGAA TGTATCTATT TATTAGTTTC 540  
 TCAATGTGAA AATGTGTCT GTAGATTTGT CAGTGCACAC CACACAGCT CACCAGAGT 600  
 TGTGCAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660  
 TATGCTATTA AAGTGATTTC ATCTGCTC

Seq ID NO: B84 Protein sequence  
 Protein Accession #: NP\_000720.1

80 1 11 21 31 41 51  
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEAP RRQLRVSRQ DGESRAHLGA 60  
 ELARYIQAR KAPSERMSIV KNLQNLDPSE RISDRYNGW MFGRRSARE YEYPS



TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

- 5 **A1 DNA SEQUENCE**  
 Gene name: endothelial differentiation, sphingolipid G-protein-coupled receptor, 1  
 Unigene number: Hs.154210  
 Probeset Accession #: M31210  
 Nucleic Acid Accession #: M31210  
 Coding sequence: 251-1396

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TCTAAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG 60  
 AACGCAACTT CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCCAAGGA 120  
 AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT 180  
 CTGGCTGCG CCTCTAGCGT TCGTCTGGAG TAGCGCCACC CGGCTTCCCT GGGGACACAG 240  
 GGTTCGGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCCACCAGA GCTCGGTCTC 300  
 TGACTACGTC AACTATGATA TCATCGTCCG GCATTACAAAC TACACGGGAA AGCTGAATAT 360  
 CAGCGCGGAC AAGGAGAACG GCATTAAACT GACCTCGGTG GTGTTCAATC TCATCTGCTG 420  
 CTTTATCATC CTGGAGAACG TCCTTGCTCT GCTGACCAT TGGAAAACCA AGAAATTCCA 480  
 CCGACCCATG TACTATTTTA TTGGCAATCT GGGCTCTCTA GACCTGTTCG CAGGAGTAGC 540  
 CTACACAGCT AACCTGCTCT TGTCTGGGCG CACCACCTAC AAGCTCACTC CCGCCCAAGT 600  
 GTTTCGCGTC GAAGGAGATA TGTCTGTGGC CCTGTCAAGC TCGGTGTTCG GTCTCTCGC 660  
 CATCGCATTT GAGCGCTATA TCACAAATGCT GAAATGAAA CTCCACAAAG GAGCAATAA 720  
 CTTCCGCTTC TCCGCTCTAA TCAGCGCTG CTGGGTCAAT TCCCTCATCC TGGGTGGCTT 780  
 GCCTATCATG GGTGGAAGT GCATCACTGC GCTGTCCAGC TGCTCCACCG TGCTGCGGCT 840  
 CTACACAGAG CACTATATCC TCTCTGCGAC CACGCTCTTC ACTCTGCTTC TGCTCTCCAT 900  
 CGTCTATTCT TACTGCAAAA TCTACTCCTT GGTCAAGACT CGGAGCCGCG GCCTGACGTT 960  
 CCGCAGAAAC ATTTCCAAAG CCGCGCGCAG CTCGAGAAT GTGGCGCTGC TCAGAACCGT 1020  
 AATTATGCTC CTGAGCGCTG TCATCGCTCG CTGGGCAACG CTCCTCATCC TGCTCTGCT 1080  
 GGATGTGGGC TGCAAGGTGA AGACCTGTGA CATCTCTCTC AGAGCGGAGT ACTTCCCTGGT 1140  
 GTTAGCTGTC CTCACCTCCG GCACCAACCC CATCATTTAC ACTCTGACCA ACAAGGAGAT 1200  
 GCGTCGGGCG TTCACTCGGA TCATGTCTCTG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG 1260  
 CAAATTCAGC CGACCCATCA TCGCGGCGAT GGAATTCAGC CGCAGCAAAAT CGGACAATTC 1320  
 CTCCACCCCG CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTAATGCTT CTGGAACGTT 1380  
 CAATCTCTCT TCTTAGAAGT GGAGGCTGTC CACCCACCGG AAGGCTCTTT TACTTGGTCTG 1440  
 CTGGCCACCC CAGTGTCTGG AAAAAAATCT CTGGGCTTGG ACTGCTGCCA GGGAGGAGCT 1500  
 GCTGCAAGCC AGAGGGAGGA AAGGGGAGAA TACGAACAGC CTGGTGGTGT CGGTGTCTGG 1560  
 TGGGTAGAGT TAGTTCCTGT GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCGCT 1620  
 GGAATATATA TTCTACCTCC CTGAGGCTTT GATTTTGCAC TGAGCCAAAG GTCTAGCATT 1680  
 GTCAAGCTCC TAAAGGTTTC ATTTGGCCCC TCCTCAAAGA CTAAATGTCC CATGTGAAAG 1740  
 GGTCTCTTTG TCTGAGGCTT TGAGGAGATG TTTTCTCTCA CTTAGTTTC AAACCCAGT 1800  
 GAGTGTGTC ACTTCTGCTT CTTTAGGGAT GGCCTGTACA TCCACACCC CACCTCCCT 1860  
 TCCTCTCATA CCCCCTCTCA ACGTCTCTTT ACTTTTACT TTAATCACT GAGAGTTATC 1920  
 AGAGCTGGG TGTGGAATG ATCGATCATC TATAGCAAT AGGCTATGTT GAGTACGTAG 1980  
 GCTGTGGGA GATGAAGATG GTTTGGAGT GTAAACAAT GTCCCTCGCT GAGGCCAAG 2040  
 TTTCCATGTA AGCGGGATCC GTTTTGTGGA ATTGGTGTGA AGTCACITG ATTTCTTTAA 2100  
 AAAACATCTT TTCAATGAAA TGTGTTACCA TTTCATATCC ATTGAAGCG AAATCTGCAT 2160  
 AAGGAAGCCC ACTTTATCTA AATGATATTA GCCAGGATCC TTGGTGTCTT AGGAGAAACA 2220  
 GACCAAGCAA ACRAAGTGA AACCGAATGG ATTAACCTTT GCAAAACCAAG GGAGATTTCT 2280  
 TAGCAATGA GTCTAACAAA TATGACATCC GTCITTOCCA CTTTGTGTGA TGTATTATTC 2340  
 AGAATCTTGT GTGATTCAT TCAAGCAACA ACATGTTGTA TTTTGTGTG TTAAGAGTAC 2400  
 TTTTCTGAT TTTTGAATGT ATTTGTTTCA GGAAGAAGTC ATTTATGGA TTTTCTAAC 2460  
 CCGTGTAAAC TTTTCTAGAA TCCACCTCTT TGTGCCCTTA AGCATTACT TAACTGGTAG 2520  
 GGAACGCCAG AACTTTTAAAG TCCAGCTATT CATFAGATAG TAATTGAAGA TATGTATAAA 2580  
 TATTACAAAG AATAAAAATA TATTACTGTC TCCTTAGTAT GGTTTTCAGT GCAATTAAAC 2640  
 CGAGAGATGT CTGTGTTTTT TAAAAAGAA AGTATTTAAT AGGTTTCTGA CTTTGTGGA 2700  
 TCATTTGCA CATAGCTTTA TCACTTTTA AACATTAATA AACTGATTTT TTAAAG

- 60 **A2 Protein sequence:**  
 Gene name: endothelial differentiation, sphingolipid G-protein-coupled receptor, 1  
 Unigene number: Hs.154210  
 Probeset Accession #: M31210  
 Protein Accession #: AAA52336  
 Signal sequence: none found  
 Transmembrane domains: 50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301  
 Cellular Localization: plasma membrane

70  
 75  
 80

1 11 21 31 41 51  
 MGPTSVPLVK AERSSVSDYV NYDIIVRHYN YTGKLNISAD KEN8IKLTSV VFILIOCFII 60  
 LENIFVLLTI WKTKKFRHFM YFIGNLALS DLLAGVATTA NLLSGATTY KLTPAQWFLR 120  
 EGGMFVALGA SVFBLALAI ERYITMLRMK LHNGBNNFRL PLLISACWVI SLILGGLPIM 180  
 GWNICISALSS CSTVLPLVHK HYILFCITVF TLLLLSIVIL YCRISLVRT RSRRLTFRKN 240  
 ISKASRSSEN VALLKTVIIV LSVPLACWAP LFILLLLDVG CKVKTCDILF RAEYFLVLAV 300  
 LNSGTNPIIY TLINKEMRRA FIRIMSCKK PSKDSAGKFK RPIIAGMBFS RSKSDNSSHP 360  
 QKDEGDNPET IMSSGNVNS S

- 80 **A3 DNA SEQUENCE**  
 Gene name: G protein-coupled receptor 51  
 Unigene number: Hs.198612  
 Probeset Accession #: AA452928  
 Nucleic Acid Accession #: NM\_004624.1

Coding sequence:

1-2826 (underlined sequences correspond to start and stop codons)

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5 1 11 21 31 41 51
| | | | | |
ATGCGCTTCCC CGCGGAGGTC CGGGCAGCCA GGGCGGCGGC CGCGGCGGCC ACCGCGGCCC 60
GCGGCGCTGC TACTGCTACT GCTGCTGCCG CTGCTGCTGC CTCTGGCGCC CGGGGCTGG 120
GGCTGGCGGC GGGGCGCCCC CGGCGCGCCG CCCAGCAGCC CGCCGCTCTC CATCATGGGC 180
CTCATGCCGC TCACCAAGGA GGTGGCCAG GGCAGCATCG GCGCGGCTGT GCTCCCGGCC 240
GTGGAAGTGG CCATCGAGCA GATCGGCAAC GAGTCACTCC TCGCGCCCTA CTTCCTCGAC 300
CTCGGGCTCT ATGACACGGA GTGCGACAAAC GCAAAAGGCT TGAAGGCTT CTACGATGCA 360
ATAAAATACG GCGCGAAGCA CTTGATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC 420
ATCATGTCAG AGTCCCTCCA AGGCTGGAAT CTGGTGCAGC TTTCTTTTGC TGCAACCAAG 480
CCTGTTCTAG CGATAAGAA AAAATACCTT TATTCTTTTC GGACCGTCCC ATCAGACAAAT 540
GCGGTGAATC CAGCCATTCT GAAGTGTCTC AAGCACTACC AGTGGAGGCG CGTGGGACAG 600
CTGACGCAAG ACCTTTCAGAG GTTCTCTGAG GTGCGGATG ACCTGACTGG AGTTCTGTAT 660
GGCGAGGACA TTGAGATTTC AGACACOGAG AGCTTCTCCA ACGATCCCTG TACCAGTGTC 720
AAAAAGCTGA AGGGGAATGA TGTGCGGATC ATCCTTGGCC AGTTTGACCA GAATATGGCA 780
GCAAAAGTGT TCTGTTGTGC ATACGAGGAG AACATGTATG GTAGTAAATA TCAGTGATC 840
ATTCCGGGCT GGTACGAGCC TTCTTGTTGG GAGCAGGTGC ACACGGAAGC CAACTCATCC 900
CGCTGCTTCC GGAAGATCTT GCTTGTCTGC ATGGAGGGCT ACATTGGCGT GGATTTGGAG 960
CCCCTGAGCT CCAAGCCGAT CAGAACCATC TCAGGAAGA CTCCACAGCA GTATGAGAGA 1020
GAGTACAACA ACAAGCGGTC AGGCGTGGGG CCCAGCAAGT TCCACGGGTA CGCCTACGAT 1080
GGCATCTGGG TCATCGCCAA GACACTGTCG ABGGCCATGG AGACACTGCA TGCCAGCAGC 1140
CGGACCCAGC GGATCCAGGA CTTCACCTAC ACGGACCACA CGCTGGGCGG GATCATCTTC 1200
AATGCCATGA ACAGAGACAA CTTCCTGGGG GTCAAGGCTC AAGTTGTATT CCGGAATGGG 1260
GAGAGAATGG GAGACCATTA ATTACTCAA TTCAAGACA GCACGGAGGT GAAGGTGGGA 1320
GAGTACAACG CTGTGGCGGA CACACTGGAG ATCATCAATG ACACCATCAG GTTCCAAGGA 1380
TCCGAACCCG CAAAAGACAA GACCATCATC CTGGAGCAGC TGCGGAAGAT CTCCTACCT 1440
CTCTACAGCA TCTCTCTGCG CCTCACCATC CTCGGGATGA TCATGGCCAG TGCCTTTCTC 1500
TTCTTCAACA TCAGAAACCG GAATCAGAAAG CTCATAAAGA TGTGAGTCC ATACATGAAC 1560
AACCTTATCA TCCCTGGAGG GATGCTCTCC TATGCTTCCA TATTCTCTT TGGCCTGTAT 1620
GGATCCTTTG TCTCTGAAA GACCTTTGAA ACACCTTGCA CCGTCAGGAC CTGGATCTTC 1680
ACCGTGGGCT ACACGACGCG TTTTGGGGCC ATGTTTGCAA AGACCTGGAG AGTCCAGGCC 1740
ATCTTCAAAA ATGTGAAAAT GAAGAAGAAG ATCATCAAG ACCAGAAACT GCTTGTGATC 1800
GTGGGGGGCA TGCTGCTGAT CGACTGTGT ATCCTGATCT GCTGGCAGGC TGTGGACCCC 1860
CTGCGAAGGA CAGTGGAGAA GTACAGCATG GAGCGGAGCC CAGCAGGACG GGTATCTCC 1920
ATCGCGCTTC TCTGGAGCA CTGTGAGAAC ACCATATGA CCATCTGGCT TGGCATCGTC 1980
TATGCCATA AGGACTTCT CATGTTGTTC GATTGTTCT TAGCTTGGGA GACCCGCAAC 2040
GTGAGCATCC CGGACTCAA CGACAGCAAG TACATCGGGA TGAGTGTCTA CAACGTGGG 2100
ATCATGTGCA TCATCGGGGC CGCTGTCTCC TTCTGACCC GGGACAGGCC CAATGTGAG 2160
TTCTGATCG TGGCTCTGGT CATCATCTTC TGACGACCA TCACCTCTG CTTGGTATTC 2220
GTGCGAAGC TCATCACTCT GAGAACAAAC CCAGATGCG CAACGAGAA CAGGCGATTC 2280
CAGTCTACT AGAATCAGAA GAAGAAGAT TCTAAACGT CCACTCTGGT CACCAGTGT 2340
AATCAAGCCA GCACATCCG OCTGGAGGCG CTACAGTCAG AAAACCATCG CCTGCGAATG 2400
AAGATCACAG AGCTGGATTA AGACTTGGAA GAGGTCAACA TGCAGTGA GACACACCA 2460
GAAAAGACCA ACTGATTAAC ACAGAACCAC TACCAAGAGC TCAATGACAT OCTCAACCTG 2520
GGAACCTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATT TAAAAATCA CCTCGATCAA 2580
AATCCCTAGC TACCTGAGAA CACAACAGAG CCTCTCGAA CATGCAAGA TCCTATAGAA 2640
50 GATATAAACT CTCAGAAACA CATCCAGCGT CGGCTGTCCC TCCAGCTCCC CATCTCCAC 2700
CACGCTTACC TCCATCCAT CGGAGCGGTG GAGCCAGCT GTGTGAGCCC CTGCGTCAAG 2760
CCCAAGCGCA GCCCGGCCA CAGACATGTG CCACCTCTCT TCCAGTCTAT GGTCTCGGGC 2820
CTGATA

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55 **A4 Protein sequence:**  
 Gene name: G protein-coupled receptor 51  
 Unigene number: Hs.198612  
 Probeset Accession #: AA452928  
 Protein Accession #: NP\_005449.1  
 60 Signal sequence: 1-42  
 Pfam domains: 7tm 3 [481-754], ANF\_receptor [130-204]  
 Transmembrane domains: 22-44, 477-499, 517-539, 552-574, 595-617, 653-675, 692-713, 722-744  
 Cellular Localization: plasma membrane

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65 1 11 21 31 41 51
| | | | | |
MASPRRSQGP GRPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP FSSPPLSING 60
IMPLTKGVAK GSIGRGVLP VELAIEQIRN ESLLRPFYLD LRLYDTECDN AKGLKAFYDA 120
IKYGNHLMV FGGVCPGVTG IIAESLQGNV LVQLSFAATT FVLADKKKYP YFFRTVPSDN 180
AVNPAILLKL KRYQMKRVGT LTQDVQRFSZ VRNDLTGVLY GEDIEI SDTE SPENDPCTGV 240
KGLKENDVRI ILGQFDQDMA AKVFCAYEE NMYGSKYQNI IPGHYEPSSW EQVHTEANSS 300
RCLRNLLAA MEGYIGVDFE PLSSKQIKTI SGKT PQQYER EYNNKRSVG PSKFHGYAYD 360
GIWVIAKTLQ RAGTITLHSS RHQRIQDFNY TDHTLGRIL NAMNETNFPG VTGQVVRNG 420
ERMGTIKFTQ PQDSREVRVG EYNAVADTLE IINDTIRPQG SEPPDKITII LEQLRKISLP 480
LYSILSALTG LGMIMASAFI FFIKNRNQK LIKMSSPYMN NLIIILGMLS YASIFLGLD 540
GSPVSEKTFE TLTFTVTMIL TVGYTTAFGA MFAKTWRVHA LFKNVKMKKK IINDQKLVI 600
VGGMLLDLCL ILICWQAVDP LRRTVEKYSM EPPDAGRDIS JRPLLEHCEN TMHTIHLGIV 660
YAYKGLMLF GCFLANEVRN VSIPALNDSK YIGMSVYNVG IMCLIGAAVS FLTRDQPNVQ 720
PCIVLVLIIF CSTITLCLNF VPKLITLRTN PDAATQNRFF QFTQNKQKED SETSTSVTSV 780
NQASTSRLEG LQSENERLRM KITELDKDLE EVMQLQDTP EKTYYIKQNH YQELNDLNL 840
GNFTSTDDG KAILNHLDD NPQLQMDTTE PSRTCDPIE DINSFERIQR RLSLQLPILH 900
HAYLPSIGGV DASCVPSCVS PTASPRHRHV PPSFRVMVSG L

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A5 DNA SEQUENCE

Gene name:

ESTs

Unigene number:

Hs.293616

Probeset Accession #:

AW043782

Nucleic Acid Accession #:

none found

Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

10 1 11 21 31 41 51  
 AGCAACGACG CGGCGCAGCG GGAGCGGCGG CGCGGCCATG TGGCTGCTGG GGCGCTGTG 60  
 CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCG GGGAACTACT TCACCAATGA 120  
 GTGCACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCTTGGCA 180  
 GTGTGACGGG CTGCCTGACT GCCTCGACAA GAGTGATGAG AAGCAGTGCC CCAAGGCTAA 240  
 15 GTCGAAATGT GGCACCAACT TCCTCCCTCG TGCCAGCGGC ATCCATTGCA TCATTGGTGG 300  
 CTTCGCGTGC AATGGGTTTG AGGACTGTCT CAGTGGCAGC GATGAAGAGA ACTGCACAGC 360  
 AAACCCCTCG CTCTGTCTCA CGGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420  
 GAGCTTCATC TGCATGGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 AAGTTCTCAA GAACCCGCGA GTGGGCGAGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540  
 20 TTACCCGAGC ATCACTTATG CCATCATCTG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 CCTGCTGGCA CTGTCTTTCG ACCACGAGCG GAAGCGGAAC AACCTCTAGA CGCTGCCCGT 660  
 GCACCGGCTG CAGCAGCGCT TGTGCTGTCT CCGCTTGGTG GTCTTGGACC ACCCCACCA 720  
 CTGCAACGCT ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780  
 GAATGCGTCG GAAGTAGGCT CCCCACCTCT CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840  
 25 TGCGTGGTAT GACTTCTCTC CACCGCCTTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900  
 CGACCTGGCC CCTTACCGCT CCGGCTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGACGC 960  
 CAGCAGCGCT CTGAGCGTGG AAGACACCGG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020  
 GGGCACTGCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080  
 AGTTATTCCA AAGTCCATAT GSBTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140  
 30 TGCTCATGGG AAGCTCTTTA AGCACCCTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 AACTATCTCT GCATTCCTCT CCTCCGCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260  
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 CACCTCTCAT TTTCACTATA TTCTGTCTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380  
 35 AAATAGCGTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440  
 CGCTGGACCC AATTCCTCTC GCTGGGTAGT TACCTTATAG CATTGGGGGA TTTGGGTTAG 1500  
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 40 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTCTA AATAGGCAGG 1800  
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 TACACCTGCT CTGCTCTGAC AGCCACTTAC CTGGTTCTG GACTGTCACT CTCOCAGCTG 1920  
 ACCTGCGCTG AGCCAGAGAA TGAGGACCTA ACTTGAGTGG GCCCAAAGTC TGACCTGGCT 1980  
 GTATGTCCCT GTGGCCACCA CCGAGCCCTG CTGCTCATT CATGCAGCCT CAACACTGGC 2040  
 45 CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTTACCT GTGCATTGGG ACTTGAGGAC 2100  
 ACTGTTTTCT ATCAGAGTGT AGAGCCATGT TCAATACCTC CAGCAGGCTC TCCTGGCTCC 2160  
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 GGTGAGGTC AGGCTCTCTC CAACATCCCA GTAGTTCTCT CTCGAGACA CATGGGCAAG 2280  
 50 AGCAATTG AGTCAGAT TTTCCATTG GATCTATTTT AAATCTTTA GAAATGCATT 2340  
 TGAAACAGTG TGTGTGTTTT TTCCCTCTTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400  
 AGCTGTCTCT TTTTGTGTTT TTCTTTTAA ACAGGTCCAA GAAAGATGCA AAAGGAGATC 2460  
 ACACCCCTG CCGCTCTGAG CCGGTGATAA CAGTCACTC CAGACTAAC TGTGTGCCAG 2520  
 ACATTGTGTC ATGTGTGAC TTTGAGGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580  
 55 AAGAGGACTC CTCTCTCCT COGTGTATAG TCTCTATGTT TGTCAGTGT TTTCTTTTTT 2640  
 TTCTCTGTGT CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACGTT 2700  
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 AACCTGTTG ACCTTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAG TGGCATTGAG 2880  
 60 TGATCTGTCT CTGTAGACTT TCTTCTCTT TTTTAACCA ATCCAAAGGA TTTTACAGAA 2940  
 AAGCTAGCCA CTGTATTTT GTTTTGTTTA AAAAAAATAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAGAG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCCTT GAGTTATTTT 3060  
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 CATTTTCATCT CCGTGTAGTC AGAAGGGCTT TATTTCTCCC TTGATGGGG CCCCTTCTTC 3180  
 65 TTCTCTGTTG CTGTGAAGTT GTTTAGAGGA AAGAACTCTA ATTTAATTA ATTGCGAGT 3240  
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 AGATAAGGGA TGCTTACTAA TGCTTTTATA AAACARACAG GGACATTTT ATTATAGATT 3360  
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 70 TTTTAACTC ATTTCAACCA GGAAGCTTTT TTATACATTG CCTAATCTA CCGCAACCA 3540  
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 75 TTATCTTTC TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAAG GWMCTAMARM 3840  
 AAAAAAAGC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCCTTCGGG 3900  
 TGGGGGGGG GGGCCACAGT AGGTACGGCG ACCACGGGG CCAACAGGG ACCCCAGAG 3960  
 GAAACCTG GCAAGAAAAA GGTGCGAGA ATTCTCCACA CCAAAAAA ACBCGCGGG 4020  
 80 GGAACCGCA GAGTPTTGC TAAACCAAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080  
 GGACTCAACC AGGAGGACCC AAGGAACCC GATAGAGTAC G

A6 Protein sequence:

Gene name:

ESTs

Unigene number: Hs.293616  
 Probeset Accession #: AN043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLA domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

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10 1      11      21      31      41      51
    MLLLGPICLL LSSAAESQLL PGNFTNECN IPGNFMCBNG RCIPGAWQCD GLEDFCFDKSD 60
    EKECPKAKSK CGPTPPFCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
    KNGLCIDKSF ICDGQNNQD NSDESECESS QEPOSGQVVF TSENQVLYYP SITYALIGSS 180
15 VIFVLVVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VULDAPHRCN VTYNVNNGIQ 240
    YVASQAQNA SFVGSPPSYS EALLDQRFAP YDLPPPPYS DTESLNQADL PPYRSRSGSA 300
    NSASSQAASS LLSVEDTSES FGQFGPQEGT ABERDSEPSQ GTEEV
  
```

20 A7 DNA SEQUENCE  
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Nucleic Acid Accession #: NM\_002205  
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

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30 1      11      21      31      41      51
    ATGGGGAGCC GGAGCCAGCA GTCCCTCTTC CACGCCGTGC AGCTGCGCTG GGGCCCCGGG 60
    CGCCGACCCC CGCTSSSTGCC GCTGCTGTTG CTGCTSSSTG CCGCCGCCAC CAGGGTCGGG 120
    GGCITCAACT TAGACGGGGA GCGCCAGCA GTACTCTCGG GGGCCCCGGG CTCCTTCTTC 180
    GGATTCTCAG TGGAGTTTTA CCGCCCGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
    CCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGACGGGTG GTGCTGTCTA CCTCTGTCTT 300
35 TGGGGTGCCA GCCCCACACA GTGACCCCCC ATTGAATTTC ACAGCAAGG CTCCTCGCTC 360
    CTGGAATCCT CACTGTCCAG CTCAGAGGGA GAGGAGCGTG TGGAGTACAA GTCCITGACG 420
    TGGTTCGGGG CAACAGTTGG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCACCTGTAC 480
    AGCTGCGGCA CAGGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGTCT CCTCTCCACA 540
    GATAACTTCA CCGGAATTCG GAGTATGCA CCTGCGCGCT CAGATTTCAG CTGGGCGACA 600
    GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCGGAGTTCA CCAAGACTGG CCGTGTGGTT 660
    TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCGAGGACAG 720
    ATTGCAAGAT CTATTATCCC CGAGTACCTG ATCAACCTGG TTCAGGCGCA GCTGCAGACT 780
    CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 840
    TTCACTGGTG ATGACACAGA AGACTTTGTT GCTGTGTGTC CCAAGGGGAA CCTCACTTAC 900
45 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCGATCCC TCTACACTT CTCAGGGGAA 960
    CAGATGCGCT CTACTTTTGG CTATGCAATG GCGCCACAG AGCTCAATGG GAGCGGCTG 1020
    GATGACTTGC TGGTGGGGGC ACCCTGCTCT ATGGATCGGA CCCCTGACGG GGGGCTCTAG 1080
    GAGGTGGGCA GAGACTAGCT CTACCTGACG CACCCAGCGG GCATAGAGCC CAGGCCACCC 1140
    CTTACCTTCA CTGCCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTBAAC CCCCTTGGGG 1200
50 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCTTTTGG TGGGAGGACC 1260
    CAGCAGGGAG TAGGTGTTGT ATTCTCTGGG GGCOCAGGAG GGCTGGGCTC TAAGCCTTCC 1320
    CAGGTTCTGC AGCCCCCTGG GGCAGCCAGC CACACCCAGG ACTTCTTTGG CTCTGCCCTT 1380
    CGAGGAGGCC GAGACCTGGA TGCAATGGA TATCCTGATC TGATTGTGGG GTCCITTTGT 1440
    GTGACAAAGG CTGTGSTAT CAGGGGCGCG CCCATCGTGT CCGCTAGTGC CTCCCTCACC 1500
55 ATCTTCCCGG CCATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
    GCCTGCATCA ACCTTAGCTT CTGCTTCAAT GCITCTGAAA AACACGTTGC TGACTCCATT 1620
    GGTITTCAGT TGAACCTTCA GCTGGAGTGG CAGAAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
    CTGTTCCTGG CCTCCAGGCA GGCACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
    CGAGAGGATT CGAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCGAGACAAA 1800
60 CTCTGCGCGA TTCACATGCG TCTCAACTTC TCCTTGGACC CCGAGGCTCC AGTGGACAGC 1860
    CACGGCCTCA GGCAGGCCCT ACATTATCAG AGCAAGAGCC GATAGAGGA CAGGCTCAG 1920
    ATCTGCTGG ACTGTGAGA AGACAACATC TGTGTGCGTG ACCTGCAGCT GGAAGTGT 1980
    GGGGAGCAGA ACCATGTGTA CTTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCATGCC 2040
    CAGAATGTGG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCTCCAGAG 2100
65 GCTGAGTACT CAGGACTCGT CAGACACCCA GGAACCTTCT CCAGCCTGAG CTGTGACTAC 2160
    TTTGCCGTGA ACCAGAGCGG CTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGAGGA 2220
    GCCAGTCTGT GGGTGGCCTT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGRAAAC 2280
    ATCCAGTTTG ACTCCAGAT CCTCAGCAAG AATCTCAACA ACTGCAAG CGACGTGTT 2340
    TCCTTTGGGC TCTCGTGA GGCCTAGGCC CAGGTCACCC TGAACGTTGT CTCCAGCCT 2400
70 GAGGCACTGC TATTCCAGT AAGCGACTGG CATCCCGAG ACCAGCTTCA GAAGGAGGAG 2460
    GACCTGGGAC CTGCTGTCCA CCAATGCTAT GAGCTCATCA ACCAGGCCOC CAGCTCCATT 2520
    AGCCAGGGTG TGCTGGAAT CAGCTGTCCC CAGGCTCTGG AAGGTACAGA GCTCCTATAT 2580
    GTACAGCAGG TTAAGGACT CAACTGCACC ACCAATCACC CCATTAACCC AAAGGGCTG 2640
    GAGTTGGATC CCGAGGGTTC CTTGCACAC CAGCAAAAC GGGAGCTCC AAGCCGCGAG 2700
75 TCTGCTTCTT CCGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTTC CAGGCTGCGC 2760
    TGTGAGCTCG GGCCTCTGCA CCAACAAGAG AGCCAAAGTC TGCAGTTGCA TTTCCGAGTC 2820
    TGGCCCAAGA CTTCCTTGA GCGGAGCAC CAGCCATTTA GCTGCACTG TGAGGCTGTG 2880
    TACAAGCCC TGAAGATGCC CTACCGAATC CTGCTCGGCG AGCTGCCCA AAAAGAGCGT 2940
    CAGGTGGCCA CAGCTGTGCA ATGGAACCA GTCAGAGGCA GCTATGGCGT CCACTGTGG 3000
80 ATCATCATCC TAGCCATCCT GTTTGGCCTC CTGCTCTAG GTCTACTCAT CTACATCTC 3060
    TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CGGCATGGA AAAAGCTCAG 3120
    CTCAGCCCTC CAGCCACCTC TGATGCCCTGA
  
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**A8 Protein sequence:**

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)  
 Unigene number: Hs.149609  
 Probeset Accession #: X06256  
 Protein Accession #: NP\_002196  
 Signal sequence: 1-42  
 Transmembrane domains: 998-1020  
 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036  
 Cellular Localization: plasma membrane

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	GFSEVFYRPG	TDGVSVLVGA	PKANTSQPGV	LQGGAVYLCP	WGASPTQCTP	IEFDSKGSRL	120
20	LESSLSSEEG	KEPVEYKSLQ	WFGATVRAHG	SSILACAPLY	SWRTEKEPLS	DPVGTCTYLS	180
	DNFTRILEYA	PCRSDFSWAA	GGYCCGGFS	AEFTKTGRVV	LGGPGSYFWQ	GQILSATQEQ	240
	IAESYYPEYL	INLVQQQLQT	RQASTYVDS	YLGYSVAVGE	FSGDDTEDFV	AGVPEKMLTY	300
	GYVTILNGSD	IRSLYNFSGE	QMASYFGYAV	AATDVNGDGL	DDLVLGAPLL	MDRTPDGRPQ	360
	EVGRVYVYLG	HPAGIEPTFT	LTLTGEDEFG	RFGSSLTPLG	DLDDQGYNDV	AIGAPFGGET	420
25	QQGVVVFVPG	GGGLGSKFSS	QVLQPLWAAS	HTPDPFGSAL	RGGRLDNGG	YPLIVGSPG	480
	VDRVAVYRGR	PVVSASASLT	IFPAMFNPEE	RSCSLEGNPV	ACINLSPLCN	ASGHVADSI	540
	GFTVELQLDN	QKQKGVRRRA	LFLASRQATL	TQTLILQNGA	REDCREMKTY	LRNSESFRDK	600
	LSPIHIALNF	SLDPQAPVDS	HGLRPALHYQ	SKSRISDKAQ	ILLDCGEDNI	CVPDLQLEVF	660
	GEQNHVYLG	KNALNLTFFA	QNVGEGGAYE	AELRVTAPEE	AEYSGLVRHP	GNFSSLSQDY	720
30	FAVQSRLLLV	COLGNEMKAS	ASLWGLRFT	VPHLRDTKKT	IQDFDQILSK	NLNNSSQSDVV	780
	SFRLSVEAQA	QVTLNGVSKP	EAVLFPSVDW	HPRDQPKKEE	DLGPAVEHVY	ELINQGPSSI	840
	SQGVLELSCP	QKQKGVRRRA	VTRVTGLNCT	TNEPINTKGL	ELDPEGSLEH	QKREAPSRSS	900
	SASSGPQILK	CPEAKCFRLR	CELGLHQQE	SQSLQLHFRV	WAKTFLQREH	QPFSLQCEAV	960
35	YKALKMPYRI	LPRQLPQKER	QVATAVQNTK	AECSYGVPLW	IIILAILFGL	LLGLLIYIL	1020
	YKLGFFKRSI	PYGTAMEKAQ	EKPPATSDA				

**A9 DNA SEQUENCE**

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Nucleic Acid Accession #: NM\_002211.1  
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
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	CAAACGATG	AAAATAGATG	TTTAAAGCA	AATGCCAAT	CATGTGAGAG	ATGTATACAA	120
	GCAGGGCCAA	ATTGTGGGTG	GTGCACAAAT	TCAACATTTT	TACAGGAAGG	AATGCTTACT	180
50	TCCTGACGAT	GTGATGATTT	AGAAGCCTTA	AAAAAGAAGG	GTTCCTCTCC	AGATGACATA	240
	GAATATCCCA	GAGGCTCCAA	AGATATAAAG	AAAAATAAAA	ATGTAAACAA	CCGTAGCAAA	300
	GGACACGACG	AGAAAGCTCA	GCCAGAGGAT	ATTACTCAGA	TCCACCCACA	GCAGTTGGTT	360
	TTGCGATTAA	GATCAGGGGA	GCCACAGACA	TTTACATTAA	AATTCAGAG	AGCTGAAGAC	420
	TATCCCATTG	ACCTCTACTA	CCTTATGGAC	CTGTCTTACT	CAATGAAGA	CGATTGGAG	480
55	AATGTAAAAA	GTCTTGGAAC	AGATCTGATG	AATGAAATGA	GGAGGATTAC	TTCCGACTTC	540
	AGAAATGGAT	TTGCTCTACT	TGTGGAAAAG	ACTGTGATGC	CTTACATTAG	CACAACACCA	600
	GCTAAGCTCA	GGAACTCTTG	CACAAGTGAA	CAGAACTGCA	CCAGCCCTTT	TAGCTACAAA	660
	AATGTGCTCA	GTCTTACTAA	TAAAGGAGAA	GTATTTAATG	AACCTGTGAG	AAAACAGGCG	720
	ATATCTGGAA	ATTTGGATTC	TCCAGAGGTT	GGTTTCGATG	CCATCATGCA	AGTTGCAGTT	780
60	TGTGGATCAC	TGATTGGCTG	GAGGAATGTT	ACACGGCTGC	TGGTGTCTTC	CACAGATGCC	840
	GGGTTTCACI	TTGCTGGAGA	TGGGAACTTT	GGTGGCATTG	TTTTACCAAA	TGATGGACAA	900
	TGTCACCTGG	AAATAATAT	GTACACAATG	AGCCATTATT	ATGATTATCC	TTCTATTGCT	960
	CACCTTGTCC	AGAACTGAG	TGAAATAAT	ATTCAGACAA	TTTTTGCACT	TACTGAAGAA	1020
	TTTCAGCCTG	TTTACAAGGA	GCTGAATAAC	TTGATCCCTA	AGTCAGCAGT	AGGAACATTA	1080
65	TCCTGCAAT	CTAGCAATGT	AATTCAGTTG	ATCATTGATG	CATACAATTC	CCITTOCTCA	1140
	GAAGTCATTT	TGGAAAACGG	CAATTTGTCA	GAAGGAGTAA	CAATAAGETA	CRAATCTTAC	1200
	TGCAAGAACG	GGGTGAATGG	AACAGGGGAA	AATGGAAGAA	AATGTTCCAA	TATTTCCATT	1260
	GGAGATGAGG	TTCAATTTGA	AATTAGCATA	ACTTCAATA	AGTGTCCAAA	AAAGGATTCT	1320
	GACAGCTTTA	AAATTAGGCC	TCTGGGCTTT	ACGGAGGAAG	TAGAGGTTAT	TCTTCAGTAC	1380
70	ATCTGTGAT	GTGAATGCCA	AAGCGAAGGC	ATCCCTGAAA	GTCCCAAGTG	TCATGAAGGA	1440
	AATGGACAT	TTGAGTGTGG	CGCGTGCAGG	TGCAATGAAG	GGCGTGTGGG	TAGACATTGT	1500
	GAATGCAGCA	CAGATGAAGT	TACAGTGAA	GACATGGATG	CTTACTGCAG	GAAGAGAAAC	1560
	AGTTCAGAAA	TCTGCAGTAA	CAATGGAGAG	TGCGTCTGCG	GACAGTGTGT	TTGTAGGAAG	1620
	AGGATATAAT	CAATGAATAT	TTATTTCTGC	AAATTTCTCG	AGTGTGATAA	TTTCAACTGT	1680
75	GATAGATCCA	ATGGCTTAAT	TTGTGGAGGA	AATGGTGTIT	GCAAGTGTGG	TGTGTGTGAG	1740
	TGCAACCCCA	ACTACACTTG	CAGTGCATGT	GACTGTTCCT	TGGATACTAG	TACTTGTGAA	1800
	CCAGCAACG	GACAGACTTG	CAATGGCCGG	GGCATCTGCG	AGTGTGGTGT	CTGTAAAGTT	1860
	ACAGATCCGA	AGTTTCAAGG	GCAAACTGTG	GAGATGTGTC	AGACCTGCCT	TGGTGTCTGT	1920
	GCTGAGCATA	AGAAATGTGT	TCAGTGCAGA	GCCTTCAATA	AAGGAGAAAA	GAAAGACACA	1980
80	TGCACACAGG	AATGTTCTTA	TTTAAACATT	ACCAAGGTAG	AAAGTCCGGA	CAAAATACCC	2040
	CAGCCGTTCC	AACCTGATCC	TGTGTCCCAT	TGTAAAGAGA	AGGATGTTGA	CGACTGTGTG	2100
	TTCTATTATC	CGTATTTCAT	GAATGGGAAC	AACGAGGTCA	TGGTTCATGT	TGTGGAGAA	2160
	CCAGAGTGTC	CCACTGGTCC	AGACATCAT	CCAATTTGTAG	CTGGTGTGGT	TGCTGGAATT	2220

GTTCCTATTG GCCCTGCATT ACTGCTGATA TGGAAAGCTTT TAATGATAAT TCATGACAGA 2280  
 AGGGAGTTTG CTAATTTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAT 2340  
 CCTATTATTA AGAGTGCCTT AACAACTGTG GTCAATCCGA AGTATGAGGG AAAATGA

**A10 Protein sequence:**

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)  
 Unigene number: Hs.287797  
 Probeset Accession #: X07979  
 Protein Accession #: NP\_002202.1  
 Signal sequence: 1-21  
 Transmembrane domains: 732-754  
 INB domain: 34-464  
 PSI domain: 26-76  
 Cellular Localization: plasma membrane

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    LRLRSGEPQT FTLKFKRAED YPIDLYYIMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDP 180
    RIGFGSFVEK TUMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKGE VFNELVGRQR 240
    ISGNLDSPEG SHYDYPSIA CGSLIGWRNV TRLLVPSTDA GFHPAGDGKL GGIVLPNDGQ 300
    CHLENNMYTM SHYDYPSIA HLVQKLSENN IQTIFAVTEE PQPVYKELN LIPKSAVGTL 360
    SAMSSNVIQL IIDAYNSLES EVILENGKLS EGVTSYKSY CKNGVNGTGE NGRKCSNISI 420
    GDEVQPEISI TSNKCPKIDS DSFKIRPLGF TSEVEVILQY ICECECQSEB IPBSPKCHSG 480
    NGTFECGACR CNEGRVGRHC BCSTDEVNSE DMDAYCRKEN SBEICSNNGE CVCGQCVCRK 540
    RDNTHBYSG KFCBCDNFNC DRNGLICGG NGVCKCRVCE CNPNYTGSAK DCSLDTSCE 600
    ASNGQICNGR GICECGVCKC TDPKFGQJTC EMCQTCLGVC ASHKCVQCR AFNKGEKKOT 660
    CTQECSTFNI TKVESRDKLP QPVQDPVSH CKEDVDDCW FYFTYSVNGN NEVMVHVVEN 720
    PECFTGEDII PIVAGVVAGI VLIGLALLLI WKLLMIHDR RRFAXFEKEK MNAKWDTGEM 780
    PIYKSAVTTV VNEKYEGK
  
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**A11 DNA SEQUENCE**

Gene name: selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

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    CACCAAAAGT ACACACACCT GGTGCAATT CAAACAAAG AAGAGATTGA GTACCTAAAC 180
    TCCATATTGA GCTATTCAAC AAGTTATTAC TGGATTGGA AAGAGAAAGT CAACAATGTG 240
    TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAAGAG CCAGAAACTG GGCTCCAGGT 300
    GAACCCACAA ATAGGCAAAA AGATGAGGAC TGGGTGGAGA TCTACATCAA GAGAGAAAAA 360
    GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAGAAAGA AGCTTGCCCT ATGCTACACA 420
    GCTGCTGATG CCAATACATC CTGCACTGGC CACGCTGAAT GTGTAGAGAC CATCAATAAT 480
    TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAAGTGT 540
    ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGTTTGCA GTCAACCACT GGGAAACTTC 600
    AGCTACAAAT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAG CAGCATGGAG 660
    ACTATGCAAT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGGT 720
    GAGTGTGATG CTGTGACAAA TCCAGCCAAAT GGGTTCGTGG AATGTTTCCA AAACCCCTGGA 780
    AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGTA ACTAATGGGA 840
    GCCAGAGGCC TTCACTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
    GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
    CTTGCTGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTAGGGA AGGCTTCATG 1020
    TTGAGGGTGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAATCCCA 1080
    GTTTGTGAAG CTFTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
    CTTCCTAGTG CTCTGTCAG TTTCCTGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
    GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
    GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCC GAAGGGTTTG 1320
    GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCTCTTG TGCTTCAGC 1380
    TGTGAGGAGG GATTGGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
    TGACAGAGAG AGGTTCCTTC CTGCCAAGTG GTAAATATGT CAAGCCTGGC AGTTCCGGGA 1500
    AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTPGGCA CTGTGTGCAA GTTCGCTGT 1560
    CTTGAAGGAT GGAAGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGCACTGG 1620
    CTGCGCTGTC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
    CTTTCTGCTG CTGACTCTC CTCTCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
    TGCTTACGGA AAGCAAGAAA ATTGTGTCCT GCCAGCAGCT GCCAAGCCT TGAATCAGAC 1800
    GGAAGCTACC AAAGCCTTC TTACATCCTT TAA
  
```

**A12 Protein sequence:**

Gene name: Selectin E (endothelial adhesion molecule 1)  
 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Protein Accession #: NP\_000441  
 Signal sequence: 1-22  
 Transmembrane domains: 555-573  
 C-lectin domain: 23-139

Cellular Localization: plasma membrane

5 1 11 21 31 41 51  
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MYDEASAYC QQRVTHLVAI QNKKEIEYLN 60  
 SILSYSPSY WIGIRKVN NVVWVGITQKFL TEEAKNNAPG EPNNRQKDED CVBIYIKREK 120  
 DVGMNNDERC SKKLLALCYT AACTNTSCSG HGEVETINN YTCKCDPGFS GLKCEQIVNC 180  
 TALESPFHGS LVCSHPLGNF SYNSSCSISG DRGYLPSSME TMQCMSGGEW SAPLPACNVV 240  
 10 ECDVNTNPAN GFVECFQNGF SFFWNTTCTF DCEBGFELMG AQSLQCTSSG NWDNEKPTCK 300  
 AVTCRAVRQP QNGSVKCSHS PAGEFTFKSS CNPTCEBGFN LQSPAQVECT TQGGNTQQIP 360  
 VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEPSCBQ GFVLKGSKRL QCGPTGEWLN 420  
 EKPTCEAVRC DAVHQPQKGL VRCASPIGE FTYKSSCAPS CEEGFELYGS TQLECTSQGQ 480  
 WTSVPBQQV VKCSLAVPG KLNMCSEGP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540  
 15 SCLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLNLRK CLRKAKKFVP ASSCQSLESD 600  
 GSYQKPSYIL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Nucleic Acid Accession #: NM\_001508  
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51  
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCAATGATCA CAGTCATGTC 60  
 CCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCITA TTCTGGTGTA CCGTATCATC 120  
 TTGCTGATGG GCGTCTCTGG GAACAGCGCC ACCATTCGGG TCACCCAGGT GCTGCAGAA 180  
 30 AAAGGATACT TCCAGAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240  
 TTGGTATTCC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTTGACC 300  
 AGGTCCAGCT ACACCCCTGC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360  
 GCTACGCTGC TGCACGTGCT GACACTCAGC TTGAGCGCT ACATCCCAT CTGTACCCCC 420  
 TTCAAGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCCTATTGG CTTGCTCTGG 480  
 35 GTCACCTCCG CCTGTGTGTC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTCG 540  
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCCCT CCAGCACCCG CCACCCAGAG 600  
 CAGCCCGAGA CTTCCAAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660  
 CAGTCCAGCA TCTTCGGGCG CTTCGTGGTC TACCTGCTGG TCTGCTCTC CGTAGCCCTC 720  
 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAGAGCCAGA AGGGCTCGCT GGCCTGGGGC 780  
 40 ACGCGGCTC CCGACTGAG GAAGTCCBAG AGCGAAGAGA GCAGBACCGC CAGGAGGCAG 840  
 ACCATCATCT TCGTAGGCT GATTGTGTG ACATTGCGC TATGCTGGAT GCCCAACAG 900  
 APTCGGAGGA TCATGCTGCG GGCCAAACCC AAGCAGGACT GGACGAGGTC CTACTTCGG 960  
 GCGTACATGA TCTCTCTCC CTTCCTGGAG ACGTTTTTCT ACCTCAGCTC GGTATCAAC 1020  
 45 CCGCTCTCTG ACACGCTGTC CTGCGAGCAG TTTCGGCGGG TGTTCCTGCA GGTGCTGTGC 1080  
 TGCCGCTCTG CCGTGCAGCA CGCCAAACAC GAGAAGCGCC TCGCGTACA TGCCACTCC 1140  
 ACCACGACA GCGCCGCTT TGTGCGCGC CGTGTCTCT TCGCTTCCG GCGCCAGTCC 1200  
 TCTGCAAGGA GAAGTGAAG GATTTTCTTA AGCACTTTC AGAGCGAGGC CGAGCCCGAG 1260  
 TCTAAGTCCC AGTCAATGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCGGCC 1320  
 50 AATTCGTCTG CAGAGAATGG TTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Protein Accession #: NM\_001508, NP\_001409  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [72-172, 224-344]  
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
 60 Cellular Localization: plasma membrane

65 1 11 21 31 41 51  
 MASPSLPGSD CSQIIDHSHV PEFVATWIK ITLLVYLII FVMGLLGNSA TIRVTQVLQK 60  
 KGYLQKEVTD RMVSLACSDI LVFLIGMPME FYSIINMELT TSSYTLCKL HTLEFEACSY 120  
 ATLLHVLTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTETPL 180  
 VNVPSHRGLT CNRSSTRHEE QPETSNNMIC TNLSSRWTFV QSSIFGAPVV YLVVLLSVAF 240  
 70 MCKMMQVLM KSQKSLAGG TRPEQLKXSE SEESRTARRQ TIIFRLRLIV TLAVCWMPNQ 300  
 IRRIMAAAKP KHDWTRSYER AYMLLPFSE TFFYLSVVIN PLLYTVSSQQ FRRVFPQVLC 360  
 CRSLQAHNE EKRLVHAHS TTDSAPVQR PLLPASRRQS SARTEKIFL STPQSEAEPP 420  
 SKQSLSLES LEFNSGAKPA NSAAENGFOE HEV

A1 ProstateA15 DNA sequence

80 Gene name: CBGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Nucleic Acid Accession #: AJ400877  
 Coding sequence: 51-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	GGGGTCCGCG	CACACCTCCC	GGGCGCGCGG	CGGCCACCGC	CGGCACTCCG	CGGCTCTGCG	60
	CGGCAACCGC	TGAGCCATCC	ATGGGGGTGG	CGGGCCGCAA	CGGTCCTGGG	GGGCTCTGGG	120
5	CGGTGCTGCT	CTGCTGCTGG	CTGCTGCTGG	CACGTGCTGCT	GCTGGCGGGG	GCGTCTCCGC	180
	CGGGTCCGGG	CGGTGCCCGG	GGGCGCGCAG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCCGACGCC	CTGTGTCTGA	ACACACCCAC	CTCCTACCAAG	TGCTCCTGCA	300
	AGCCTGGCTA	CCAAGGGGAA	GGCAGGCGAG	GTGAGGACAT	CGATGAATGT	GGAATGAGC	360
	TCAATGGAGG	CTGTGTCCAT	GACTGTCTGA	ATATTCCAGG	CAATTATCGT	TGCACTTGT	420
10	TTGATGGCTT	CATGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGGAC	GAGTGCCTGG	480
	AGAACCAATG	CGGCTGCCAG	CATACCTGTG	TCAACGTCTA	GGGGAGCTAT	GAGTGTGCT	540
	GCAAGGAGGG	GTCTTTCCTG	AGTGACAATC	AGCACACCTG	CATTCAACGC	TCGGAAGAGG	600
	GCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCAAT	CTGCAAGGAG	GCCCAAGGG	660
	GCAGCGTGGC	CTGTGAGTGC	AGGCCCTGGT	TTGAGCTGGC	CAAGAACCAG	AGAGACTGCA	720
15	TCTTGACCTG	TAACCATGGG	AACGGTGGGT	GCCAGCACTC	CTGTGACGAT	ACAGCCGATG	780
	GCOCAGAGTG	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGCTGCCCTG	840
	ABCGAGAGGG	AGATGAGGAG	GAGGTGACAG	AGAGCAACAC	CACATCAGTG	GTGGATGGGG	900
	ATAAAGGGGT	GAAACGGCGG	CTGCTCATGG	AAACGTGTGC	TGTCAACAT	GGAGGCTGTG	960
	ACCGCACCTG	TAAGGATACT	TGAGCAGGTG	TCCACTGCAG	TTGTCTCTGT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGTAGAGCA	TGTAAAGATA	TTGATGAGTG	CCAGACCCGC	AATGGAGGTT	1080
	GTGATCATTT	CTGCAAAAC	ATCGTGGGCA	GTPTTGAAGT	CGGCTGCAGG	AAAGGATTTA	1140
	AATATTAAAC	AGATGAGGAG	TCTTGCCCAAG	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACACACG	CTGCATCAAC	CACCTTGCCA	CATTGTCTTG	TGCTTGCAAC	CGAGGATACA	1260
	CCCTGTATGG	CTTCACCCAC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
25	GTGACGAGTG	CTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGGCAC	CCTGGGTACA	1380
	AGCTCCACTG	GATTAAGAAA	GACTGTGTGG	AAGTGAAGGG	GCTCCTGCCC	ACAAGTGTGT	1440
	CACCCCGTGT	GTCCCTGCAC	TGCGTAAGA	GTGGTGGAGG	AGACGGGTGC	TTCTCTAGAT	1500
	GTCACTCTGG	CATTCACTTC	TCTTCAGATG	TCACCACCAT	CAGGACAGAT	GTAACCTTTA	1560
	AGCTAAATGA	AGGCAAGTGT	AGTTTGAAGA	ATGCTGAGCT	GTTCCTCCAG	GGTCTGCGAC	1620
30	CAGCACTACC	CAGGAAGCAC	AGCTCAGTAA	AAGAGAGCTT	CCGCTACGTA	AACCTTACAT	1680
	GCAGCTCTGG	CAGCAAGTTC	CCAGGAGGCC	CTGGCCGACC	AAGCACCCCT	AAGGAATGT	1740
	TTATCACTGT	TGAGTTTGAAG	CTTGAAACTA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGCGA	ACGAGAGAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
	AGGCCGTCCA	CAGGGAGCAG	TTTCACTTCC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
35	AAAAGCCTCC	CAGAACATCT	GAAOCCGAGG	CAGAGTCTCT	TGGAGTGGGC	CAGGTCATG	1980
	CAGAAAACCA	ATGTGTCACT	TGCGGGGCTG	GGACCTATTA	TGATGAGACA	CGAGAACGCT	2040
	GCAATTTATG	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAATTTCT	GGGGCCCTGA	AGACCCACGA	AGCTTGGAA	ATGTCGTGAAT	2160
	GTGGAGGTCT	GTGTCAACCT	GGTGAATATT	CTGCAGATGG	CTTTGCACTT	TGCCAGCTCT	2220
40	GTGCCCTGGG	CACGTTCCTAG	CCTGAAGCTG	GTGGAACCTC	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGCCAC	CAACATCTAG	GGAGCTACTT	CCCTTCAGGA	CTGTGAACCC	AGAGTTCAAT	2340
	GTTCACCTGT	ACATTTCTAC	AACACCAACA	CTCACCGATG	TATTCTGTGC	CCAGTGGGAA	2400
	CATACCGACC	TGAATTTGGA	AAAATAAATT	GTGTTTCTTG	CCAGGGAAT	ACTACGACTG	2460
	ACTTTGATGG	CTCCACAAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	2520
45	GAGATTTTCA	TGGGTACATT	GAAATCCCAA	ACTACCCAGG	CAATTACCCA	GCCAAACCCG	2580
	AGTGTACGTG	GACCATCAAC	CCACCCCCCA	AGGCGCGCAT	CTGTATCGTG	GTCCCTGAGA	2640
	TCTTCTGGCC	CATGAGGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
	CCAATTCGTG	GACACATAT	GAAACCTGCC	AGAACCTAGA	ACGCCCATC	GCCTTCACCT	2760
	CCAGGTCAAA	GAAGCTGTGG	ATTCACTTCA	AGTCCAAATG	AGGGAACGCG	GCTAGAGGGT	2820
50	TCCAGGTCCC	ATACGTTGAC	TATGATGAGG	ACTACCAAGA	ACTCATGAAA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAAC	ATCAGGAAT	ACTTAAGGAT	AAGAACTTA	2940
	TCAGGGCTCT	GTTTGTATGC	CTGGCCCATC	CCAGAACTA	TTTCAAGTAC	ACAGCCGAGG	3000
	AGTCCGAGAG	GATGTTTCCA	AGATGTTTCA	TCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
	TTTTGAGACC	TTACAAATGA	CTCAGCCAC	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	3120
55	GGTGTGGTGG	ACAGAGCTGT	CTTCTTCTG	CATGTACAGA	CAGTCCGGTA	TTGCTGCTCT	3180
	CCGTATCAGT	GACTCATATG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
	GAACCTGGTT	TTTCTTTCCC	AGCATCTGCG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
	CAGCTTCTCA	CTGCTGTGGG	CGGATGTCTT	GGATAGATCA	CGGGCTGGCT	GAGCTGGACT	3360
	TTGGTTCAGC	TAGGTGAGAC	TCACCTGTTC	TTCTGGGGTC	TTACTCTCTC	TCAAGGATTC	3420
60	TGTAGTGGAA	AGGAGGGCCAC	AGATAAGCT	GCTTATTCTG	AACTTTCAGC	TTCTCTAGC	3480
	CCGCCCCCTC	CTAAGGGAGC	CCCTGTCACT	CGTGTGACAG	CTCTGACCA	GACAAACAGG	3540
	CAAGAGGGGA	GGGAAGGAGA	CCCTGTCACT	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGTATC	CAGGAACCTG	3660
	AGTTCTAAGC	AGTGCTCGTG	AAAAAAGAAA	GCAGAAAGAA	TTAGAAATAA	ATAAAACTA	3720
65	AGCACTTCTG	GAGACAT					

**Al6 Protein sequence**

Gene name: CBGP1  
 Unigene number: Hs.222399  
 Probeset Accession #: AA256485  
 Protein Accession #: CAB92285  
 Signal sequence: 1-31  
 Transmembrane domains: none  
 PFAM domains: EGF-like domains [49-84,132-167,177-213,286-321,407-442]  
 CUB domain [809-918]  
 Cellular Localization: may be secreted

1	11	21	31	41	51	
MGVAGRNRP	AAWAVILL	LLPPLILL	AVFPGRGA	GFQEDVDE	QGLDDCHAD	60
LCQNTPTSY	CSCKGYG	GRQCEDID	GNELNGCV	DCLNTPGMY	CTCFDGFML	120
HDGHNCLDV	ECLENNGC	HTCVNVMG	ECCKEGFPL	SDNQHTCI	SEBGLSCMN	180
DEGCSHICKE	AFRGVAC	RGFELAKN	RDCILTCNH	NGGCQHS	TDGPECSC	240
POYKMHIDGR	SCLEREDTV	EVTESNTTS	VDGDKRVKR	LLMETCAV	GGCDRTCKD	300



STGVHCSCPV GFILQLDQKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK XGFKLLTDEK 360  
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLVGFTH CGDTNECSIN NGGCGQVCVN 420  
 TVGSEYECQH PGYKLNHNRK DCEVFKGLLP TSVSFVSLH CGKSGGDDGC FLRCHSGIHL 480  
 SSDVTTIRTS VTFKLMEGKC SLKNAELFPE GLRPALEPKH SSVKESFRYV NLTCSGKQV 540  
 PGAPGRPSTP KEMFITVBEF LETNQKEVTA SCDLSCIVKR TEKRLKKAIR TLRKAVHREQ 600  
 FHLQLSGMNL DVAKKPPRTS ERQASSCGVG OGHAEQCVR CRAGTYDGA RERCILCFNG 660  
 TFOQESQMT CEPCPRPQNS GALKTPAWN MSECGGLQCP GEYSADGFAP COLCALGTFO 720  
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSFGHPY NTHHRCIRC FVGTYQPEFG 780  
 KNNCVSCPGN TTIDFDGSTN ITQCKNRRCG GELGDFGTGY ESNYPGNYP ANTECTWTIN 840  
 PPPKRRILIV VPBIFLPIED DCGDYLVMRK TSSNSVTYI ETCQTYERPI APTSRSKLW 900  
 IQPKSNBQNS ARGFQVPYVT YDEDYQSLIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960  
 LAHPQNYFKY TAQESREMF RSFIRLLR8K VSRFLRPYK

**A17 DNA sequence**

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Nucleic Acid Accession #: none found  
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

1 11 21 31 41 51  
 | | | | |  
 CAAAAGAGAA TAGATAAAAT AAATGGAAAA TTAGAAGAGT CTCCTGATAA TGATGGTTTT 60  
 CTGAAGGCTC CCTGCAGAAAT GAAAGTTTCT ATTCCAACCTA AAGCCTTAGA ATTGATGGAC 120  
 ATGCAAACTT TCAAAAGCAGA GCTCCCGAG AAGCCATCTG CCTTCGAGCC TGCCATTGAA 180  
 ATGCAAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240  
 GATCAGATGT TCCTTCAGAA ATCAAAACAA AAGAAGSTTG AAGAAATTC TTGGGATTCT 300  
 GAGAGTCTCC GTGAGACTGT TTTACAGAA GATGTGTGTG TACCCAAAGC TACACATCAA 360  
 AAAGAATAG ATAAATAAAG TGGAAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420  
 GATACAGTTC ATTCTTGTGA AAGAACAAGG GAACCTCAA AAGACCCCTG TGACCCACGT 480  
 TCAGGAAAA

**A18 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.293102  
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272  
 Protein Accession #: none found  
 Signal sequence: none  
 Transmembrane domains: none  
 Cellular Localization: nuclear

1 11 21 31 41 51  
 | | | | |  
 QKEIDKINGK LESPNDNGF LKAPCRMVSV IPTKALELMD MQTFKAEPPE KPSAFEPAPB 60  
 MQKGVFNEAL ELKNEQTLRA DQMFPSSEKQ KKVEENSWDS ESLRETVSQK DVCVFKATHQ 120  
 KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDPDPR SGK

**Breast****A19 DNA SEQUENCE**

Gene name: TMFR593a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 ACCGGGCACC GGACGGCTCG GGTACTTTCT TTCTTAATTA GGTGATGCCC GTGTGAGCCA 60  
 GGAAAGGGCT GTGTTTATGS GAAGCCAGTA ACACGTGAGC CTACTATCTC TTCCGTGGTG 120  
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180  
 AGAGGTCTTG AATAGTTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240  
 TCATTCGGAT CGCTTTTGGG CCTTGATGAT TTGAAATATA GTCTGTGTGC ACCGATGCA 300  
 GATGCTGTTC CTGCACAGAT CCTGTCACTG CTGCCATGTA AGTTTFTTCC AATCAATGTC 360  
 ATTGGGATCA TTGCATGTAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420  
 TCAGGGAAGT ACAGATGTCT CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCCTGGAAGA CCATGTGCTC CGATGACTGC 600  
 AAGGTTCACT ACGCAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660  
 GATAACCTCA GAGTGAAGTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTG GCCACGTGGT TACCTTGCAG TGCCACAGCT GTGTCATAG AAGGGGCTAC 840  
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCTCAG 900  
 CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCCTCTGCA TCAGGCCCTT GTGGATCATC 960  
 ACTGCTGCAC ACTGTGTTTA TGACTGTGAC CTCCCAGAT CATGAGCCAT CCAAGTGGGT 1020  
 CTAGTTTCCC TGTGAGACAA TCAGGCCCA TCCCACCTGG TGGAGAGAT TGTCTACAC 1080  
 AGCAGATACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCAGGCTCA 1140  
 CTCACCTTCA ATCAAGATAT CCAGCCTGTG TGCCCTGCCA ACTCTGAGA GAACCTTCCC 1200  
 GATGGAAAG TGTGCTGGAC GTCCAGGATG GGGGCCACAG AGGATGAGAC AGGTGACGCC 1260  
 TCCCTGTCC TGAACACAGC GGCCGTCCCT TGATTTTCCA ACAAGATCTG CAACCCAGCC 1320  
 GACGTGTACG GTGGCATCAT CTCGCCCTCC ATGCTCTGCG GGGCTTACTT GACGGGTGCG 1380

5  
10  
15  
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GTGGACAGCT GCCAGGCGGA CAGCGGGGG CCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGACAA GCCTGGGGTG 1500
TACACCGGTG TCACCTCCCTT CCTGGAGTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTTG AGGTGATGAA GACAGCCCGA 1620
TCCTCCCGTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAACTTT 1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800
AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCC CCACCACACC CAACTAATTT 1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
CCTCAATGA TGTGCTGCTT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
ACGCTTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
AGGGCGGCGT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGTCTTGG AAAATTCCTG 2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAGCCACCC AACAGCCACT CAGAAAAGAC 2220
GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCAGAA 2280
CCAAACCCAC CTTTCTTACT TCRAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
ATGACTCGTT TAAGGCCTAT TTTCTGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
TTGTCTTGTG ATTCCAAATA ATATGTTTCC TTCCTCATA AAAAAAATA AAAAAAATA 2460
AAAAAATA

```

A20 Protein sequence:

25  
30

```

Gene name: TMPRSS3a
Unigene number: Es.298241
Probeset Accession #: AI538613
Protein Accession #: BAB20077
Signal sequence: none found
Transmembrane domains: 43-65, 239-261
Tryp_SPC domain: 216-444
Cellular Localization: not determined

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35  
40

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1 11 21 31 41 51
| | | | |
MGENDPPAVE APFSERSLFG LDDLKISPVA FDADAVAAQI LSLLEPLKFFP IIVIGIILI 60
LALAIGLGIH FDCSGKRYCR SSKKIELIA RCDGVSDCKD GEDEYRCVRV GGNNAVLOVF 120
TAASWKTMCSS DDWKGHYANV ACAGLGFPYS VSSDNLRVSS LEQQFREEFV SIDHLLPDDK 180
VTALHSHYV REGCASGEVV TLQCTACGER RGYSSRIVGG NMBLLSQWPW QASLQFQBYH 240
LOGGSHVTPV WITTAHCVY DLXLPKSWTI QVGLVSLDDN PAPSRLVEKI VYHSKYKPKR 300
LGNLIALMKL AGPLTFNEMI QPVCLPNSSE NFPGDKVCWT SGWGATEDGA GDASFVLNHA 360
AVPLISNKIC NHRDVYGGII SP6MLCAGYL TGGVDSQQGD SGGPLVCQER RLWLKVGATS 420
FGIGCAEWNK PGVYTRVTSF LDWIEHQMER DLKT

```

A21 DNA SEQUENCE

45  
50

```

Gene name: ESTs; opposite strand to TRPS1
Unigene number: none
Probeset Accession #: AA428090
Nucleic Acid Accession #: AA428090
Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

```

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
ATGAAGCCCA GTTTGAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAT AGACCAAGG 60
CAGTGTGTG GAGAAGAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAC 120
TTTTAGACA CAGATGATCT TATGTCATA GTGGAGGAAT CAGACAGCTG CTACAACTG 180
GATTCTGTG GGCCTCTCGG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240
GGAAAAACAA CTAACTCAG CCNTTTGCCC AATTTCCACC TTGCTAGTGA TCAGAGTTCA 300
CTATTGTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGGAAAT TATTCTGAGC 360
AAGTGTTTT TTCAGCTTGC AGTATTAATA CAAAAAATC ATTGCCCTCA GCTGCAAGC 420
AAGGGCATTS CCATTATGAA AGCCCTCAA AGACTCTCTG CTATTTTCAA AACATGGAAA 480
GAAAAAGGGA AAAAAAGAAA AAAAAATAA ATTAGAAGGA TTTGTTCTCT AATTTGGGCT 540
CCCAAAATG AGAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAACTCTC 600
CAAGCAATC TTCTGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTGTATT 660
TTTCTCTCT GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCCTTCTT ATCTGGATCT 720
GTTCTGCTC ATTTCTCTTT CAAAGTCATC TTTGAGGGA CTGCGCTGGA TTAATTGAT 780
TTTAAACCAA CAAATAAGAT ATTGATATA TTAATTAAAA CTTTGTGAGA TGATTGATTA 840
GGAATTGCAAT CATGTTTACA TGAGTATACC GAATTCAGG TTAACCTTCA TAAGCAGGAG 900
TTTTTACACA TGTATAACA ATCATTTACC AATACTGAC ACTCAATATT TGATACTCAA 960
CTGAATGTTT TTGAATAAAA CACATTTTFA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020
CTTTTATGAG AAAATATATC AGTGAGAGAG TGTGTGTTTA AGAAAAAAA TCAAGGCACA 1080
ACAGTTTGA AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTGTAGA ATGGTGATT 1140
GATTTCACA TTTTCAATCA GCAGAGCTG TATATATATA TATATATATA TATATATATA 1200
TATATATATA TATATATATA TATATTACAA TGATCTGTAT TTCCTATTGC TAGAAGGATG 1260
AAGTGAATC CATATAAACC ATACCAAGCC CGTTATGTGT AACTGTGTGT AAAACTTTAT 1320
TATTCAGTT TAGATGTAA AGACATCTTT GCTGCTGGA GATTGTTTGC ATAAGAATA 1380
CACCAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAACACAAA ATAAATATA 1440
ACGAAAAAT TFCATGTGTT GTAGAACAG AACTATTATA GCCAATCTC TAGTATTCAA 1500
ATCAGGACTA CAAATTGAAT TCTTTTCTT AGCAACATGA AATCATTTCA TATGAAGAC 1560
ATTTCTGCT GGTGAATATT GCTGTAAATT AATTTTACA TTGGCATTTT GAGATGTTCC 1620
CCCTCTATG CTCCCCAAA GTTTTCCATG TGGTTGTCAA ATAGTCCG

```

A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1  
 Unigene number: none  
 Probeset Accession #: AA428090  
 Protein Accession #: none found  
 Signal sequence: none found  
 Transmembrane domains: 113-129  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MKPSLKEHWAD IKMFSEIDQR QVVGEEIHLQ VVSVSYLVEN FSDTDDLMSI VEESDSCYNR 60  
 DSVGLPGRAG DRLPKTKPR GKTNNLSHLP NFHLASYQSS LLFKLQGSYY GNLLVEFELS 120  
 KCFVQLAVLK QKKHCLQLQS KGIAIMKAPQ RLSAIFKTKW EKGKKEKKII IRRITCSLIWA 180  
 PKNEK

#### A23 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Nucleic Acid Accession #: AL133619  
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGAGCGGTG CCGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCCGAC CCGGGGCTCT 60  
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG 120  
 CTCAGGCAGA GCGACCCGCA GAAACGGAA CTTGGACCTG AGAAAAGCCT GCAGTTCCTG 180  
 CAGCAGCAGC ACTCGGAGAT GCTGGCCCAAG CTCATGAGG AGATCGAGCA TCTGAAGGGG 240  
 GAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCCGGCC TGCTCCCA GGCACACTCA 300  
 ACACGTCCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CTTGGGCTCA 360  
 GGGGGAACAC AGGACGGGGA GCCCTTCCAG ACTGTCTTG CCCACCTGGC TGCACTGGCC 420  
 CCTGTATGCC AACCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480  
 AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCAGC TGCTGCTCTC GGGAAAGCCCA 540  
 GGGCCTGAGG TCATTGCAAG GCGCAGGTG GCCACAGGCT GCTCCCGAGA CCTCCCTCCT 600  
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CTTGGGCTGC TAGATCTTTG 660  
 CCTCAGATTG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720  
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780  
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTGTG TTCTTGGCCA CTGTGCCAAG 840  
 GCACCTCCCC ATCTGACAGC CGGCCCCAC CCAGCCAGG ATCTCTGGCT GTGGTCTCAA 900  
 GCTCACTCC CATATCTTT GGGCTGGGG CTGACATCAG GAGGACTCT GACTGGTGA 960  
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCTTA GGGCTCTGCC TTCCAGGGA 1020  
 GACATGGAGA AGGGGTGTA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCCAGTAG 1080  
 CTGTCTGGG CAAAGTCTGG CCAAGTCTGG CAGCCCGAGC CTTGCACTGC TGGGACGCT 1140  
 GACAGGACAC GGGAGAGGCG CATGCTTTCC CTGCGGACCT GCTGTTCAT GTGTCCCAAG 1200  
 CCTCTCTACT TTCCAGATGG CCGCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG 1260  
 GGGCTCTGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCC 1320  
 AGGCTGAGAG AGGGCTCTCT ACAGACACAC AGGCCAGGAG CGAAGCGTGG GCGTCTTGG 1380  
 GGGGTAGAG CCGGCGGGGC ACACCCCGCA ATGATCTGCG CCGTCTCCCT AAGCTTCCAG 1440  
 TCGTCAAGT CCACTCTTAA TTCAGCCAA TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500  
 TCCCTCAACA AGCAGATGAC AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560  
 CCGCTACTTC ACAACAGCAA CTTGGACAAA GTTCTGTGGG TACAAGGGCA GGCCGAAG 1620  
 GAGAAAGCAG AGGCTCTTAA TGCCAGAGCT GCGTGTATGG GGAACAGCCA GCACAGGGC 1680  
 AGGAGATGG GGGCGGGGCG ACACCCCGCA ATGATCTGCG CCGTCTCCCT AAGCTTCCAG 1740  
 ACCACACTTA GGCAGTGCBA AGTGTCTATC CGCAGCTGTG GGAATACCAA CCTCTGCGAG 1800  
 ACCCAAGGC TGCAGCAGCT CAGTCCCTC CTGGAAGGGA GGCAGAGGCT CAGGAGGCT 1860  
 CCGAGGGAAG CTAGCTTTCC CAGGACCAA GAAGCCAGC ATTTCCCAA GGTCTCCACC 1920  
 AAGAGCCTCT CCAAGAAATG CTTGAGCCCA CCGTGTGGCG AGCGTGCCAT CTTGCCCGCA 1980  
 CTGAGCAGA CCCGAAGAA CAACCTTTGCC GAGAGGCGA AGAGGCTGCA GGCAGTGCAG 2040  
 AAACGGCGCC TGCATCGCTC AGTGCCTTGA

#### A24 Protein sequence:

Gene name: ESTs  
 Unigene number: Hs.29383  
 Probeset Accession #: AW207206  
 Protein Accession #: T43457  
 Signal sequence: none found  
 Transmembrane domains: 303-322  
 Cellular Localization: not determined

1 11 21 31 41 51  
 MSGAGVAAGT RPPSSPTPGS RRRQRPSVG VQSLRFQSPQ LRQSDPQKRN LDLEKSLQFL 60  
 QQHSEFMLAK LHEEIEHLKR ENKGEPARGP RPAFPQAHG TLPLPQEBNT AINSSTRLQS 120  
 GGTODGEPLQ TVLRLAALA FVQPSGYRF WGTWDAATS SRGWTMLCSQ AQHVLSSGP 180  
 GPEVIAGRQV ATGCSFDLFP PSRAEMGRNP WDSPPCARSL PQIAAVARPR ISSFMALSPH 240  
 MLGAQGIWTH SIQSSLPAIN AATNGITKGS RVLFPCLSK ALPHPDGSPH PAQDPGLWSQ 300  
 AHFFLSLGLG LITSGGLTGG WSQPGNLAAG AVRRALPSQG DMEKGVGGP FPSRCGNSSS 360  
 LFWAKCGPSR QPQPCAGDA DRTEERAMLS LGTCCSMCEK PSCFFDGPFG NELSASAPL 420  
 GARWVCINOV WEPGGPSPA BLKEGSSRTH RFGGKRGLA GGSADTVRSP ADSLMSSSFQ 480  
 SVKSTISNSAN SQKARPQPG SFNRQDSKAD VSQKADLEE PLLANSKLDK VPGVQQAARK 540

EKAESNAGA ACMGNSQBQ RQMGAHAHP MILPLPLRKP TLLRQCEVLI RELWNTNLLQ 600  
 TQELRHLKSL LBSQRFPQA PEEASPPRDQ EATHFVKVST KSLSKKCLSP PVAERAILPA 660  
 LKQTFKNMFA ERQKRLQAMQ KRRLHRSVL

**A25 DNA SEQUENCE**

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Nucleic Acid Accession #: NM\_000949  
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 15 GAGGCTGAA ATCCCCAGAC GCGGTTTTC TGGCTGGGC TTCTGCTTA CTCACCTCTT 60  
 CTCCCTCTTT CTGGATTITA CCGACCGTTC GCGAACACAGC TTCCACACA ATGGAGCTTC 120  
 ATGTCTCTGT GCAGGAAGTA CTGATCGACT GATGTGGCAG ACTTGTCTCC CTGACAAAAC 180  
 TAAAGAACCT TCCTATTTCAT GAGGCGGAAC ACAGAGGATG CTTTCCACAT GAAACCTGAA 240  
 GTGAATCTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300  
 20 CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCTTCTG AATGGACAGT 360  
 TACCTCTCTG AAAACCTGAG ATCTTTAAAT GTGCTTCTCC CAATAAGGAA ACATTACACT 420  
 GCTGTGGGAG GCCTGGGACA GATGGAGGAC TTCTACCAA TTATTCAGT ACTTACCACA 480  
 GGGAGGAGAG GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC CCAACTCTCT 540  
 GGCACCTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600  
 25 CTAACAGAT GGGAGCAGT TTCTCGGATG AACTTTATGT GGAGGTGACT TACATAGTTC 660  
 AGCCAGACCC TCCTTTGAGG CTGGCTGTGG AAGTAAACAA GCCAGAAGAC AGAAAACCTT 720  
 ACTGTGGGAT TTAATGTGCT CCACCTACCC TGATTGACTT AAAAAGTGGT TGGTTCAAGC 780  
 TCCTGTATGA AATTCTGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGTCT 840  
 GGCAGCAAA CAGATTTTAA ATTCTCAGCC TACATCCAGG ACAGAAATAC CTGTGCCAGG 900  
 30 TTGCTGCAAA ACCAGACCAT GGATACTGGA GTGCTGGAG TCCAGCGACC TTCATTGAGA 960  
 TACCTAGTGA CTTCACCATG AATGATACAA CGGTGTGGAT CTCTGTGGCT GTCCCTTCTG 1020  
 CTGTCTCTGT TTGTATTAT GTCTGGGCAG TGGCTTGAAG GGGCTATAGC ATGGTGACCT 1080  
 GCATCTTCC GCCAGTTCTT GGGCCAAAAG TAAAGGATT TGATGCTCAT CTGTGGAGA 1140  
 35 AGGCAAGTC TGAGGAACCTA CTGAGTGCCT TGGGATGCCA AGACTTTCTT CCCACTCTG 1200  
 ACTATGAGGA CTGCTGTGTG GAGTATTAG AAGTAGATGA TAGTGGGAC CAGCATCTAA 1260  
 TGTCACTCCA TTCAAAGAA CACCCAGTTC AAGGTATGAA ACCACATAC CTGGATCCTG 1320  
 ACATGACTC AGGCCGGGG AGCTGTGACA GCGCTTCCCT TTGTCTGAA AAGTGTGAGG 1380  
 AACCCAGGC CAATCCCTCC ACATCTCATG ATCCTGAGGT CATTGAGAGG CCAGAGATC 1440  
 CTGAACAAC CACACCTGG GACCCCAAGT GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500  
 40 TTCTATCTGG TGATCCAAA TGTTCACAT GGCCTTACC ACAGCCAGC CAGCACACC 1560  
 CCAATCTCTC TTACCAAAAT ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG 1620  
 CACCGCCAC CTCTGTGTAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAACACATTA 1680  
 AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAGCTTC CATCTGAGA 1740  
 45 CTGACAGGA TACGCCCTGG CTGCTGCCCC AGGAGAAAC CCCCCTTGGC TCCGCTAAGC 1800  
 CCTTGGATTA TGTGGAGATT CACAAGTCA ACAAGATGG TGCATTATCA TTGCTACCAA 1860  
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGAC TCCTGAGAAC AATAAGGAGT 1920  
 ATGCCAAGGT GTCCGGGGTC ATGATAACA ACATCCTGGT GTTGGTGCCA GATCCACATG 1980  
 CTAATAACCT GGCCTGCTTT GAAGAATCAG CCAAGAGGC CCCACCATCA CTTGAACAGA 2040  
 50 ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100  
 TGGGTGGTTT GATATACCTG GATCCCGCAT GTTTTACACA CTCCCTTCC CAGTACCTTG 2160  
 ACTAATGGA TGAATTGTTA AAATGTGATT TTCTTCAGG TAACACTACA GAGTACGTGA 2220  
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAGCTC CCAGCTCCTT TCATGCTCCA 2280  
 TTTTAAACCA CTGGCTCTTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCTT 2340  
 55 AACTGTGATT FTKLSTLHPG CTTTGTCTG TTAGTTATAA AACTATGTT TCAATGAAAT 2400  
 AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAG 2460  
 GCCTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTG TCAAAATTGT TTACCATAGA 2520  
 AAGATGACAA AAGAAAATT TCCACATAGG AATAATGCTT GAAATTTGCT TTTGAAAAC 2580  
 AACTGCATAA CCTTTACACT CCGTCTCCAT TTTATTAGGA TTACCCAAAT ATAACCAATT 2640  
 60 AAAGAAAGAA TGCAATCCAG AACAAATTGT TTACATAAGT TCCEATACCT TACTGACACA 2700  
 TTGCTGATAT GCAAGTAAAG AAT

**A26 Protein sequence:**

Gene name: ESTs; prolactin receptor  
 Unigene number: Hs.25252  
 Probeset Accession #: AA057193  
 Protein Accession #: NP\_000940  
 Signal sequence: 1-23  
 Transmembrane domains: 237-253  
 70 FN3 domains: 28-112, 127-215  
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51  
 MKENVASATV FTLLLFNLTC LLNGQLPPGK FEIFKCRSPN KETFTCWWRP GTDGLPTNY 60  
 SLTYHREGET LMHECPDYIT GGNSCHFGK QYTSMWRTYI MMVATNQMG SSFSDLYVD 120  
 80 VTYIVQDPP LELAVSVKQP EDRKPYLWIK NSPFTLDLX TGNFTLLYEI RLKPEKAAEW 180  
 EIHVAGQQT EFKLSLHPG KYLVQVRCKP DHGYWSAWSP ATFQIPSDF TMDTIVWIS 240  
 VAVLSAVICL IIVWAVALKG YSMVTCIFPP VPGPKIKGFD AHLLKQKSE ELLSALGQD 300  
 FEPTSDYDEL LVEYLEWDDH EDQHLMSVHS KEHPSQMKP TYLDPTDQ9 RGSCDQPSLL 360  
 SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDPQCISME GKPIFYHAGG SKCSTWPLPQ 420

PSQENPRSSY HNTITDVCELA VGPAGAPATL LNEAGKDALX SSQTIKSREE GKATQQREVE 480  
 SFHSETDQDT PWLLPQEKTP PGSAPLDDYV EIEKVNKQGA LSLLPKQREN SGKPKKPGTP 540  
 ENNKEYAKVS GVMNNILVL VEDPEAKNVA CFESAKEAP PSLEQNQAEK ALANFTATSS 600  
 KRLQLGLD YLDPACFTHS FH

**A27 DNA SEQUENCE**

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)  
 Unigene number: Hs.169266  
 Probeset Accession #: L07615  
 Nucleic Acid Accession #: NM\_000909.1  
 Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CATCCACC CTTCTCTT TAATAAGCAG GAGCGAAAA GACAAATTC AAAGAGGATT 60  
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATT CAATATCGGG 120  
 AATAAGATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTATAA 180  
 ATATCTATA ACAACCAAA CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTGAAAAA 240  
 TCATTCAGTC CACTCTAAAT TCTCAGAGAA GAATGCCAG CTTCTGGCTT TTGAAATGA 300  
 TGATGTGTCAT CTGCCCTTGG CCATGATATT TACCTTAGCT CTTGCTTAGT GAGCTGTGAT 360  
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAAC AAAAGGAGAT 420  
 GAGAAATGTT ACCACATACC TGATGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480  
 CATGTGTCTC CCTTTTACAT TTGTCTACAC ACTTATGGAC CACTGGGTCT TTGGTGAGGC 540  
 GATGTGTGAG TTGAATCCCT TTGTGCAATG TGTTCATC ACTGTGTCCA TTTTCTCTCT 600  
 GGTTCTCATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660  
 TAATAGACAT GCTTATGTAG GTATTGCTGT GATTGGGTC CTGCTGTGAG CTTCTCTCTT 720  
 GCCTTTCTCG ATCTACCAAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTGTGATG 780  
 GTACAAAGAC AAATAGTGTG GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTTTA 840  
 TACCCTCTC CTCTTGTGTC TGCAATATTG TGGTCCACTT TGTTTTATAT TTATTGTCTA 900  
 CTTCAAGATA TATATACGCC TAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960  
 TAAGTACAGG TCCAGTGAAA CCAAAAGAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020  
 ATTTGCAATC TGCTGGCTCC CTCTTACCCT CTTTACACT GTGTTTGATT GGAATCATCA 1080  
 GATCATTTCT ACCTGCAACC ACAATCTGTT ATCTCTGCTC TGCCACTTCA CAGCAATGAT 1140  
 ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGTAAC AAAAATCTCC AGAGAGACTT 1200  
 GCAGTCTCTC TTCAACTTTT GTGATTTCCG GTCTCGGATG GATGATTATG AAACAATAGC 1260  
 CATGTCCACG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC 1320  
 ATTTAAAAAA ATCAACACAA ATGATGATAA TGAATAAATC TGAACACTAT TATAGCCCTAT 1380  
 GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACTGTC AACATACCTT GATTACCTGT 1440  
 TCTCCCAAGG AATAGGGGTTG AATCATTTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500  
 TACTGCTTTT TGTGTGATTT GTCTAATTA CATTGGAAC AAAAGGTGTG GGCCTTGGGG 1560  
 TCTTCTGAAA ATAGTTTGA CCAGACATCT TTGAAGTGTCT TTTTGTGAAT TTATGCATAT 1620  
 AATATAAGA CTTTATATCT GTACTTATG GAATGAAATT TCTTTAAGT ATTACGATGC 1680  
 GCTGACTTCA GAAGTACCTG CCATCCAAAT CGGTCAATAG ATTGGGTCAT CTTGATTAGA 1740  
 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCTTCA CTTTATGATA GGCATCATTT 1800  
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860  
 GAAGTCATTC AGAAGTGTG TTGAGTTTCT GTTTTGTGTT GGTTTTGTGTT TGTTTTGTGTT 1920  
 TTTTTCACG TTAAGGGAGG CTTTCATTTT CTCCGACTG ATTGTCACTT AAATCAAAAT 1980  
 TTAATAATGA ATAAAAAGAC ATACTTCTCA GCTGCAATA TTATGGAGAA TGGGGCACCC 2040  
 ACAGGAATGA AGAGAGAAAG CAGCTCCCCA ACTTCAAAAC CATTTTGGTA CCTGACAAAC 2100  
 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160  
 TATATTTATT TGAATGTATG GTCAAGAGAT TTCCATTTT TTTTACAGAC TGTTCAGGT 2220  
 TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTCAAT TTGTAGAAAC 2280  
 ACAAATATCG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAAC TTTCAATGTC 2340  
 CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAGG GAATATTCAC TTTACCTAGC 2400  
 AGGAAATAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAAT TGTATAAAT 2460  
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TTAATGAATA GTTGTGTCAT 2520  
 GTTAATGTGC CTAATTTTAT GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTGAGAG 2580  
 AAATATATTT TTAAGAACA AGACATACCT CAATGTATTA TACAGATAAA GTATTACATG 2640  
 TGTTTGATTT TAAAGGGCGG GACATTTTAT TAAATCAAT ATTTTGTGTT CTTTTCCTGA 2700  
 GGAGCTCTCT TCAGTTTCAT TTTTCTCAT CCCATGACTT CCTTCGATG GT

**A28 Protein sequence:**

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds  
 Unigene number: Hs.169266  
 Probeset Accession #: L07615  
 Protein Accession #: NP\_000900.1  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [57-91]  
 Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286, 300-322  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MNSTLFSQVE NRSVSNSEFE KNAQLLAFEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA 60  
 LIIILKQKE MRNVNIIIV NLFSDDLVA IMCLPFTFVY TIMDHWVGE AMCKLNPFVQ 120  
 CVSITVSIYS LVLLAVERBQ LIINPGRWRP NRRHAYVGLA VIWVLAVASS LPFLIYQVMT 180  
 DRPQMVTLID AYKDKYVCFD QPPSDSHRLS YTTLLVLQY FGPLCFIFIC YPKIYIRLKR 240  
 RNNMMDKMRD NKYRSSETER INTMLLSIVV AFAVCWLELT IFNTVFDWNH QIIATCQHNH 300  
 LFLLCBLTAM ISTCVNPIFY GFLNKNFQRD LQFFNFNCFD RSRDDVYETI AMSTMMDVVS 360

KTSLSQASPV AFKKINNDD NEKI

**A29 DNA SEQUENCE**

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM\_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCACACCG TGGTACGTC CGGACCCAAC GGGTCTGGG GGGCACCGGC CAAAGCCTCC 60
GGCTGCCCGG GCTGTGGGCG CAAGGCTTCG GACGGCCAG TCCCTTCGCC GCGGGCCGTG 120
GACGCCTGGC TCGTGCCTCT CTTCTTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC 180
TCGCTGGTCA TCTAGTCAT CTGCGGCCAC AAGCCGATGC GGACCTGAC CAACTTCTAC 240
ATGCCCAACC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGGCTCCC CTTCAAGGCC 300
CTGCTGTACC CCGTGCCTCG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT GGTCAACTAC 360
ATCCAGCAGG TCTCGGTGCA GGCACGTTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
TGGTACGTGA CCGTGTTCCT GTTGCGCGCC CTGCACCGCC GCACGCCCCG CCGGGCGCTG 480
GCTGTGAGCC TCAGCATCTG GGTAGGCTCT GCGCGGTGT CTGCGCGCGT GCTCGCCCTG 540
CACCGCTGTG CACCGCGGCG GCGCGCTTAC TGCACTGAGG CTTTCCCGAG CCGCGCCCTG 600
GAGCGCGCCT TCAGCATCTG CAACTTGTCT GCGCTGTACC TGTGCGCGCT GCTCGCCACC 660
TGCGCGCTGT ATCGGCTGCA GCTCGGCCAC CTGGCGCGCG TCGCGCTGCG CCGCGCGCCC 720
GCCGATAGCG CCGTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGCGCGCGT GCGGGCCAGG 780
GTCTCGCGCG TGGTGGCGCG CCGTGTCTCT CTCTTCGCGG CTTGCTGGGG CCGCATCTAC 840
CTCTTCTCTG TGCTGCAGGC GCTGGGCGCG GCGGCTCTCT GGCACCCACG CAGCTACCGC 900
GCCTAGCGCG TTAAGACCTG GGTCTACTGC ATGTCTCTCA GCAACTCGCG GCTGAACCCG 960
CTGCTCTACG CTTCTCTGGG CTGCACTTCC CGACAGGCGT TCGCGCGCGT CTGCGCTTGC 1020
GCGCGCGCGC GCGCGCGCGC CCGCGCGCGG CCGGACCCCT CCGACCCCGC AGCCCGACAC 1080
GCGGAGCTGC ACCGCTTGGG GTCCACCCCG GCGCGCGCGC GCGCGCGCGC GCTGAAGGAG 1140
AGTGGGCTGG CCGCGCGCGG GCTGTGCTTC CTGGGGGAGG ACAAGCGCCC TCTCTGA

```

**A30 Protein sequence**

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

Pfam domains: 7tm\_1 [59-323]

Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
METVATSGPN ASWGAPANAS GCPGCGANAS DGFVPSRAV DAWLVPLPFA ALMLLGLVGN 60
SLVIYVICRH KPMRTVTNFX IANLAATDVT FLCCVPTFTA LLYPLPGWVL GDFNCKFVNY 120
IQQVSVQATC ATITAMSVDR WYVTVEPLRA LHRRTPLRAL AVGLSIWVGS AAVSAFVLAL 180
HRLSPGFRAY CSEAPPSRAL ERAPALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
ADSLAQGVQL AERAGAVRAK VSRLLVAAVVL LFAACNGBIQ LFLVLQALGP AGSMHPRSYA 300
AYALKTNABC MYSYENALNP LLYAFLGSHF RQAFRRVPCP APRRRPRPRP PGPSPDPAAPH 360
AELHRLGSHP AFARAGKPGS SGLAARGLCV LGEDNAPL

```

**A31 DNA SEQUENCE**

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM\_014246

Nucleic Acid Accession #: NM\_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGCGCGCG CGCGCGCGCG CTGCTGCGCC GTGCTGCTGC TCCTGGCGCG CGCGCGCGCG 60
CTGCGCGCGA TGGGGCTGCG AGCGCGCGCG TGCGAGCGCG GCGTACCGCG CGGGACCGCG 120
GCCTTCGCCC TCGCGCGCGG CTGTACTTAC GCGGTGGGCG CCGCTTGACG GCGCGCGCGG 180
CGCGCGGAGC TGCTGGAGCT GGGCGCGGAT GCGCGGCTGG CAGGAAGTGG GCGCGTCTCG 240
GGCGCGGGCG GCGCGCTGCC GCTGCAAGTC CGCTTGGTGG CCGCGCACTG CCGGACCGCG 300
CTGAGCGCGC GCGTGCAGGC GCGCACGCGC CTTCGCGGCT GCGGAGCGCG TGCGCGGCTC 360
TGGGGAACCG GTGCGCGGCT CTGCGCGGCG CTCTGCTTCC CCGTCCCGCG CGGCTGCGCG 420
GCGCGCGAGC ATTGCGGCT CTGAGCTCGG ACCACTTAC CCGCGCTCGG CTGCGCGCGG 480
CGCGCGAGCG CCGCTGCTGC GCGCGTCCG CTCTGCTGCG GCGCGGCGCG CTGCGTCCCG 540
CTGCGCTGCG TGTGCGCGCT GCGCGCGCGG GCTGCGCGCG TCGCGGTGGG ACTGCGCGCT 600
GAGGCGCGCA CCGCGCGGAC GCGCTCGCGG TCGCATCCCG CATGCGCGCG CCGCGCGCGG 660
AACTGCGCGG AAGCGCGGCG GCGCGCGCGG CGACCGCGCG GCGCGCGCAC GAGCGCGAGA 720
GGGAGCGCTG AGTTTCCGAT GCCCAACTAC CAGGTGGCGT TGTITGAGAA CGAACCGCGG 780
GCGACCGCTA TCCTCCAGCT GCACGCGCAC TACACCATCG AGGGCGAGGA GGAGCGCGTG 840
AGCTATTACA TGGAGGGGCT GTTCGACGAG CGCTCCCGGG GCTACTTCCG AATCGACTCT 900
GCCACCGCGG CCGTGAGCAC GGCACGCTA CTGAGCGCGG AGACCAAGGA GAGCGCGCTC 960
CTCAGGGTGA AAGCGGTGGA CTACAGTACG CCGCGCGCTG CCGCGCACAC CTACATCACT 1020
GTCTTGGTCA AAGACACCAA CGACCAACAG CCGGTCTTCG AGCAGTCCGA GTACCGCGAG 1080
CGCGTGGCGG AGAACCTGGA GGTGGGCTAC GAGGTGCTGA CCATCGCGCG CAGCGACCGC 1140

```

843

	GGCGGCATCT	GGTGGCCACA	GACCAAGTTC	GGGCAGCCGG	CTGCGGTGDC	ATGCCCTAAG	6240
	GGATCCCGTTG	GAATGCGGT	CCGACACTGC	AGCGGGGAGA	AGGGCTGGCT	GCCCCAGAG	6300
	CTCTTTAACT	GTACCACCAT	CTCCTTCGTG	GACCTCAGGG	CCATGATGGA	GAAGCTGAGC	6360
5	CGCAATGAGA	CGCAGGTGGA	CGGCGCCAGG	GGCTCTGCAGC	TGGTGAGGGC	GCTGCGCAGT	6420
	GCTACACAGC	ACACGGGCAC	GCTCTTTGGC	AATGACGTGC	GCACCGCCTA	CCAGCTGCTG	6480
	GGCCACGTCC	TTCAGCAAGA	GAGCTGGCAG	CAGGGCTTCG	ACCTGGCAGC	CACGACAGAC	6540
	GGCGACTTTC	ACGAGGACGT	CATCCACTCG	GGCAGCGCCC	TCTTGGCCCC	AGCCACCAGG	6600
	GCGGCGTGGG	AGCAGATCCA	GCGGAGCGAG	GGCGGCAEGG	CACAGCTGCT	CCGGCGCTCT	6660
10	GAGGGCTACT	TCAGCAACGT	GGCAGCGAAC	GTGCGGCGGA	CGTACCTGCG	GCCCTTCGTC	6720
	ATCGTCAACG	CCACCATGAT	TCTTGTCTGC	GACATCTTTG	ACAAGTTCAA	CTTTACGGGA	6780
	GCCAGGGTCC	CGCGATTGGA	CACCATCCAT	GAAGAGTTCC	CCAGGGAGCT	GGAGTCTTCC	6840
	GTCTCCTTCC	CAGCGGACTT	CTTCAGACCA	CCTGAAGAAA	AAGAAGGCCG	CCTGCTGAGG	6900
	CCGGCTGGCC	GGAGGACAC	CCCGCAGACC	ACGCGGCCGG	GGCTTGCCAC	CGAGAGGGAG	6960
15	GCCCCGATCA	GCAGGCGGAG	GGGACACCTT	GATGACGCTG	GCCAGTTCGC	CGTCTCTCTG	7020
	GTCACTATT	ACGCGACCTT	GGGCGAGCTC	CTGCGCGAGC	GCTACGACCC	CGACCGTCCG	7080
	AGCCTCOGCT	TGCTCTCAGC	GGCCATCATT	AATACCCCGA	TGGTGAGCAC	CGTGGTGTAC	7140
	AGCGAGGGGG	TTCCGCTCCC	GAGACCCCTG	GAGAGGCCCG	TCTTGGTGGG	GTTCGCCCTG	7200
	CTGGAGGTGG	AGGAGCGAAC	CAGGCTCTTC	TGCGTGTCTT	GGAACCACTC	CCTGGCCGTT	7260
20	GGTGGGAGCG	GAGGGTGGTC	TGCCCGGGGC	TGCGAGCTCC	TGTCCAGGAA	CCGGACACAT	7320
	GTCCGCTGCC	CCACCATGAT	CACAGCCAGC	TTTGCGGTGC	TGATGATAT	CTCCAGGGGT	7380
	GAGAACGGGG	AGGTCTCTGC	TCTGAAGATT	GTCACTTATG	CCGCTGTGTC	CTTGTCACTG	7440
	GCAGCCCTGC	CTCGCTCTCC	CGTCTCTCTT	AGCTTGGTCC	GATGCTGCTG	CTCCAACCTG	7500
	CACAGCATTC	ACAAGCACTT	CCCGTGGCGG	CTCTTCTCTT	CTCAGCTGGT	GTTCGTGATT	7560
25	GGGATCAACC	AGACCGAAAA	CCCGTTTCTG	TGCACAGTGG	TTGCCATCTT	CCTCACTTAC	7620
	ATCTACATGA	GCACCTTTTC	CTGACCCCTC	GTGGAGAGCC	TGCATGTCTA	CCGATGCTG	7680
	ACCGAGGTGC	GCACATCGA	CACGGGGCCC	ATCGGGTCTT	ACTACGTCTG	GGGCTGGGGC	7740
	ATCCCGGGCC	TTGTTCACCG	ACTGGCGGTC	GGCTTGAGCC	CCAGGGCTTA	CGGGAATCCG	7800
	GACTTCTGCT	GGCTGTGCTT	TCAGACACCC	CTGATTGGA	GCTTTGCGGG	GCCCATCGGA	7860
30	GCTGTATATA	ATCTCAACAC	AGTCACCTTC	GTCTTATCTG	CAAAGGTTTC	CTGCCAAGA	7920
	AAGACCACTT	TCAGTGGGAA	AAAAGGGATC	GTCTCCCTGC	TGAGGACCCG	ATTCTCTCTG	7980
	CTGCTGTCTA	TCAGCGCCAC	CTGGCTGTCTG	GGGCTGTCTG	CTGTGAACCG	CGATGCACCTG	8040
	AGCTTTCACT	ACCTCTTTCG	CATCTTCAGC	GGCTTACAGG	GCCCTTCTGT	CCTCTCTTTC	8100
	CACCTGCTGC	TCACACAGGA	GGTCCGGGAG	CACTGAAGG	GGTGTCTCGG	CGGAGGGAAG	8160
35	CTGCACCTGG	AGGACTCCGC	CACCAACAGG	GGCACCCTGC	TGACGCGCTC	CCTCAACTGC	8220
	AACACCACTT	TCAGTGGGAG	GGCTGACATG	CTGGCGACAG	ACTTGGGGGA	GTCCACCGCC	8280
	TGGCTGGGCA	GCATCGTCAG	GGATGAAGGG	ATCCAGAAAG	TGGGCGTGTG	CTCTGGGCTG	8340
	GTGAGGGGCA	GCCACGGAGA	GCCAGACCGG	TCCCTCATGC	CCAGGAGCTG	CAAGGATCCG	8400
	CCTGGCCACG	ATTCGCACTC	AGATAGCGAG	CTGTCCCTGG	ATGAGCAGAG	CAGCTCTTAC	8460
40	GCTCTCTCAC	ACTGCTCAGA	CAGCGAGGAC	GATGGGGTGG	GAGCTGAGGA	AAAATGGGAC	8520
	CGGGCCAGGG	GCGCCGTCCA	CAGCACCCCC	AAAGGGGAGG	CTGTGGCCAA	CCACGTTCCG	8580
	GCCGCTGTGC	CCGACCCAGG	CCTGGCTGAG	AGTGACAGTG	AGGACCCCGG	CGGCAAGCCC	8640
	CGCCTGAAGG	TGGAGAGCAA	GGTCAAGCTG	GAGCTGCACC	GCGAGGAGCA	GGGCAATCAC	8700
	CGTGGAGAGT	AGCCCCCGGA	CCAGGAGAGC	GGGGCGCCAG	CCAGGCTTGC	TAGCAGCCAG	8760
45	CCCCAGAGGC	AGAGGGAAGG	CATCTTGAAA	AATAAGTCA	CCTACCCCGC	GGCGCTGAGC	8820
	CTGACGGAGC	AGACGCTGAA	GGGCGGGCTC	CGGGAGAGAG	TGGCGGACTG	TGAGCAGAGC	8880
	CCCACATCTT	CGGCGACGTC	TTCTCTGGGC	TCTGGCGGCC	CCGACTGGGC	CATCAGAGTC	8940
	AAGAGCCCTG	GGAGGGGAGC	GGGGCGTGAC	CACCTCAAGC	GGGTGGCCCT	GAATGTGCGC	9000
	ACTGGGAGCG	CCCAGGCCGA	TGGCTCCBAC	TCTGAGAAAC	CGTGAGGCAA	GCCCCTCACC	9060
50	CCACACAGGC	TGCGGCATCA	CCCTCAGACC	TTGGAGCCCA	AGGGGGCACT	GCCCTTGAGG	9120
	TGGAGTGGGC	CCAGAGTGTG	GGGTCTCCCA	TGGTGGCAGC	CCCGGACTG	ATCATCCAGA	9180
	CACAAAGGTC	TTGGTTCTCC	CAGGAGCTCA	GGGCCCTGCA	GACCTGGTGA	CAAAGTCCAA	9240
	AGGCCACAGG	CGTGGGAGAG	GGTGGGAGCA	CTGGGCCAGC	ACCGCTGAGT	CCTAAGACTG	9300
	CAGTCAAAAG	CAGAACTGAG	AGGGGACCCC	AGACTGGGCG	CAGAGGCTGG	CCAGAGTTCA	9360
55	GGAAAGCCGG	GCACAGACCA	AGAACCGCGG	TCCAGCCCGG	CCCAAGCGGG	CATCTCATGG	9420
	CAGTGGCGAC	CCGTGGCTGG	CAGCCCGGGC	AGTCTTTTGC	AAAGGCAACC	CTTGTCTTAA	9480
	AATCACTTCG	CTATGTGGGA	AAGGTGGAGA	TACTTTTATA	TATTTGTATG	GAAGTCTGAG	9540
	GAGGTGCAAC	CTGTATATAT	ATGTGATTCG	TGCTGACTTT	GTATCCCGGA	GAGATCCATG	9600
	CAATGATCTC	TGCTGTCTCT	CTCTGTCAAG	ATTGCACAGT	TGTACTTGAA	TCTGGCATGT	9660
60	GTTGACGAAA	CTGGTGCCCC	AGCAGATCAA	AGGTGGGAAA	TAGCTCAGCA	GTGGGGCTAA	9720
	AACCAAGCGG	CTAGAAAGCC	TACAGCTGCC	TGCGGCCAGG	AAGTGAGGAT	GGTGTGGGCC	9780
	CTCCCGCGCG	GCCCCCTGGG	TCCCCAGTGT	TGCTGTGTG	TGCGTTTGTG	CTCTGCTGCC	9840
	ATCTGCCCCG	GCTGTGTGAA	TTCAAGACAG	GGCAGTGCA	CACCTAGGCG	GTGTGAGGAG	9900
	CCCTGCTGAG	GTCACTGTGG	GGCACGGTTG	CCACACGGCT	GTCAATTTTC	ACCTGGTCAT	9960
65	CTGTGACCA	CCACCCCTTC	CCCTCACCGC	CTCCAGGTG	GCCCCGGAGC	TGCAGGTGGG	10020
	GATGGCTTTG	TCTTTTGTCT	CTGCTCCCGG	TGGGACCTGG	GACCTTAAAG	CGTTGCAGGT	10080
	TCTGTATTGG	GACAGAGGTG	TGGGGCTTTC	CAGGCGGTTA	CATACCTCCT	GCCATTTCTC	10140
	TAACTCTCTG	AGACTGCGAG	GATCTCCAGG	CAGGGTCTTC	CCCTCTGGAG	TCTGACCAAT	10200
	TACTTCAATT	TGCTTCAAAT	GGCCAAATGT	GACAGGGGAC	AAAGCCACAG	CCACACTCTT	10260
70	CAAGGTTAC	CAAACTGTTT	TTGGAATTC	ACACCAAGGT	CGGGCCCACT	GCAGGCACTT	10320
	GGCAGAGGCT	GGCCCGAGGG	GCTGTGGAAC	GGGTCCCGGA	ACTGTGAGAC	ATGTTTGATT	10380
	TTAGCGTTTC	CTTTGTTCCT	CAAACTCAGT	GCCCCAATAA	GTGATCAGCA	CAGCTGCTTC	10440
	CAAAATAGAG	AAACCATGAA	AATCAAGTAA	AATGCAAGAA	AATGCAAGAA	TGTCCACACT	10500
	GTTTTAAACT	TGACCCGTAT	GAATAATGTA	GCATGTTAG	CAGATGCCCTA	TGGGAGAGGA	10560
75	AAAGCGTATC	TGAAAATGGT	CCAGGACAGG	AGGATGAAAT	GAGATCCAGG	AGTCTCACCA	10620
	CCTGAATGAA	TTATACATGT	GCCTTACCAG	GTGAGTGGTC	TTTCGAAGAT	AAAAAACTCT	10680
	AGTCCCTTTA	AACGTTTGCC	CCTGGCGTTT	CCTAAGTACG	AAAAGGTTTT	TAGTCTCTCG	10740
	AACAGTCTCC	TTTCAATGAT	TTAACAGGAT	TCTGCCCTCT	GAGGTGTAAAT	TTTTTTGTTC	10800
	TATTTTCTTC	CAGGTACTCC	ACAGCCCAACA	TACAGAGGTG	TAAATTTTAA	TTTGATCAGA	10860
80	ACTGTACCA	AAAAACAAT	GTCAATTTTA	TTGAGATGGG	AAAAATGTAA	ACCTAATTTT	10920
	ATTACTTAAG	ACTTTATGGG	AGAGATTAGA	CAGTGGAGGT	TTTTAACAGA	AGTGTATTTT	10980
	ATTATGTTTC	AAAAACACTG	AATTACAAAT	GAGAAGATGC	TACAATAAAT	TAAATTTTTT	11040
	GAATTTGTAC	TCTGCGGTGG	CTGGTCTTTC	TCCACAAACA	CCCCCGCCCC	TOCCCATGCC	11100
	CAGGGTGGCC	GTGGAGAGGA	CGGTTTACGG	ACGTGCAGCT	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGAACGCT	GCCGGAACCT	TTTGTCCATT	CCCTAGTAGG	CCTGCCACAG	11220



CCTAGATGGG CAGTTTTTGT CTTTCACCAA ATTGAGGAC TTTTTTTTTT TGCCATTATT 11280  
 TCTTCAGTTT TCTTTCTCTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340  
 AGACGTTAGA CTTCTGTATG TTTTCCCACT GGTCCCTGAG GCTCTGTTT

### A32 Protein Sequence

Gene name: CH22\_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo  
 (Drosophila) homolog (CELSR1),  
 Hs.252387  
 Unigene number:  
 Protein Accession #: NP\_055061  
 Signal sequence: 1-20  
 Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092,  
 1110-1199  
 Pfam domains: Laminin\_EGF [2003-2048], 7tm\_2 [2465-2708]  
 Latrophilin/GPS domains: 2407-2460  
 Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MAPPPPPVLP VLLLLAAAA LPAMGLRAAA WEPRVPGGTR AFALRPGCTY AVGAACFPRA 60  
 PRELLDVGRD GRLAGRRRVG GAGREPLPQV RLVARSAFTA LSRRRLKARTH LPGCGARARL 120  
 CGTGARLCSA LCFPPVGGCA AAQHSALAAP TTLPACRCPP RPRPRCPGRP ICLPPGGSVR 180  
 LRLCALRAA AGAVRVGLAL EAATAGTSPA SPSPSPPLPP NLPEARAGPA RRARRGTSGR 240  
 GSLKFPMPNY QVALFENFPA GTLLQLLHAM YTIEGEEKV SYVMEGLFDE RSRGYFRIDS 300  
 ATGAVSTDSV LDRETKETHV LRKAVDYST PERSATTYIT VLKEDTNDHS PVFEQSEYRE 360  
 RVRENLEVGX EVLTTRASDR DSPINANLRY KVLGGANDVP QLNSSSGVVS TRAVLDREBA 420  
 ASYQLLVEM DGQRNEGELS ATATVYIEVE DEMONYPOFS EQNYVVQVPE DVGLMTAVLR 480  
 VQATDRDQGG NAAHYSLIS GNVAGQFYIH SLSGILDVIN PLDFEDVQKY SLSTKAQDGG 540  
 RPPLINSSGV VSVQVLVDVD NEPIFVSSPF QATVLENVPL GYPVVEIQAV DADSGENARL 600  
 HYRLVDTAET FLGGGSAGPK NEAPTDFDFF QIENSSGWIT VCABLEREEV RHYSFGVEAV 660  
 DHGSPMSSS TSVSITVLGV MNDPVPFTQP TYELRLNEDA AVGSSVLTQ ARDRDANSVI 720  
 TYQLTGGRN NRFALESORG GGLITLALFL DYKQEQYVVL AVTASDSTRS RTARVLIINV 780  
 DANTRFPVPG SSHYIVSVBE DRPVGTSLAT LSANDRTGE NARITYVIQD PVPQFRIDPD 840  
 SGTMYTMML DYENQVATIL TIMAQDNGIP QKSDTTILBI LILDANDNAP QFLWDFYQGS 900  
 IFEDAPPSTS ILQVATDRD SQPNRGLLYT FQGGDGDGDG FYIEPTSGVI RTQRRLDREN 960  
 VAVYNLMALA VDRGSPFPLS ASVEIQVTL DINDNAPMFE KDELELFVEE NNPVGSVVAK 1020  
 IRANDEDEGE NAQIMYQIVE GDMRBEFQID LLNGDLRAMV ELDFEVRREY VLVVQATSAP 1080  
 LVSRATVHIL LVDQDNPPV LPDFQILFNN YVTNKNSFP TGVIQCIAPH DEDVSDSLNY 1140  
 TFVQGNELRL LLLDPATGEL QLSRDLNNR PLBALMEVSV EDGIHSVTAI CTLRVTTITD 1200  
 IMLTNSITVR LBNMFSQKFL SPFLALFVEG VAAVLSTTKD DVFPVNVQND TDVSSNINLV 1260  
 TFALALEGVV RQGFSTPLS QEQIYLNRTL LTTISTQRLV PFDDNICLRE PCENYMECVS 1320  
 VLFDFBSAPF LSTTVLFRP IHPINGLRCA CPFGTGDVYC ETEIDLCYSO PCJANGRCRS 1380  
 REGGYTCECF EDFTGEHCEV DARSGRGANG VCKNGGTCVN LLIGGFHCVC PPGSEYRPHYC 1440  
 EVTRSEPPQ SVFTFRGLRQ RFHFTISLTP ATQERNGLLL YNGRFNEKED FIALEIVDEQ 1500  
 VQLTFBAGET TTTVAPKVPK GVSIDGRHWS QVQYINKPNI GHLGLFEGPS GEKMAVTVVD 1560  
 DCOTMAVRF KQDIGNYSCA AQGTQTGSKK SLDLTLGLLL GGVPNLPEDF FVBNKQFVGC 1620  
 MRNLSDGKN VDMAGFIANN GTREGCAZER NFCDGRRCQN GGTCVVRNMM YLCBCLPFRG 1680  
 GKNCQAMPH PQLFSGESVV SWSDLNIIIS VPWYLGMPF TRKEDSVLME ATSGGPTSF 1740  
 LQILNNYLPQ EVSHGSPDVE SVMLSGLRVT DGBWHLLIE LKNVKEDSEM XHLVTMTLDY 1800  
 GMDQNKADIG GMLPGLTVRS VVVGASSEDK VSVRRGRFC MQGVRMGGTP TNVATLMMNN 1860  
 ALKRVKQDC DVDDPCTSSP CPFNRSCHDA WEDYSCVCDK GYLGINCVDA CELNFCENMG 1920  
 ACVRSPGSPQ GIVCEGSPSH YGFCENKLD LDCPRWMMGN FVCGSPCEAV SKGDFDPCNK 1980  
 TNGCQCKEN YKLLAQDTL LDCDPPHGS HSRTCDMATG QCACKPGVIG RQCNRCNPF 2040  
 AEVTLGCEV IYNGCPKAF AGIHWPTKP GPAAVECPK GSVGNVREH SGEKWLFP 2100  
 LYNCTTISFV DLRAMNEKLS RNETQVDGAR ALQVRLARS ATQSTGTLEF NDVRYATYQLL 2160  
 GVLQHSBEG IQKLGVSSGL ADPHEDVLHS GSALLAPATR AAWEQIQRSE GDTQQLLELL 2220  
 EGYFSNVARN VRTYLRPFV IVTANMILAV DIFDKPFTG ARVPRDTTH HEPFRELESS 2280  
 VSPADFPFP PREEKGFLLR PAGRRTTPTQ TRPQPGTERE APISRRRRHF DDAGQFAVAL 2340  
 VIYRTLQQL LPRYDFDRR SLRLPHRP11 NTPMVSTLVY SEGAPLPRPL RRFVLVEFAL 2400  
 LEVEERTKPV CVFWNHSALV GGTGWSARG CELLSNRNTE VACQCSHTAS FAVLMDISRR 2460  
 ENGEVLPLKI VTYAANVSL AALLVAFVLL SLVRMLRSNL HSLHKLAVA LFLSQLVFI 2520  
 GINQNTENFL CTVAALLHY IYMTFAWTL VESLHVYRML TEVRNIDTGP MRFYVVGVG 2580  
 IPAIVTGLAV GLDPQGYGNT DFCNLSLQDT LIWSFAGPIG AVIINTVTS VLSAKVSCDR 2640  
 KHYYGKGI VSLRTAFLL LLLISATWLL GLLAVNRDAL SFHYLFAIPS GLQGFVLLF 2700  
 HCVLNQVRK HLKGLVGGK LHLKDSATTR ATLLTRSLNC NTTFDGDGDM LRIDLGESTA 2760  
 SLDSIVRDEG IQKLGVSSGL VRGSGEPDA SLMPRSCKDP PGHDSDSSE LSLDQSSSY 2820  
 ASSHSSDSO DGVGAEKWD PARGAVHSTP KGDVAVNHVP AGWFDQSLAE SDSDFPGKP 2880  
 RLKVTKLSV ELHREBQSGH RGEYFDQES GGAARLASSQ PPEQRKGILK NKVTYPPPLT 2940  
 LTEQTLKRL REKLADCEQS PTSSRTSSLG SGGEDCAITV KSPGRPGRD HINGVAMVR 3000  
 TBSAQADGSD SEKP

### A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3  
 Unigene number: Hs.198252  
 Probeset Accession #: X95876  
 Nucleic Acid Accession #: X95876  
 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CCAACCAAA GCACCAAGC AGAGGGGCG AGAGCACACC ACCCAGCAGC CAGAGCACCA 60  
 GCCCAGCCAT GGTCTTTCAG GTGAGTGACC ACCAAGTGCT AAATGACGCC GAGGTTGCCG 120

5	CCCTCCTGGA	GAACCTTCAGC	TCTTCCTATG	ACTATGGAGA	AAACGAGAGT	GACTCGTGCT	180
	GTACCTCCCC	GCCTTGCCCA	CAGGACTTCA	GCCTGAACCT	CGACCGGGCC	TTCTGSCCAG	240
	CCCTCTACAG	CTCCTCTCTT	CTGCTGGGGC	TGCTGGGGCA	CGGCGCGGTG	GCAGCCGTGC	300
	TGCTGAGCCG	GCGGACAGCC	CTGAGCAGCA	CCGACACCTT	CCTGCTCCAC	CTAGCTGTAG	360
	CAGACAGSCT	GCTGGTGCTG	ACACTGCCGC	TCTGGGCAGT	GGACGCTGCC	GTCCAGTGGG	420
	TCITTTGGCTC	TGGCCTCTGC	AAAGTGGCAG	GTGCCCCCTT	CAACATCAAC	TTCTACGCAG	480
	GAGCCCTCCT	GCTGGCCTGC	ATCAGCTTTG	ACCGCTACCT	GAACATAGTT	CATGCCAACC	540
	AGCTCTACCG	CCGGGGGGCC	CCGGCCCCGC	TGACCTCTAC	CTGCTTGGCT	GTCTGGGGGC	600
10	TCITGCTGCT	TTTCGCCCTC	CCAGACTTCA	TCTTCCTGTC	GGCCCAACAC	GACGAGCGCC	660
	TCACAGCCAC	CCACTGCCAA	TACAACTTCC	CACAGGTGGG	CCGACCGGCT	CTGCGGGTGC	720
	TGCAGCTGGT	GGCTGGCTTT	CTGCTGGCCC	TGCTGGTCAT	GGCTTACTGC	TATGCCACCA	780
	TCCTGGCCGT	GCTGGCTGCT	TCCAGGGGCC	AGCGGGCCCT	GCGGGCCATG	CGGCTGGTGG	840
	TGGTGGTGGT	GGTGGCTTTT	GCCCTCTGCT	GGACCCCTTA	TCACCTGGTG	GTGCTGGTGG	900
15	ACATCCTCAT	GGACCTGGGC	GCTTTGGCCC	GCAACTGTGG	CCGAGAAAGC	AGGGTAGAAG	960
	TGGCCAAGTC	GGTCACTTCA	GGCCTGGGCT	ACATGCAGTG	CTGCTCTAAC	CGGCTGCTCT	1020
	ATGCTCTTGT	AGGGGTCAAG	TTCCGGGAGC	GGATGTGGAT	GCTGCTCTTG	CGGCTGGGCT	1080
	GCCCAACCA	GAGGTGGCTC	CAGAGGCAGC	CATCGTCTTC	CCGCGGGGAT	TCACTCTGGT	1140
	CTGAGACCTC	AGAGGGCTCC	TACTCGGGCT	TGTGAGGCGG	GAATCCGGGC	TCCCTTTTGG	1200
20	CCCACAGTCT	GACTTCCCGG	CATTCCAGGC	TCTTCCCTCC	CTCTGCCCGC	TCCTGGCTCTC	1260
	CCCATATATCC	TCGCTCCCGG	GACTCACTGG	CAGCCCCAGC	ACCACCCAGG	CTCCCGGGAA	1320
	GCCACCTTCC	CAGCTCTGAG	GACTGCACCA	TTGCTGCTCC	TTAGCTGCCA	AGCCCATCTC	1380
	TGCGGCGCGT	GCTGGCTGCT	TGGAGCCCCA	CTGCGCTTCT	CATTTCGAAA	CTAAAACTTC	1440
	ATCTTCCCCA	AGTGGCGGGA	GTACAGGCA	TGGCGTAGAG	GGTGTGCCCC	CATGAAGTCA	1500
25	CAGCCAGGCC	CTCCAGTCTA	GCAGTGACTG	TGGCCATGGT	CCCCAAGAGC	TCTATATTTC	1560
	CTCTTTTATT	TTTATGTCTA	AAATCTGCT	TAAAACTTTT	CAATAAACRA	GATCGTCAGG	1620
	ACCAAAAAAA	AAAAAAAATA	AAAAAAAATA	AAAAAAAATA	AAAAAAAATA	BHCLITERAT	1680
	UREBHCBLAS	TFEHCBLAS	LOGUESMOUS	ECXCRMVLEV	SERQVLDASD	PAPLLENSTH	1740
	PYDXGENESD	FSDSPPCPDQ	FSLNFDRTFL	PALYSLLFLL	GLLNGAVAA	VLLSRTALSL	1800
30	STDTFLHLHL	VADVLLVLTLL	PLMAVDAAVQ	WVFGPLCKV	AGALFNINFX	AGAPLLACTIS	1860
	FDRYLSIVHA	TQIYRRDPV	RVALTCIVVW	GLCLLFLALPD	FTYLSANYDQ	RLNATHCQYN	1920
	FPQVGRITLR	VLGQVAGFL	PLVMAYCYA	HILAVLVSR	GQRRFRAMRL	VVVVVAFAV	1980
	CNTFYHLAVL	VDILMDVGV	AENCRESRE	DVAKSVTSGM	GVMHCLNPL	LYAFVGVKFR	2040
	BQMMLFTRL	GRSDQGRFQR	QPSRRRRESS	NSETTEASYL	GL		
35	<b>A34 Protein sequence</b>						
	Gene name:			CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3			
	Unigene number:			Hs.198252			
40	Protein Accession #:			P49682			
	Signal sequence:			none found			
	Pfam domains:			7tm 1 [70-318]			
	Transmembrane domains:			57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323			
	DRY box:			148-149			
45	Cellular Localization:			plasma membrane			
50	1	11	21	31	41	51	
	MLVLEVSDEQV	INDAEVAALL	ENFSSSYDYG	ENESDSCTTS	PPCPQDFSLN	FDRAFLPALY	60
	SLLFLILGLL	NGAVAAVLLS	RRTALESSTDT	FLHLAVADT	LLVLTLPLMA	VDAAVQWVFG	120
	SGLCKVAGAL	FNINFYAGAL	LLACTSFDRY	LNIVHATQLY	RRGPPARVYL	TCLAVHGLCL	180
	LFALPDYFPL	SAHDERILNA	THCQYNFPQV	GRTALRLVLQ	VAGELLLPLV	MAYCAEILLA	240
	VLLVSRGQRR	LRAMRLVVVV	VVAFALCWT	YHLVVLVDIL	MDLGALAEAC	GRESRVDAK	300
55	SVTSGLYME	CCLEPLLYAF	VGKFRERMM	MLLLRLGCEN	QRGLQRQFSS	SRRDSWSSET	360
	SEASYGL						
60	<b>A35 DNA SEQUENCE</b>						
	Gene name:			Differentially expressed C016 gene (clone MGC:5257)			
	Unigene number:			Hs.69517			
	Probeset Accession #:			AA447522			
	Nucleic Acid Accession #:			BC001291			
	Coding sequence:			44-541 (start and stop codons are underlined)			
65	1	11	21	31	41	51	
	GGGGGCGCGG	CGCGCTGACC	CTCCCTGGGC	ACCGCTGGGG	ACGATGGCGC	TGCTCGCCTT	60
	GCTGCTGGTC	GTGGCCCTAC	CGCGGGTGTG	GACAGACGCT	AACCTGACTG	CGAGACAACG	120
70	AGATCCAGAG	GACTCCGAGC	GAACGGACGA	GGGTGACAAT	AGAGTGTGGT	GTCTGTTTGG	180
	TGAGAGAGAA	AACACTTTGG	AGTGCCAGAA	CCCAAGGAGG	TGCAATGGCA	CAGAGCCATA	240
	CTGCTTTATA	GCGGCCGTGA	AAATATTTCT	ACGTTTTCCT	ATGGTTGCGA	AGCAGTGTCT	300
	CGCTGGTTGT	GCAGCGATGG	AGAGACCCAA	GCCAGAGGAG	AAGCGTTTTC	TCTGGGAAGA	360
	GCCCATGCCC	TTCTTTTACC	TCAAGTGTGG	TAAATTTGCG	TACTGCAATT	TAGAGGGGCC	420
75	ACCTATCAAC	TCATCAGTGT	TCAAAGAATA	TGCTGGGAGC	ATGGGTGAGA	GCTGTGGTGG	480
	GCTGTGGCTG	GCCATCTCTC	TGCTGCTGGC	CTCCATTGCA	GCGGGCTTCA	GCTGTGCTTG	540
	AGCCACGGGA	CTGCCACAGA	CTGAGCCTTC	CGAGCATGGG	ACTGCTTCCA	GACCGTTGTC	600
	ACCTGTTGCA	TTAAACTTGT	TTTCTGTTGA	TTACCTCTTG	GTTTGACTTC	CCAGGCTCTT	660
	GGGATGGGAG	AGTGGGATGC	AGGTGCAGTT	GGCTCTTAAC	CCCTCAAGGT	TCCTTAACATC	720
80	ACATTCAGAG	GAAGTCCAGA	TCCTCTGAGT	AGTGATTTTG	GTGACAGATT	TTTCTCTTTG	780
	AAATCAAAAC	TTGTAACTCA	TTTATTGCTG	ATGGCCACTC	TTTTCCTTGA	CTCCCTCTTG	840
	CCTCTGAGGG	CTTCACTATT	GATGGGGAGG	GAGGCCCTAG	TACCACTCAT	GGAGAGTATG	900
	TGCTGAGATG	CTTCCGACCT	TTCAAGTGAC	GCAGGAACAC	TGGGGGAGTC	TGAATGATTG	960
	GGGTGAAGAC	ATCCCTGGAG	TGAAGGACTC	CTCAGCATGG	GGGGCAGTGG	GGCACAAGTT	1020
	AGGGCTGCCC	CCATTCAGAT	GGTGGAGGCG	CTGTGGATGG	CTGCTTTTCC	TCAACCTTTC	1080

CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTG AAGAACTTA GACTTCACCC 1140  
 ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200  
 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTCTCTGTG AAGATGAGC 1260  
 CATCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAACAAAT ACAAGGGGAC 1320  
 TTCAAAGTT CACGAAAAA AAAAAAATA AAAAAAATA AAAAAAATA AAA

# A36 Protein sequence:

Gene name: Differentially expressed CO16 gene (clone MGC:5257)  
 Unigene number: Hs.69517  
 ProbeSet Accession #: AA447522  
 Protein Accession #: AAK01291  
 Signal sequence: 1-17 (first underlined sequence)  
 Transmembrane domain: 146 - 162  
 Cellular localization: plasma membrane

1 11 21 31 41 51  
 MALLALLLVV ALPRVWTDAN LTARQDFED SQRTDESDNR VMCHVCEREN TFEQNPRRC 60  
 KWTPEYCVIA AVKIPRPFPM VAKQCSAGCA AMERPKPEEK RFLLEPMFMY FYLKCKKIRY 120  
 CNLEGPPIINS SVEKEYAGSM GESCGGLWLA ILELLASIAA GLSLLS

# A37 DNA SEQUENCE

Gene name: ESTs  
 Unigene number: Hs.293616  
 ProbeSet Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51  
 AGCAACGACG CCGGCGAGCG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCGCGTGTG 60  
 CCTGCTGCTG AGCAGCGCGG CGGAGAGGCA GCTGCTCCCC GGAACAACT TCACCANTGA 120  
 GTGCAACATA CCGGCAACT TCATGTGAGC CATGGAGCGG TGCATCCCGG GCGCTGGCA 180  
 GTGTGACGGG CTGCGTGAAT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240  
 GTCGAAATGT GGCCCAAGCT TCTTCCCTTG TGCCAGCGCG ATCCATTGCA TCATTGTCG 300  
 CTTCGCGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAGAGA ACTGCACAGC 360  
 AAACCCCTCG CTCTGCTCCA CGCCCGCTA CCACTGCAAG AACGGCTCT GTATTGACAA 420  
 GAGCTTCATC TGGATGGAC AGAATAACTG TCAGACAAC AGTGATGAGG AAAGCTGTGA 480  
 AAGTTCCTCA GAACCCCGCA GTGGGCAAGT GTTTGTGACT TCAGAGAAC AACITGTGTA 540  
 TTAACCCAGC ATCACCCTAT CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600  
 CCTGCTGGCA CTGGTCTTGC ACCACCAAGG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660  
 GCACCGGCTG CAGCACCCTG TGTGCTGTG CCGCTGGTGT GTCCCTGGAC ACCCCACCA 720  
 CTGCAACGTC ACCTACAAGG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGCGGAGCA 780  
 GAATGCGTGG GAATGAGGCT CCCCACCCCT CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840  
 TGGTGGTGTG GAACCTCTTC CACCGCCCTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900  
 CGACCTGCCC CCTTACCGCT CCGGCTCCGG GAGTGCCAC AGTGCCAGCT CCCAGSCAGC 960  
 CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020  
 GGGCACTGCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAGAGAG TATAAGTCCC 1080  
 AGTATTCTCA AAGTCCATAT GGGTAAATCT GCTCTGACTT GTTGCCATTG TAAATATTG 1140  
 TGCTGAGTGG AACTCTCTTA AGCACCCTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200  
 AACTATCTCT GCATCCCTCT CCTCCCCAGC ACTTCAGAGA TGTTTTCTG CGCTCTCAGT 1260  
 TGACATGATC TGTGTGTGGT CTTTCTGTG AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320  
 CACCCCTATT TTTCACATTA TTCTGTATCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380  
 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCGAGAGA 1440  
 CGCTGGACCC AATCTCTCTT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500  
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCAACCCCG CAAAAAATT CCATTTGAGC 1560  
 ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCAG TTCCAGAGAG TCAGTGGCCA 1620  
 AAGAAACTT TGGAGGTGAG TAACACCCCT CAGCAGTGGC AAGCTTATT TTGGTTTGTG 1680  
 AAGGACTCTG AACCATCTTA CCTGTATTA ATCTGCGCT TAGAAATTTG CCCAAGATG 1740  
 CTCATTCTGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800  
 GAGCCCTCC CATGAGTTTA TCCAGTTCT CAGCTCTTAA AATGCAAGCT GCCAAGACCC 1860  
 TACACCTGCC CTGGCTTAC AGCCACTTAC CTGGTTCTG GACTGTCACT CTCCAGCTG 1920  
 ACCTGCCCGT AGCCAGGGA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TBACTGGCT 1980  
 GTATGTCCCT GTGGCCCA CAACGCTGT CTTCGTCATT CATGCAAGCT CAACACTGGC 2040  
 CTCAAAAGTT CCTTAAACAC TTGCAAGTTC CTTTTACCT GTGCAATTGG ACTTGAGGAC 2100  
 ACTGGTTTCT ATCAGAGTGA AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCGCTCTCC 2160  
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220  
 GGTGAGGTC AGGCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGCAAG 2280  
 AGACAATTG GAGTCAAGAT TTTCATTG GATCTATTTT AAATCTTTTA GAAATGCAAT 2340  
 TGAACAGTGG TTTTGTGTTT TTCCCTTCTA GTTAAGGAC TATTTATATG TGTATAGGAA 2400  
 AGCTGTCTCT TTTTGTGTTT TTCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAGGAGATC 2460  
 ACACCCCTGC CCGCTGAGC CCGGTGATA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520  
 ACATTGTGTC ATTGTGTCAC TTGAGGTTA TTATTATCA AGTCTGTGAA GGAAGCAGAA 2580  
 AGAGGAGACT CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640  
 TTCTCTGTGT CAGCTCAGCC OCTCCCTGCA GGAATAAGGG GTAAAACTTT 2700  
 AGGTGTTTGT TGGCAGAGAA CCACACTGAC TGATGAGGGG TAAATGGGAA CCAGGTAGAG 2760  
 CCACCTCGGG CAGCTCTCAC CCATTCAGAA CTCTCTTCCB CAGCTGAGAA ATGTTCAGT 2820  
 AACCTGTGTT ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAGG TGGCATTGAG 2880  
 TGATCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACAA ATCCAAAGGA TGTATCAGAA 2940  
 AAGCTAGCCA CTGTATTTT GTTTTGTGTT AAAAAAATA AAGAAAGAAA AAGAAAGAAA 3000

AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTTAA AATAGCACTT GAGTTATTTT 3060  
 CTGAGTAATC CAATAAGAA CTTTGTATGA CAGCCAGAAI GTGTTAGAAC TCTGGCTGAA 3120  
 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TAITTTCTCC TTGTATGGGG CCCCTTCTTC 3180  
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAAATTA ATTGCGCAGT 3240  
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATGT 3300  
 AGATAAGGGA TGCCCTACTAA TGCTTTTITA AAACAAACAG GGACATTTT ATTATAGATT 3360  
 TGATTTTITT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420  
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480  
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACACG 3540  
 AAAATAGTCT CATCTCTTTT TTTCTCAAT GAGATCCGTG TTTTATTTTA GCATTAATTT 3600  
 AGTTACACAG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATGACA 3660  
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720  
 GAAAGGTTGT GTGTGTTGTC TTTTGTGTTT TGTGTTAGGC TTGGTTTGT TTTTAAATTT 3780  
 TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTCTGTTT TGTGCAAAWG GNMCTAMARM 3840  
 AAMMAAAAC ANYWTTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTAAACA CCACCTCGGG 3900  
 TGGGGCGGGG GGGCCACGCT AGGTACGGCG ACCACGGCGG CCCAAACGGG ACCCCAGAGG 3960  
 GAAACCTCGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAAGAAAAA ACGCGCGGG 4020  
 GGAACCCGCA GAGTGTGCG TAAACACAC CCAAGAGAG AACTCAGAG CACACAAGCG 4080  
 GGACTCAAC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

**A38 Protein sequence:**

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AN043782  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDL domains: 28-66, 70-108, 112-149  
 Cellular localization: plasma membrane

1 11 21 31 41 51  
 MLLGLFLCLL LSSAAESQLL PGMNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60  
 EKECPKAKSK CGPTFPFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTAMP ILCSTARYHC 120  
 KNGLCIDKSF ICDGQNNQD NSDEBSCSS QEPGSGQVVF TSENQLVYYP SITTAIIGSS 180  
 VLPVLVVALL ALVLHQRKR NMLMTLPVHR LQHPVLLSRL VVLDEPHCN VTYNVNNGIQ 240  
 YVASQABQNA SEVSGPPSYS EALLDQREAW YDLPPPPYS DTESLNQADL PPYRSRSGSA 300  
 NSASSQAABS LLSVELTSHS PQPGPQEGT AEPRDSEPSQ GTEEV

**A39 DNA sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGCTGCTCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCAGTA CACTCCCGGA 60  
 GGAAAGAAAC TTCCGTGGGA GGCCTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCGAG 120  
 GACCGGAGAG GGGAGAGCCG SCCGGAGGCT GCGGGGCTCC TGTGGGACCG CGCTGAGGCC 180  
 GGGGAGGCGG AAGAGGGGAA CCGGGGCGAG CCGCCCGCCT GGAATCCGCG CCAGCAGCAG 240  
 CCGGGGCGCG CGCCAGCTGG GCAGGCTCCG GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300  
 CGCTGCGCTC CTGAGGCTTC CCGGGGAGG GTCCGCTTGC CAGTGAACCT TCAGAGGCTT 360  
 TCCGAGCAGC AGCCCGGGGG GCCTTCTGAC TGATCCCGGA GATTTCATC AGCGAGTGCA 420  
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTTCTGGAC CTAGGCGCGG CGGTCTGTCG CTCTGGGGCG TCGCGGCAGA GGGAGTGGC 540  
 CCGCGCGGAA AGCGCGCGCG GACAGTCACT GACGAGGCCG GGGGGTCCGC GGGGCCACGA 600  
 CTCTCTGGAG ACCGTCCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGGCA 660  
 TGTGGGGCGC TCGCGCTCGG TCCGTCTCCT CATCTCTGAA CCGCGCTCG CTCTGACGC 720  
 TGCTGCTGGC TGCGCTGCTG GCGGCGGGGG CGAGGCGCCA GCGGCGAGTA CTGCCAGCGC 780  
 TGCTGAGAG CGCAGGGGCT CTGGCGCATC GGTCTCCAGT GTCCGAGCGC CTTCGACGCG 840  
 GCGGACGCCA CCATCTGCTG CGGCGAGCTG GCGFTGCGCT ACTGCTGCTC CAGCGCGAG 900  
 GCGCGCTGG ACCAGGGCGG CTGCGACAAAT GACCGCCAGC AGGCGGCTGG CGAGCCTGGC 960  
 CGGGCGGACA AAGACCGGCC CCGACGGCTC GGCAGGGCTT CATGCTTAG GGGTACCCAA 1020  
 GGAGACGGCG AGGGTGGCGC CCACCCGCTG AGGCGCTGGC AGCGGTGCTC CCTGAAGGC 1080  
 TCCCGGAAG GAAGGCGAGT CCTCAGGCTT TTCCCGGGCG TGTGCGCCCG TGCAGAGCGC 1140  
 CGCGGATTCC CATCTCTCTT ACAGCGCGGC CCTCTCCCT TGCAGCGGCT CGCCTTGGCC 1200  
 ATCTACGTGC GGTCTCCCAT TGTGGCTCC GTGTTTGTGG CCTTATCAT CTTGGGGTCC 1260  
 CTGGTGGCAG CCTGTTGCTG CAGATGCTCT CCGCTTAAGC AGGATCCCCA GCAGAGCTCA 1320  
 GCGGAGGGG GTACCGCTT GATGGAGACC ATCCCCATGA TCCCCAGTGC CAGCACTCC 1380  
 CCGGGGTGCT CCTCAGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACCTC 1440  
 GGGGCCCGGG CGCCGCCAAC AAGGTACAG ACCAAGTGT GCTTGCAGGA AGGGACCATG 1500  
 AACACGTTGT ATGTCAACAT GCCACCAAT TTCTCTGTGC TGAAGTGTCA GCGGCCAC 1560  
 CAGATTGTGC CACATCAAGG GAGATATCTG CATCCOCTAT ACBTGGGTA CAGGTTGAG 1620  
 CAGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCTTGGCTAC 1680  
 AGGCAAGTTC AGTCCCCCTT CCTTCAACCC AACAGTGAAC AGAAGATGTA CCGAGCGGTG 1740  
 ACTGTATAAC CAGAGTACAC TGGTGGGTTT CTTACTGAA GCGAGACGAA GCGAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTCG GTGGTATTGA TGGCAGGATT CCTTGGATG 1860  
 GCTTCATTTG CCCCCAGACT GTATGAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920  
 CATCCAGGAT ATCATTGATT TATGATGGAA AACCGGCTC AGCTGGAGAT GACCTGTATG 1980  
 TTGCTGATGG GTGTATAACA AATGCTTAG TCCGAAGTGC CCTTGAATA TGGTTGACGA 2040  
 AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCCTTT 2100

5  
 10  
 15  
 20  
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TTGTTGTTGA CTGCACAGGA TC AAAATGCC TGTTATCTCC CTFTTACTGG GACTTTTTTT 2160
TTTTTTTTTT TTTTTTTTAA TCAGACAGGG ICTTGCCTCG TTGCCCAGGC TGGAGTGCAG 2220
TGGTGCATCT TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCCAAC CTCTGCCTC 2280
AGCCTCCAC CTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTAATTTT 2340
TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCTCGA CCTCAAGCAA 2400
TCGCGCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
TGAGCCTTTT TTTTTTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
ATTCTAAAAG GAAACCTGTT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
GGCACACCTT AATTTCAATG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640
GGGCTATTTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTTACA 2700
TTAAAAGAG ACTGAAATAA ATTTATATGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAAACCATT CATCCCTTC 2820
TTGATTGAT CTAAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCCTTTT 2880
TATATTGAAA TCATAAACTA TCACCCGCTG CTTCCTGAG TTACTTTTAA TTTTGCCCTG 2940
TGGTTATGGT TTGGGCTTTC CTCTGTTTG GTTTTCAGAG CCCATGTCT ATATATCTCT 3000
GAGTGCAGT AATTACTATA CTCTGTAATG AAGATCAGTA TTCTGCTTA GATCTGATAA 3060
AAAAATTTTC TTGCTTTTAT TATAAAATTT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
TAGCTCCTCA GCCATTAACCT GAGACTTGGG ATGAAATTTA AACCATATAC GATTTACTTT 3180
GCAGATCTA AGGCTTTTTA TACTCTTGTT ATCAAAATGG CTATTTTTT AGGCACTAAG 3240
GATTGTTAAG AGAAAGCTT TTCACGAAG GATTGCTTTT CTCTCCAC ACTGTCTCTG 3300
ATTTCTCTC TCCTTCAGGC CTCACAGGC ACTGTATCTA TTGCCAATGT TCCAAATTAT 3360
CAAAATTCAG TGAATCTTAT TGTTGTTTCT TTACTTATAT AAAAAAGAT AACTTTAAGG 3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCATGATT TTGTAATTA ACAAATCTCT 3480
GTATGTTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTCTATTTC 3540
TGTTCATGTA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATCTCA 3600
TTTTTAATA ACCAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
TGAAAAA AAAA AAAA
  
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30  
 35

**A40 Protein sequence**  
 Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular localization: not determined

40  
 45  
 50

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1 11 21 31 41 51
| | | | |
MLSGFLMSPS TQRRAYTTPG GKLLPWEAST GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
GEAEKGNRGE PPWIRAOQQ PRPPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPEEA 120
SGRQPRGFSO CTPRPPSASA TEKAVPKGTG PPAEDCGDLG APGPRARRRR LLGVAAEGSG 180
PRGRRRGTVS DEARGSPGPR LLGDRPALSG DALSAPEVVP OGALAARPEP HPGTFLRSCS 240
CCWLRCWRRG RGPSPGEYCHG WLDAGVWRI GFQCPERFDG GDATICGSGC ALRYCCSSAE 300
ARLDQGGCDN DRQGGAGBPG RADKDGPRRL GRASCLRGQT GDGEGAPPPV RAWQRCSPEB 360
SPKCRQLLRA RPKQDFPRRR RGFSSSPRGG PSPLQRPALP IYVFFLIVGS VFAVFIILGS 420
LVAACCCRCCL RPKQDFPQSR APGGNRLMET IPMIFSASTS RGSSSRSOST AASSSSSANS 480
GARAPPTRSQ TNCLPEGIM NNIVYVMPIN FSVLNCQQAT QIVFHQQYXL HPPYVGYTVQ 540
HDSVPMTAVP PFMDGLQPGY RQIQSFPFPH NSEQRMYPAY TV
  
```

55

**A41 DNA SEQUENCE:**  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

60  
 65  
 70  
 75

```

1 11 21 31 41 51
| | | | |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCTCTTCA CTGCTACAG TTTCTTCCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAAGAG GCTCTCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACCCTGA GATTGTGCAA TACTCTCAAG CACTAAGAA AGTATTGGCC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAATTT ATCACTGAT GGGCAATATG TGCTAGAAAT CATGTTGTA 420
GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAGAT ACTTAAACAG ATTGTACACA 480
TATGAGCCTC GGGATTACT CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAAGAGT CAAATTTTAT 600
GAAGAAACCT CTGGGACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGAATA 660
TTACTATTTA GTTTTTTAA TGTGTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
TCTGAAAAA AAAAAA AAAA
  
```

80

**A42 Protein sequence:**  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

1 11 21 31 41 51  
 5 MMLHSAIGLC LLLVTVSSNL AIAIKKRRP PQTLSRGWD DITWVQTYEE GLFYAQSKR 60  
 PLMVHHELED CQYSQALKKV PAQNEEIQEM AQNKFMIMNL MRETTDKNLS PDGQYVPRIM 120  
 FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

**A43 DNA SEQUENCE**

Gene name: ATPase, Ca++ transporting, type 2C, member 1

Unigene number: Hs.106778

Probeset Accession #: N51919

Nucleic Acid Accession #: AF189723

Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 20 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120  
 TTTCATGGCT GGAATGAGTT TGATATTACT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCTGGCCT CTGCAGTCAT CAGTGTTTTA 240  
 25 ATGCATCAGT TTGATGATGC CFTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300  
 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACITGTGCCA 360  
 CCAGAAATGCC ATTTGTGTGC TGAAGGAAAA TTGAGGACATA CACTTGGCCC AGACTTGCTT 420  
 CCAGGTGATA CAGTTTGGCT TCTGTGTGGG GATAGAGTTC CTGTGACTT ACGCTTGTTT 480  
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTCT 540  
 AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600  
 30 GCCTTTATGG GAACACTGCT CAGATGTGGC AAGACAAAGG GTGTGTGCAT TGGACACGGA 660  
 GAAATTTCTG AATTGTGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTACTC CTTGGGTATA 780  
 ATAGGAATCA TCATGTGTGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840  
 35 ATTAGTGTAA GTTGTGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTACACAGT 900  
 ACGCTAGCTC TTGCTTTTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960  
 ATAGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGGA AACACTGACG 1020  
 AAGAAATGAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080  
 GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTTGTTGAT GTGATGTTGT TCATGGATTCT 1140  
 40 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200  
 AGAAACAAAT CTCCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260  
 ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320  
 GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380  
 TGTTTTATGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440  
 45 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACGC 1500  
 ATGGGCTCAG CCGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTTGAACT GGGACAGCTG 1560  
 ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620  
 ACAACACTCA TTGCTTCAGG AGTATCAATA AAAATGATTA CTGGAGATTCT ACAGGAGACT 1680  
 GCAGTTGCAA TGCCAGCTCG TCTGGGATTG TATTCCAAAA CTTCOCAGTC AGTCTCAGGA 1740  
 50 GAAGAAATAG ATGCAATGGA TGTFACAGAG CTTTCACAAA TAGTACCAAA GGTTCAGTA 1800  
 TTTTACAGAG CTAGCCCAAG GCACAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860  
 TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920  
 ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTCCA AAGAGGCAGC AGCATGATC 1980  
 CTAGTGCATG ATATTTTCCA AACCAATATG TCTGCARTCG AAGAGGGTAA AGGGATTAT 2040  
 55 AATAACATTA AAAATTTCTG TAGATTCCAG CTGAGCAGCA GTATAGCAGC ATTAACCTTA 2100  
 ATCTCATTGG CTACATTAT GAACCTTCTC AATCCTCTCA ATGCCATGCA GATTTTGTG 2160  
 ATCAATATTA TTATGGATGG ACCCCCAAGT CAGAGCCTTG GAGTGAACCC AGTGGATATA 2220  
 GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGTACTA AAATGTGATA 2280  
 CTTAAATATC TTGTTTCATC AATAATCAAT GTTTGTGGGA CTTTGTGTTG CTTCTGGGCT 2340  
 60 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACACAA TGACCTTCAC ATGCTTTGTG 2400  
 TTTTGTGACA TGTTCAATGC ACTAAGTTCC AGATCCGAGA CCAAGCTCTG GTTTGAGATT 2460  
 GGACTCTGCA GTAAATAGAA GTTTTGTCTAT GCAGTTCTTG GATCCATCAT GGGACAAATTA 2520  
 CTAGTTATTT ACTTCTCTCC GCTACAGAA GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580  
 65 GATCTGTGTT TCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640  
 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700  
 CTTGAAGTAT GA

**A44 Protein sequence:**

Gene name: ATPase, Ca++ transporting, type 2C, member 1

Unigene number: Hs.106778

Probeset Accession #: N51919

Protein Accession #: AAF27813

Signal sequence: none found

Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878

Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C

[744-889]

Cellular Localization: not determined

1 11 21 31 41 51  
 80 MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRA FRGWNEFDIS EDEPLWKYI 60  
 SQPKNPLIML LLASAVISVL MEQFDDAVSI TVAILIVTV AVVQYRSEK SLEELSKLVP 120  
 PECHCVREBK LEHILARDLV PGDTVCLSVG DRVFDLRLF EAVDLSIDES SLTGETTPCS 180  
 KVTAPQPAAT NGDILASRNTI AFMGTLVRCG KRGVVIGTG ENSEFGEVFK MNQAEAPKT 240  
 PLQKSMOLLG KQLSPYSPGI IGIIMLVGWL LSKDILEMPT ISVSLAVAAI PEGLPVVTV 300

5	TLALGVMRMV	KKRAIVKKLP	IVETLGCCNV	ICSDKTGTLT	KNEMTVTHIF	TSDGLHAEVT	360
	GVGYNQFGEV	IYDGDVHGF	YNPAVSRIVE	AGCVCNDAVI	RNNTLMGKPT	BGALIALAMK	420
	MGLDGLQQDY	IRKABYPFSS	EQKMWAVKCV	HRTQQDRPEI	CFMKGAYBQV	IKYCTTYQSK	480
	GQILTLTUTQ	RDVYQOEKAR	MGSAGLRVLA	LASGPBLGQL	TFLGLVGIID	PPRTGVKRAV	540
	TTLIASGVSI	KMITGDSQET	AVAIASRLGL	YKTSQSQSVS	BEIDAMDVQQ	LSQIVPKVAV	600
	FYRASPRHKM	KIKSLQKNG	SVVAMTGDGV	NDAVALKAAD	IGVAMSQTGT	DVCKEADAMI	660
	LVDDDFQTIM	SAIEEGKGIY	NNIKNFVRPQ	LSTSIALLTL	ISLATLMNFP	NFLNAMQILW	720
	INIIMDGPPA	QSLGVEPVDK	DVIRKPPRW	KDSILTKNLI	LKILVSSIII	VOGTLFVFWR	780
10	ELRDNVITFR	DTIMTFTCFV	FFDMFNALSS	RSQTKSVFEI	GLCSNRMFCY	AVLGSIMGQL	840
	LVYIFPPLQK	VQTESLSIL	DLLPILGLTS	SVCIVAEIHK	KVEREREKIQ	KEVSTSSSP	900
	LEV						

A45 DNA sequence

15	Gene name:	ESTs
	Unigene number:	Hs.157601
	Probeset Accession #:	W07459
	Nucleic Acid Accession #:	AC005383
20	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GACAGTGTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
25	TTTTATTTCG	AGACCTGGGC	CGATGCGGCT	TTAAAAAAGC	CGAGGGGCTC	TATGCACTTC	120
	CCTGGCGGTA	GTTCTCTCGA	CCTCAGCCGG	GTCGGGTCTGT	GCCGCGCTCT	CCCAGGAGAG	180
	ACAAACAGGT	GTCACACGTG	GCAGCCCGGC	CCCGGGCGCC	CCTCCTGTGA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCCGGC	CGGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TGCGCGCTCT	CCTTCGGTGA	TATCAACATG	CCCCCTTTCC	TGTTGCTGGA	GCGCGTCTGT	360
30	GTTTTCCTGT	TTTTCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAAGCAA	420
	GAACACATCG	GGAAGATTTT	AGCTGCCAGC	AAATGATGT	GCTGCTCGGC	TGCAGTGGAC	480
	ATCATGTTTC	TGTTAGATCG	GTCTAACAGC	GTCCGGAAAG	GGAGCTTTGA	AAGGTCCAGG	540
	CACCTTGCCA	TACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCAGT	TGATTTCCAC	TCTCTATCTG	GAATTCCTCT	TGGATTCAAT	TTCAACCCAA	660
35	CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTTTCAAG	GAGGGCGCAC	GGAGACGGAA	720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCCTGAG	GCAGAAATGC	TTCTGTGCCC	780
	CAGATCCTCA	TCACTGTCAC	TGATGGGAAG	TCCCAGGGGG	ATGTGSCACT	GCCATCCAAG	840
	CAGCTGAAGG	AAAGGGGTGT	CACCTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
	GAGCTGCATG	CATGCGCCAG	CGAGCCCTGA	GGGACGACCG	TGCTGTGGGC	TGAGCAGGTC	960
40	GAGGATGCCA	CCAAACGCTT	CPTCAGCACC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020
	ACGCCAGACT	GCAGGGTCCA	GGCTCACCCC	TGTGAGCACA	GGAGCTGGGA	GATGGTCCGG	1080
	GAGTTGCTGT	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGAGCTTTGC	GCTGCTGGCT	1140
	GCACACTGTC	CCCTTCTACG	GTGGAGAGAG	GTGTTCTTAA	CCACCCCTGC	CACCTGTAC	1200
	AGGACCACTT	GCCGAGGCC	CTGTGACTCG	CAGCCCTGCC	AGATGGAGG	CACATGTGTT	1260
45	CAGGAAGTGA	TGAGCGCTCA	CCAGTGCCTC	TGCCCGCTGG	CCCTTGGAGG	GGAGGCTAAC	1320
	TGTGCTCTGA	AGCTGAGCCT	GGAATGCAGG	GTGCACTTCC	TCTTCTGCT	GGACAGCTCT	1380
	GCGGGCACCA	CTCTGAGCGG	CTTCTGCGGG	GCCAAAGTCT	TGTTGAAGCG	GTTTGTGCGG	1440
	GCGGTGCTGA	GCGAGGACTG	TGCGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
	CTGTGTGGGG	TGCTGTGGGG	GGAGTACCAG	GATGTGCTGT	ACCTGTGCTG	GAGCCTCGAT	1560
50	GGCATTCCTT	TCCGTGGTGG	CCCAACCTTG	ACGGGCGATG	CCCTTGGGCA	GCGGCGAGAG	1620
	CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTGT	1680
	CTCAGTGAAT	CACACTCCGA	GGATGAGGTT	GCGGGCCAG	CGCTTACCTC	AAGGGCGCGA	1740
	GAGCTGCTCC	TGCTGGGTGT	AGGCACTGAG	GCTGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
	GGCAGGCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
55	GAGCTGCAGG	GGAGCTGTG	CAGCCGCGAG	CGGCCAGGGT	GCGGACACA	AGCCCTGGAC	1920
	CTCGCTTCA	TGTTGACAC	CTCTGCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	1980
	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGAGCTGAC	ACAGGTCCGC	2040
	CTGTGTGTGT	ATGCGAGCCA	GGTGCAGACT	GCCTTGGGGC	TGGACACCAA	ACCCACCCGG	2100
	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
60	ACCGCTCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGC	CCGGCTGTGT	2220
	GTCCCAAGAG	CTGTGTGTGT	GCTCAGAGGC	GGGAGAGGGC	CAGAGGATGC	AGCCGTTTCT	2280
	GCCCAAGAGC	TGAGGAACAA	TGGCATCTCT	GTCTTGGTGG	TGGGCGTGGG	GCCTGTCTTA	2340
	AGTGAGGATC	TGCGAGGGCT	TGCAGGTCCC	CGGATTCCTC	TGATCCAGCT	GGCAGCTTAC	2400
	GCCGACCTGC	GGTACCAACA	GGAGCTGCTC	ATTGAGTGGC	TGTGTGAGGA	AGCCAGCGAG	2460
65	CCAGTCAACG	TCTGCAAAAC	CAGCCGCTGC	ATGAATGAGG	GCAGCTGGGT	CCTGCAGAAT	2520
	GGGAGCTACC	GCTGCAAGTG	TGCGGATGGC	TGGGAGGGCC	CCCACTGCGA	GAACCGTGAG	2580
	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATTC	TTGAGACGCC	CCTGAGGCAC	2640
	ATGCTCTCCG	TGCAGGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAGGGCCCT	2700
	GGCACTGAAA	TGCTGCTTAC	CTTCTGGAAT	GTCTGTGCCC	CAGGTCTCTA	GAATGTCTGC	2760
70	TTCCCGCCGT	GGCCAGGACC	ACTATTTCTA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC	2820
	ATGCTGCTTA	GAGACAAGAA	AGCAGCTGAT	GTCAACCCACA	AACGATGTTG	TTGAAAAGTT	2880
	TGATGTGTGA	AGTAAATACC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGTAG	GCTATGTGAT	2940
	CTGCCACCTT	TCCCTTGAGG	ATAAACAGGG	GGTCTGGAAG	ACTTAAATTT	AGCGGCTTGA	3000
	CGTTCCTTTG	CACACAATCA	ATGCTGCGCA	GAATGTGTGT	GACACAGTAA	TGCCAGCAGG	3060
75	AGGCTTTTAC	TAGAGCATCC	TTTGAGCGGC	GAAGGCCACG	GCCTTTCAAG	ATGGAAAGCA	3120
	GCAGCTTTTC	CACCTTCCCA	GAGACATCTT	GGATGCATTT	GCAITGAGTC	TGAAAGGGGG	3180
	CTTGAGGGAC	GTTTGTGACT	TCTTGGCGAC	TGCCCTTTTGT	GTGTGGAAGA	GACTTGGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGCA	GGGGCTGAGT	3300
80	TGTGCATGGG	CCAGGTCTGT	GAGGGCCACG	TAAATCTGTT	CTGAGTCTGT	AGCAGTGTCC	3360
	ACCTTGAAGG	TCTTCT					

A45 Protein sequence

Gene name: ESTs

Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGN domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

10 1 11 21 31 41 51  
 | | | | |  
 MPPFLLEAV CVPLFSRVPP SLPLQSEVHS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60  
 SVGKGSFERS KHEAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120  
 15 MVFKGGRTST ELALKYLLHR GLPGGRNASV PQILIIIVTDG KQGDVALPS QQLKRGVTV 180  
 FAVGVPRPRW EELEALASEP RGQHVLLAEQ VEDAINGLFS TLSSSAICSS ATPDCRVEAH 240  
 FCHRTLEMV RSPAGNAPCH RGSRRTLAVL AAHCPPFYSWK RVFLTHPATC VRTTCGPGCD 300  
 SQPCQNGGTC VPEGLDGYQC LCPLAFGBEA NCALKLSLEC RVDLLFLDLS SAGITLDGFL 360  
 RAKVFFVRV RAVLSSEDSRA RVGVATYSRE LLVAVPVGEY QDVPLVWSL DGIPFRGPT 420  
 20 LTGSALROAA ERGFGSATRT QDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVS 480  
 EAVRALEBI TGSPKHVMVY SDPQDLFNQI PELQGLCSR QRPGRCTQAL DLVFMLOTS 540  
 SVGFENFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKET RAAMLRAISQ 600  
 APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPEKVVVLT GSGGASDAV PAQKLNNNGI 660  
 SVLVVGVGVF LSEGLRLLAG PRDSLIHVAA YADLYEYQDV LIEMLCGEAK QFVNLCKPSP 720  
 CMNKGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETFLR HMAFVQEGSS 780  
 25 RTPPSNYREG LGTEMVPTFW NVCAFGP

## COLON

30 A47 DNA SEQUENCE:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 35 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51  
 | | | | |  
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60  
 CTACACTCAG CTITGGGCTCT CTGCTCTCTA CTCTCACAG TTTCTTCCAA CCTTGGCATT 120  
 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180  
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240  
 45 ATGGTTATTC ATCAGCTGGA GGATTGTCTA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300  
 CAAATGAAAG AAATACRAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360  
 GAAACCACTG ATAAGAAATT ATCAGCTGAT GGGCAATATG TGCTAGAAAT CATGTTTGTA 420  
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
 TATGAGGCTC GGGATTATCC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540  
 50 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAAAGT CAAATTTTAT 600  
 GAAGAAACC 1CTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660  
 TTACTATTTA GTTTTITTA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTITTA 720  
 TCTGAAAAA AAAAAA AAAAAA

55 A48 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 60 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

65 1 11 21 31 41 51  
 | | | | |  
 MMLHSAALGLC LLVTVSSNL AIAIKGEKRP PQTLSRONGD DITWVQTYEE GLFYAQKSKK 60  
 PLWVIHLED QYSAALKKV PAQNEEIQEM AQNKFIHLNL MHSTTDKNLS PDGQYVPRIM 120  
 70 FVDPSLVVRA DIAGRYSNRL TYTERDLFL LIENMKALR LIQSEL

75 A49 DNA SEQUENCE  
 Gene name: G protein-coupled receptor 56  
 Unigene number: Hs.6527  
 Probeset Accession #: AA478599  
 Nucleic Acid Accession #: NM\_005682  
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 | | | | |  
 CGGCAGCAGG GTCTCGCTCT GTACACACAG CTGGAGTGCA GTGGTGATG CTGGCTCAT 60  
 CGTAACCTCC ACCTCCGGG TCAAGTGAT TCTCATGCT CAGCTCCCG AGTAGCTGG 120  
 ATTACAGGTG GTGACTTCA AGATGACTC GTCGAGGA AAATGACTCC CCAGTCTGCTG 180



5 CTGCAGACGA CACTGTTCTT GCTGAGTCTG CTCTTCTCTG TCCAAGGTGC CCAOCCGAGG 240  
 GGCCACAGGG AAGACTTTGG CTCTGTCAGC CAGCGGAACC AGACACACAG GAGCAGCTTC 300  
 CACTACAAAC CCACACACAG CCGTCCGATC TCCATCGAGA ACTCCGAAGA GGCCTTCACA 360  
 GTCCATGCCC CTTTCCCTGC AGCCCCACCT GCTTCCCGAT CCTTCCCTGA CCCCAGGGGC 420  
 CTCTACCACT TCTGCTCTTA CTGGAACCGA CATGCTGGGA GATTACATCT TCTCTATGGC 480  
 AAGCGTGACT TCTTGTCTGAG TGACAAAGCC TCTAGCTTCC TCTGCTTCCA GCACCAGGAG 540  
 GAGAGCCTGG CTCAGGCGCC CCCGCTGTTA GCCACTTCTG TCACCTCTCG GTGGAGCCTC 600  
 CAGAACATCA GCCTGCCAGG TGCCGCCAGC TTCACCTTCT CTTTCCACAG TCCTCCCCAC 660  
 10 ACGCCCGCTC ACAATGCCCT GGTGGACATG TGGGAGCTCA AAAGGGACCT CCAGCTGCTC 720  
 AGCCAGTTCC TCTCCCTCCG CCAGAAGGCC TCAGGAGGCC CCGTCCGCTG CCCCAGGAGC 780  
 CAGCAGTTCC AGAGCCTCGA GTCCGAACTG ACCTCTGTGA GATTATGCTG GGACATGCTG 840  
 TCCTTCGAGG AGGACCCGAT CAACGCCACG GTATGGAAGC TCCAGCCAC ABCCGCGCTC 900  
 CAGGACCTGC ACATCCACTC CCGGCAGGAG GAGGAGCAGA BCAGATCAT GGAGTACTCG 960  
 GTGCTGCTGC CTCGAACACT CTTCCAGAGG ACGAAAGGCC GGAGCGGGGA GGCTGAGAAG 1020  
 15 AGACTCTTCC TCTCCCTCCG CAGCAGCCAA GCCCTGTTCC AGGACAAGAA TTCCAGCCAA 1080  
 GTCTGCTGGT AGAAGGTCTT GGGGATTGTG GTACAGAACA CCAAGTAGC CAACCTCACG 1140  
 GAGCCCGTGG TGCTCACTTT CCAGCACCAG CTACAGCCGA AGAATGTGAC TCTGCAATGT 1200  
 GTTCTCTGGG TTGAAGACCC CACATTGAGC AGCCCGGGGC ATTGGAGCAG TGCTGGGTGT 1260  
 20 GAGACCTGCA GGAGAGAACC CCAACATCCG TGCTTCTGCA ACCACTTGAC CTACTTTGCA 1320  
 GTCTGATGAG TCTCTCTGGT GAGGTGGGAC GCGGTGCACA AGCACTACCT GAGCCTCTCTC 1380  
 TCTTACGTGG GCTGTGTGCT CTCCTGCCCTG GCCCTGCTTG TCACCATGCT CGCCTACCTC 1440  
 TGCTCCAGG GTGCTCCGCT GTGCAGGAGG AAACCTCGGG ACTACACCAT CAGGTGCTCA 1500  
 ATGAACCTGC TGCTGGCCGT CTTCTGCTG GACACGAGCT TCCTGCTCAG CGAGCCGCTG 1560  
 25 GCCTTGACAG GCTCTGAGGC TGCTGCTGCA GCCAGTCCCA TCTTCTGCTG CTCTCTCCCTG 1620  
 CTCACTCTGC TTCTCTGGAT GGGCTCGAGG GGGTACAACC TCTACCGACT CGTGTGGGAG 1680  
 GTCTTTGGCA CTTATGTCTC TGCTTACCTA CTCAGCTGGA GCGCCATGGG CTGGGGCTTC 1740  
 CCACTCTTTC TGCTCAAGCT GGTGGCCCTG GTGGATGTGG ACAACTATGG CCCCCTATC 1800  
 TTGCTGTGTC ATAGGACTCC AGAGGCGCTC ATCTACCTTT CCAATGTCTG GATCGGGGAC 1860  
 30 TCCTTGCTCA GCTACATCAC CAACCTGGGC CTCTTCAGCC TGGTGTCTCT GTTCAACATG 1920  
 GCCATGCTAG CCACCATGGT GGTGCAGATC CTGCGGCTGC GCCCCACAC CCAAAAGTGG 1980  
 TCACATGTGT TGACACTGCT GGGGCTCAGC CTGTCTCTTG GCTTGGCTCG GGCCTTATC 2040  
 TTCTTCTCTT TGCTCTCGG CACCTTCCAG CTTGTCTGCT TCTACCTTTT CAGCATCATC 2100  
 ACCTCTCTTC AAGGCTTCTT CATCTTCATC TGCTACTGGT CCATGCGGCT GCAGGCCCGG 2160  
 35 GGTGGCCCTT CCGCTCTGAA GAGCAACTCA GACTGCGCCA GGCTCTCCAT CAGCTCGGGC 2220  
 AGCACTCTGT CAGCCCGCAT CTAGGCTTCC AGCCCACTG CCAATGTGAT GAAGCAGAGA 2280  
 TGCGGCTCTG TGCCACACTG CCGTGTGCCC CCGAGCCCA GGCAGTCTAG 2340  
 CCGCAACTT TGGAAGCCG AOCAGCCAG GAGAGATGGG CCGTTGCCAT GGTGGACGGA 2400  
 40 CTCGCGGGG TGCGGCTTTT GAATGCGCTT TGGGGACTAC TCGGCTCTCA CTCAGCTCCC 2460  
 ACGGACTCA GAAGTGGCCG GCAATGCTGC CTAGGGTACT GTCCCACTAT CTGTCCCAAC 2520  
 CCGACTGGAG GCGCTGCTCT TCCTTACAA CCGTGGGCCC AGCCTCATAT CTGGGGGCCA 2580  
 GGCCTTGGAT CTTGAGGGTC TGCCACATCC TTAATCTCTG GCCCTGCTCT GGGACAGAAA 2640  
 45 TGTTGGCTCA GTTCTCTCTT CTCTGCTGCT CACCTTGGG GCACTCTGCA TCCTCTGTCA 2700  
 TTTTAACTTC AGGTGGCACC CAGGCGCAAT GGGGCCCCAG GCAGACCTTC AGGCGCAGAG 2760  
 CCGTGGCGGA GGAGAGGCC TTTGCCAGGA GCACAGCAGC AGCTCGCCTA CCTCTGAGCC 2820  
 G

**A50 Protein sequence**

50 Gene name: G protein-coupled receptor 56  
 Unigene number: Hs.6527  
 Protein Accession #: NM\_005682.1  
 Signal sequence: 1-26  
 55 GFS domain: 342-394  
 Pfam domain: 7tm\_2[400-665]  
 Transmembrane domains: 410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659  
 Cellular localization: plasma membrane

60 1 11 21 31 41 51  
 MTPQSLLQTT LFLLSLLPLV QGABRGHRE DFRFCSQRNQ THRSSLHYKP TPDLRISTEN 60  
 SSEALTVHAP FPAHPASRS FPDPRGLYHF CLYWNHAGR LHLLYGRDF LLSDKASSLL 120  
 CFQDEESLA QGPPELLTSV TSWNSPQNIS LPSAASFTFS FHSPPHTAAH NASVDMCEBK 180  
 65 RDLQLLSQFL KHPPKASRRP SAAPASQQLQ SLESKLTSVR FMGDMVSPFE DRINATVWKL 240  
 QPTAGLQDLH IHSRQREBQS HIMEYSVLLP RTLPORTKGR SGEAREKRLLL VDFSSQALFQ 300  
 DKNSSQVLGE KVLGIUVQNT KVANLTSPVV LTFQEQQLQPK NVTLQCVFVW EDPFLSSPGH 360  
 WSSAGCTFVR RETQTSCEFN HLTTFVAVLMV SVSEVDAVHK HYLSSLSYVG CVVSALACLV 420  
 TIAAYLCGRV PLPCRRKPRD YTIKVRMNL LAFVLLDTSE LLSEFVALTG SEAGCRASAI 480  
 70 FLNPSLLTCL SWMGLGYNL YRLVVEVFGT YVPGYLLKLS AMGWGFPIFL VTLVALVDVD 540  
 NYGPILLAVE RTPGVVYPS MCWIRDSLVS YITNLGLFSL VFLENMAMLA TMVVQILRLR 600  
 PHTQKWSHVL TLLGLSLVLG LPWALIFFSF ASGTFOVLVVL YLFSIITSFQ GLFIPIWYWS 660  
 MRLQARGGPS PLKMSDCAR LPISGGSTSS SRI

**A51 DNA SEQUENCE**

75 Gene name: Hypothetical protein FLJ20063  
 Unigene number: Hs.5940  
 Probeset Accession #: AA053660  
 Nucleic Acid Accession #: AA053660  
 80 Coding sequence: 218-1360 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CCCCCATGAC TTTGTACAGC TACTTCACTG CTTCCCCCA ATTAGTACAC ATAGTCTCTC 60

5	CACAAATTCCT	ACACCTGCTC	CCCCATAAT	CAGTACACAT	AGTTCCCTCA	CAATTCCTAT	120
	ACCTACTGCT	GCAGACAGTG	AGTCAACCCAC	AAATGTAAAT	TCATTAGCTA	CCTCTGACAT	180
	AATCACCGCT	TCATCTCCAA	ATGATGGATT	AATCACAAATG	GTTCCTTCTG	AAACACAAAG	240
	TAACAATGAA	ATGTCCCCCA	CCACAGAAGA	CAATCAATCA	TCAGGGCCTC	CCACTGGCAC	300
	CGCTTTATTG	GAGACCCAGCA	COCTAAACAG	CACAGGTCCC	AGCAATCCTT	GCCAAAGATGA	360
	TCCCTGTGCA	GATAATTCGT	TATGTGTAA	GCTGCATAAT	ACAAGTTTTT	GCTGTGTTT	420
	AGAAGGGTAT	TACTACAAC	CTTTACATG	TAAGAAAGGA	AAGGTATTCC	CTGGGAAGAT	480
	TTAGTGACA	GTATCAGAAA	CATTGACCC	AGAAGAGAAA	CATTCCATGG	CCTATCAAGA	540
10	CTTGATAGT	GAAATTACTA	GCTTGTTAA	AGATGTATT	GGCAGATCTG	TTTATGGACA	600
	GATCTGAATT	CTTACTGTAA	GCACATCTCT	GTCAACAGA	TCTGAAATGC	GTGCTGATGA	660
	CAAGTTTGT	GATGTAAACRA	TAGTAACAT	TTTGGCAGAA	ACCACAAATG	ACAATGAGAA	720
	GACTGTGACT	CAGAAAGATTA	ATAAAGCAAT	TAGAAGTAGC	TCAAGCAACT	TCTAAACTA	780
	TGATTTGACC	CTTCGGGTGG	ATTATTATGG	CTGTAACCAAG	ACTGCGGATG	ACTGCCTCAA	840
15	TGGTTAGCA	TGCAATTGCA	AATCTGACCT	GCAAAGGCCCT	AACCCACAGA	GCCCTTTCTG	900
	CGTTGCTTCC	AGTCTCAAGT	GTCTGATGC	CTGCAACGCA	CAGCACAGC	AATGCTTAAT	960
	AAAGAAGAGT	GGTGGGGCCC	CTGAGTGTGC	GTGCGTGCCT	GGCTACCCAG	AAGATGCTAA	1020
	TGGGAACCTG	CAGAAAGTGC	CATTGGGCTA	CAGTGGACTC	GACTGTAAAG	ACAAATTTCA	1080
	GCTGATCTCT	ACTATTGTGG	GCACCATCGC	TGGCATTGTC	ATTCTCAGCA	TGATAATTGC	1140
20	ATTGATTGTC	ACAGCAAGAT	CAAATAACRA	AACGAAGCAT	ATTGAAGAAG	AGAATCTGAT	1200
	TGACCAACAC	TTTCAAAATC	TAAAACCTGG	GTGACAGGC	TTCAACCAATC	TTGGAGCAGA	1260
	AGGGAGCGTC	TTTCTTAAGG	TCAGGATAAC	GGCCTCCAGA	GACAGCCAGA	TGCAAAATCC	1320
	CTATTCAGAA	CAGAAAGTGC	TGCCCCGCC	TGACTATTAG	AATCATAAGA	ATGTGGAAC	1380
	CGCCATGGCC	CCCAACCAAT	GTACAAGCTA	TTATTTAGAG	TGTTTAGAAA	GACTGATGGA	1440
25	GAAGTGAGCA	CCAGTAAGA	TCGGGCTCC	GGGGTTTTTC	TTCCATCTGA	CATCTGCCAG	1500
	CCTCTCTGAA	TGGAAGTTGT	GAATGTTTGC	AACGAATCCA	GCTCACTTGC	TAAATAAGAA	1560
	TCTATGACAT	TAAATGTAGT	AGATGCTATT	AGCGCTTGTG	AGAGAGGTGG	TTTCTTCAA	1620
	TCAGTACAAA	GTACTGAGAC	AATGGTTAGG	GTGTTTTTCT	TAAATCTTTT	CCTGGTAGGG	1680
	CAACAAGAAC	CATTTCCAAAT	CTAGAGGAAA	GCTCCCCAGC	ATTGCTTGTCT	CCTGGGCAAA	1740
30	CATTGCTCTT	GAGTTAAGTG	ACCTAATTCC	CCTGGGAGAC	ATAAGCATCA	ACTGTGGAGG	1800
	TCCGAGGGGA	TGAGAAGGGA	TACCCACCAT	CTTCAAGGG	TCACAAGCTC	ACTCTCTGAC	1860
	AAGTCAGAAAT	AGGGACACTG	CTTCTATCCC	TCCCAATGGAG	AGATTCTGGC	AACCTTTGAA	1920
	CAGCCAGAG	CTTGCAACCT	AGCCTCAACC	AAGAAGACTG	GAAAGAGACA	TATCTCTCAG	1980
	CTTTTTCAGG	AGGCGTCCCT	GGGAATCCAG	GAACTTTTTG	ATGCTAATTA	GAAGGCTCTG	2040
35	ACTAAAAATG	TCCACTATGG	GGTGCACTCT	ACAGTTTTTG	AAATGCTTAGG	AGGCAGAGG	2100
	GGCAGAGAGT	AAAAACATC	ACCTGGTAGA	AGGAAGAGAG	GCAAGGAAA	CTGGGTGGGG	2160
	AGGATCAATT	AGAGAGGAGG	CACCTGGGAT	CCACCTCTCT	CCTTAGGTCC	CCTCCTCCAT	2220
	CAGCAAAAGGA	GCACCTCTCT	AATCATGCCC	TCCCGAAGAC	TGGCTGGGAG	AAGGTTTAAA	2280
	AACAAAAAAT	CCAGGAGTAA	GAGCCTTAGG	TCAGTTTGAA	ATTGGAGACA	AATGTCCTGG	2340
40	CAAAGGGTGC	GAGAGGGAGC	TGTGCTCAG	GAGTCCAGCC	GTCCAGCCTC	GGGGTGTAGG	2400
	TTTCTGAGGT	GTGCCATTGG	GGCCTCAGCC	TTCTCTGGTG	ACAGAGGCTC	AGCTGTGGCC	2460
	ACCAACACAC	AACCAACAC	ACACAACAC	ACACAACAAAT	GGGGGCAACC	ACATCCAGTA	2520
	CAGCTTTTAA	CAAAATTTAT	TAGTGCTCTT	TTTATTTTCT	AATGCCCTGT	OCTCTTAAA	2580
45	GTATTTTAT	TTGTTATTAT	TATTTGTTCT	TGACTGTAA	TTGTGAATGG	TAAATCAATA	2640
	AAGTGCCCTT	GTATAGTGT	GAATAAAAAA	AAAAAATAAA	AAAAAATAAA	A	

**A52 Protein sequence:**

Gene name:	Hypothetical protein FLJ20063
Unigene number:	Hs.5940
Probeset Accession #:	AA053660
Protein Accession #:	none found
Signal sequence:	none found
Transmembrane domains:	289-311
EGF domain:	45-74
SEA domain:	80-196
Cellular Localization:	plasma membrane

60	1	11	21	31	41	51	
	MVPSETQSMN	ENSPPTEDNQ	SSGPPPTGTAL	LETSTLNSTG	PENPCQDDPC	ADNSLCVKLH	60
	NTSFCLELEG	YYNSSTCKK	GKVPFGKISV	TVSETFDPEE	KHSMAYQDLH	SRITSLFKDV	120
	FETSVYQTV	ILTVSTSLSP	RSEMRADDKF	VDVTIVTILA	ETSDNEKTV	TEKINKAIRS	180
65	SSSNFLNYDL	TLRCDYVGCN	QTADDCLNGL	ACDCKSDLQR	ENFQSPFCVA	SSLKCPDACN	240
	AQHKQLIKK	SGGAPEACV	PQYQEDANGN	CQKCAFQYSG	LDCCKDFQLI	ITVIGTLAGI	300
	VILSMIALI	VTARSMNKTK	HIEKENLIDE	DFQNLKLRST	GETNLGAREG	VFPKVRITAS	360
	RDSQMNPYS	RHSSMRPRPY					

**A53 DNA SEQUENCE**

Gene name:	TMPS883a
Unigene number:	Hs.298241
Probeset Accession #:	AI538613
Nucleic Acid Accession #:	AB038157
Coding sequence:	202-1566 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	ACCGGGCACC	GGACGGCTCG	GCTACTTTCG	TTCTTAATTA	GGTCATGCC	GTGTGAGCCA	60
	GGAAAGGGCT	GTGTTTATGG	GAAGCCAGTA	ACACTGTGGC	CTACTATCTC	TTCCGTGGTG	120
	CCATCTACAT	TTTTGGGACT	CGGGAATTAT	GAGGTAGAGG	TGGAGCGGGA	GCGGATGTC	180
	AGAGGTCTCT	AAATAGTCAC	CATGGGGGAA	AATGATCCGC	CTGCTGTTGA	AGCCCCCTTC	240

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TCATTCGGAT CGCTTTTGG CCTTGATGAT TTGAAATAA GTCCGTGTTGC ACCAGATGCA 300
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTITTTCC AATCATCGTC 360
ATTGGGATCA TTGCATTTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
TCAGGGAAAGT ACAGATGTGC CTATCCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
GGAGTCTCGG ATTGCAAGA CGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
AAGGGTCACT ACGCAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
TGTGCCCTCG GCCAGTGGT TACCTTGCAG TGCACAGCCT GTGTGATAG AAGGGGCTAC 840
AGCTACGCA TCGTGGGTGG AACATGTGCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
ACTGTGTCAC ACTGTGTTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCAGGGCCA 1140
CTCAAGTTCA ATGAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200
GATGGAAGA TGTGCTGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
TCOCCGTGCC TGAACACGCG GCGCGTCCCT TTGATTTCCA ACAAGATCTG CAACCCAGG 1320
GACGTGTACG GTGGGATCAT CTCCCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACCA CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
TACACCCGTC TCACCTCTCT CTTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAAGGGGACA AGTATGCCAC TGAGTTCTCG AGGTGATGAA GACAGCCCGA 1620
TCTTCCCTCG GACTCCCTGG TAGGAACCTB CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGCG CGAAGAGAG CACCCCTCCA TCTGATTTCCA GCACAACCTT 1740
CAAGCTGCTT TTTGTTTITT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
AGTGCAGTGG CGAATCCCTT GCTCACTGCA GCTTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
TTGCCCTCAG TTTCCCACTA GCTGGGACCA CAGGTGCCCG CCACCAACAC CAACTAATT 1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GCTGCTCTC AAACCCCTGA 1980
CCTCAAATGA TGTGCTGCT TCAAGCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
AGCCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
AGGGCCGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTTG 2160
ACBAGATAAG CAGTATGTGT ACCTCACGTC CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCTCTCTA GGGACCAGAA 2280
CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
ATGACTCGTT TAAGGCTTAT TTTCATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
TGTGCTTTG ATTCCAAATA ATATGTTTC TTCCCTCAAA AAAAAAANA AAAAAAANA 2460
AAAAAANA

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**A54 Protein sequence:**

Gene name: TMFRSS3a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

55  
60

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1 11 21 31 41 51
MGENDPPAVE APPSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFFP IIVIGIILI 60
LALAIGLGIH FDCGKYRCR SSKFCIELIA RCDGVSDCED GEDEYRCVRV GGNNAVLIQVF 120
TAASWXTMCS DDWKGHYANV ACAQLGFPSY VSSDNLKVS LBGQFREFV SIDHLLPDK 180
VTALHHSVIV REGCAGHV VLTQCTACHR RGYSSRIVGG NMSLLSQWPF QASIQFGYH 240
LCGGVITPL WIITAARCVY DLYLPKSWTI QVGLVSDLDN PAPSHLVEKI VYHSRYKPKR 300
LGNDIALMKL AGPLTFNEMI QPVCLFNSBE MFPDQKVCWT SGWATEDGA GDASFVLEHA 360
AVPLISNKKC MERIVYGGII SPSMLCAGYL TGGVDSQGD SGGPLVCQER RLWKLWGATS 420
PGIGCAEVNK PGVTRVTSF LDWHEQMER DKRT

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**A55 DNA SEQUENCE**

Gene name: Putative G protein-coupled receptor GPCR150  
 Unigene number: Hs.97101  
 Probeset Accession #: AA215333  
 Nucleic Acid Accession #: NM\_014373  
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

70  
75  
80

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1 11 21 31 41 51
GTGGCTCGA GGTGGTGGCA GGGCCGCCCC CTGCACTCCG GAGACGAACG CACGGACCGG 60
GCCTCCGGAG GCAGGTTCCG CTGGAAGGAA CCGCTCTCCG TTGCTCTTAC ACTTGCGCAA 120
ATGTCTCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180
AAATAACATA ATTGAAGGCA GTAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240
GACCACTGG AGAGGACAGA AAATGAAGCA GTGTTTATC ATGTGTATT TTTTCAAGT 300
TCTTGAATTT TAACATAAAA TAAGACTGCT CTCTCTTCCG AGAAGTCTC TTTTCACTAC 360
CAGTACGTC AAACAAACCA GCCCTTAGAC GTTAAGTATC TGCTATTCTT GATCATACTT 420
GGGAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAT 480
TTATGGAAT ATTTTTCAT TTTCACTAGC TTGTTTATC TTTTACTTTT GGTAAACATT 540
TCCATTATAT TGTATTTCAG GGATTTTGTG CTTTAAACCA TTAGGTTTAC TAAATACCAC 600
ATCTGCCAT TTTACTCAAT TATTTCCCTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC 660
CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCAAAA CAACCAAGCT TTTCTTTAAG 720
TGTCAAATAT TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTTCACT CTTTCTTATT 780

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5	GTCTTGGGAG ACCCAGCCAT CTACCAAGGC CTGAAGGCAC AGAATGCITA TTCTCGTCAC 840
	TGTCCTTTCT ATGTCAGCAT TCAGAGTTAC TGGCTGTCAT TTTTCATGGT GATGATTTTA 900
	TTGTAGCTTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960
	ACTTCCTATA TGAATGAAAC TATCTTATAT TTTCTTTTTC CATCCCACTC CAGTTATACT 1020
	GTGAGACTTA AAAAATATAT CTATCCCAAG CTCATTGTCT GTTTTCTCAG TACCTGGTTA 1080
	CCATTTGTAC TACTTCAGGT AATCATTGTT TTACTTAAAG TTCAGATTCC AGCATATATT 1140
	GAGATGAATA TTCCCTGGTT ATACTTTGTC AATAGTTTTC TCATTGCTAC AGTGTATTGG 1200
	TTTAATTGTC ACAAGCTTAA TTAAAGAGC ATTGGATTAC CTTTGGATCC ATTTGTCAAC 1260
10	TGGAAGTGCT GCTTCATTCC ACTTACAAAT CCAATCTTTC AGCAAATTGA AAAGCCTATA 1320
	TCATAATGA TTTGTTAATA TTATTAATTA AAAGTTACAG CTGTCAATAG ATCATAATTT 1380
	TATGAACAGA AAGAACTCAG GACATATTAA AAAATAAACT GAACTAAAAC AACTTTTGCC 1440
	CCCTGACTGA TAGCATTTC AATGTGTCT TTTGAAGGGC TATACCAGTT ATTAAATAGT 1500
	GTTFATTTT AAAACAAA TAATTCCAAAG AAGTTTTTAT AGTTATTCAG GCACACTATA 1560
15	TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGAATAG AGTTAACATT TGGCTATATT 1620
	GATGTTTGTG TTACTCAAAA AAACACTGAG ATGCAACTG TTATGTAAAT CTGAGATTTC 1680
	ACRGACAACT TTAAGATATC AACCTAAACA TTTTATTAA ATGTTCAAAT GTAAGCAAGA 1740
	AAAAAAA

20	<u>A56 Protein sequence</u>
	Gene name: Putative G protein-coupled receptor GPCR150
	Unigene number: Hs.97101
	Protein Accession #: NP_055188
	Signal sequence: none found
25	Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297
	Cellular Localization: plasma membrane

30	1 11 21 31 41 51
	MTALSSENC FQYQLRQTNQ PLDVNYLLFL IILGKYLNI LTLGMRKNT CQNFMEYFCI 60
	SLAFVDLLL VMSIILYFR DFVLLSIREF KYHICLPTQI ISFTYGLFHY PVFLTACIDY 120
	CLNPSKTKL SPKCKQLFYF FTVILINISV LAYVLGDPAL YQSLKAQNAV SRKCFYVSI 180
	QSYWLSFMV MILEVAFITC WEEVTLVQA IRTSYNMET ILYPFSSSES SYTVRSKKIF 240
35	LKSLIVCFIS TMLPFFVLQV IIVLLKVQIP AYIEMNIPWL YFVNSFLIAT VYWFNCHRLN 300
	LKDGLPLDP FVMKKCCFIP MTIPNLEQIE KPISIMIC

40	<u>A57 DNA SEQUENCE</u>
	Gene name: ESTs, Weakly similar to CGH07L collagen alpha 1(III) chain precursor [H.sapiens]
	Unigene number: Hs.19322
	Probeset Accession #: AA088458
	Nucleic Acid Accession #: AA088458
	Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

45	1 11 21 31 41 51
	GCCCTTGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CAGGAGGACA CTGACATGGA 60
	CTGAAGAAA AGGAGCTGGA GCAGGAGAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
50	GCGCGGGGCC GCTACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
	CTGGCCAGA GCAGAGCCAG CCGCCACTTT GGGGCTGCAG GAGGCCCCCG CTTACTGGGG 240
	CGGCTACTGC CCAAGGTGCA AGAGGTGGCC CGGTGCTTGG GGGAGCTGCT GGCTGCAGCC 300
	TGTGCCAGCC GGGCCCTGCC CCGCTCCTCC TCGGGGCCCG CTTGCCCTGC CTTGACCTCC 360
55	ACCTCACCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACGAGCTC 420
	CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCAAGC AGCTGGAGCA GGAGAAAGTC 480
	GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCGCTGAGCC AGCAGGACGG GGGACCTCTG 540
	GATTCCACCT TCATCTAGTC CTGTGGGGCC GGTGGGGCCC CAGGGGCCAG CTTGGCACTC 600
	AGCCCTTCGA GGGTGGGCGC CCATCGCAC CCACCTCTC TGGCTGGAGA CCCCCGGCAG 660
60	GCCAGGCGAC AGTCCCGGAG TGGGCGCCTT CTTGCCCGCC TTGCCAGATG GGCYCCCCAG 720
	GCCCTGCCCC GGTCTGGTCC CCGACCGAGC GCTTGACTCC GTTTGGCTC CTGGTTGTTG 780
	ACATGGGCTG GGGCTCTCTT TGAGTCCGCA TAGTCCGCG CTACTACTGG CCGCTGTGAG 840
	TGGACAGTGG GGTACCCCTC CATGAGTTAG GGTCCCGCCG TTTCCAGCGG TGCCGCCCCTG 900
	GGTCCCATCT TCAGGGAAG GCATCGCCCA CGCCAGGCTG CACTTCCAA CACGGGCGAG 960
65	AGAGGCGCG GGGCGGCTCC GAAGCGGGTC CAGGGCGAGC TTCCCGCTCA ACCAGGGCAC 1020
	CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
	GTAAGCGGG GGTGCTGTCG TGGCTGGGGA GCGCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
	CTGGCCAGG CTGAGGAGCC CTGGCTGCAG CGGATCGGCA GCGCCGGGTG GCGAGAGCTT 1200
	GGCTGCACTG TGCTCTCCAC AGACCTCTGG GTGATGGCTT TCCCTCTCTT GGCCTGGGACG 1260
70	TTGCCCCAG TTGAGTCCCA CACAACATCC TGTGAGCTTG GCTCCCCAGG AGGGCCCCCA 1320
	GACAGCTCCC AGGCACTGTA TAGGCAAGGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380
	CTGGGGTCTT GCTCACCCCC CTTTGCTCTC AGGCCCGGCC TGTCCCCAGG TTTCACTGCT 1440
	GAGAGGCCAC CTCCCTCAGC CAGGAAACCG GAGAAACCCC AGGGTACAGG AGGAGGCTGG 1500
	GGCAGGTCCC CTGGGTGTC ACTCCCTCAG CCGCTGCCCA GGCCTACTCC CGCTGGTCTC 1560
75	GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620
	GAACCAAGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CAGGGGCCCC CGATGCGGG 1680
	TCAGTGTGTC TGGGGGCGAG GGCCTCCGAT GCGGGGCTAG TGGTGGGGG GCGCAGGGCC 1740
	CCGATGTCGG GGTCACTGCG TGGGGGGGCG AGGGGCCCTT CGTGTCCAGG GCACCTTTGGT 1800
	ACACTGTCCC ACAAGGCACC TGCTCTCAGG GAGGGGCCCT GGCAGGCAGC GTGGCACTC 1860
80	CCTTCCGAG CCGAGCTCCA TGCTAACCTG CCGACAGCAA CCGCACAGAG CCACATTCCC 1920
	TGCTGCACCT GGTCTGCAGG GGTGTCCCG GACAGGCCCA AGTCAGGCCA GCATGCAGCT 1980
	GCCCTCCTAC CTTGAAGATG GAGATGGGCT TTCCAGGGGA CATAAGGATG TCAGGCTTGG 2040
	ACCTCTTGG CAGGAAAGGG TGCAAGTCTT GAGGGCCTGT GCGCCACAGC CCGACGACCC 2100
	AGGTGGAAGT CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GAGAAAGCCC CCGCTCAGCA 2160
	GCTGGGGTC TGCCCAACAG GGCTCCCCCA GCTCTGCCTT TGAGGGTGCC TGCCATGCC 2220

5	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TGAGGAGACC	GCCCAACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCCTCG	GAAAAACCTGC	CTTTGAGCCT	TGGTGTTCGG	TGCAGGTGTA	2400
	AAAGAAATAG	GTCTTCCGAG	TTTACAGCTT	GAATCAGGCG	TAGTGAATGG	CCCTGGAGAC	2460
	CACGAGGGGA	GAATTTAAAG	GCCCGGCGTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCCTG	CTGGAGGCTT	GCCCTAGGAC	GCTGGGCGGG	TGAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CTGGGCTCTT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAGGT	ACATACACGT	2640
	GCGTGCACAC	TGTATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
10	CAGAAGTGTG	CCGAGTTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTGTGTGTT	ATCAAGTTCC	AAGGAAAAGG	AACATCTCAG	CGGGGCGTGG	TGGTTACGCG	2820
	CTGGAATCCC	AGCAGTTGAG	GCCAGGAGTT	CCAGAGCAGC	CTGGGCAACG	CAGTGAGAGA	2880
	CCCCATCTCT	ACAARAAAAA	AAAAAGAAAG	AAAGAAAATG	AGAGATCCAG	GTTTAAAAAT	2940
	TCATAAACAC	CACAAGGAAA	CAATACACTA	TGAGACCCAG	CAGAGCAAC	AGATTGACTC	3000
15	TAGACCCAGA	TACTAGAAIT	ATCAGAGAGA	ATATAAAGTA	ACAGTGTGTT	ATATATCTAA	3060
	AGAAATAAAA	GAGATTCTTG	GAAACATGAA	AAAAAA			

A58 DNA sequence

	Gene name:	ESTs
	Unigene number:	Hs.157601
20	Probeset Accession #:	N07459
	Nucleic Acid Accession #:	AC005383
	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

25	1	11	21	31	41	51	
	GACAGTGTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
	TTTATTATTG	AGACCTGGGC	CBATGCGCGT	TTAAAAAAGG	CGAGGGGCTC	TATGCACCTC	120
	CCTGGCGGTA	GTCTCTCCGA	CCTCAGCCCG	GTGGGGTCTG	GCCGCGCTCT	CCCAGGAGAG	180
30	ACAAACAGGT	GTCCCAAGTG	GCAGCGCGCG	CCCGGGCGCC	CCTCTCTGTA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TGCGCGCTCT	CCCTCCGTTA	TATCAACATG	CCCTCTTTCC	TGTTGCTGGA	GGCGGTCTGT	360
	GTCTTCTCTG	TTTCCAGAGT	GCCGCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAAA	420
	GAACCCATCG	GGAAGATTTC	AGCTGCCAGC	AAATGATGTG	GGTGTCTCGC	TGCAGTGGAC	480
35	ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTGGGAAAG	GGAGCTTTGA	AAAGTCCAAG	540
	CACCTTGCCA	TACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCCAGT	TCAATTCAC	TCCTCATCTG	GAATTCCTCT	TGGATTCAIT	TTCAACCCAA	660
	CAGGAAGTGA	AGGCAAGAA	CAGAGGATG	GTCTTCAAG	GAGGGCGCAC	GGAGACGGAA	720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCTGGAG	GCAGAAATGC	TTCTGTGCCC	780
40	CAGATCTCTA	TCATGCTCAC	TGATGGGAAG	TCCACGGGGG	ATGTGGCAGT	GCCATCCAAG	840
	CAGCTGAAGG	AAAGGGGTGT	CACGTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
	GAGCTGCATG	CACCTGGCAG	CGAGCCTAGA	GGGCAGCAGG	TGCTGTGGCG	TGAGCAGGTG	960
	GAGGATGCCA	CCAACGGGCT	CTTCAGCACC	CTCAGCAGCT	CGGCGATCTG	CTCCAGCGCC	1020
	ACGCCAGACT	GCAGGGTCCA	GGCTCACCCC	TGTAGACACA	GGAGCTGGA	GATGGTCCGG	1080
45	GAGTTGCTG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGACCTTTGC	GGTGTGGCT	1140
	GCACACTGTC	CTCTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCAACCTCG	CACCTGCTAC	1200
	AGGACCACTT	GCCCCGGCCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
	CCAGAAAGAC	TGGACGGCTA	CCAGTGCCTC	TGCCCCCTGG	CCCTTTGGAG	GGAGGCTAAC	1320
	TGTGCCCTGA	AGCTGAGCCT	GGAATGCAGG	GTGACCTTCC	TCTTCTGCT	GGACAGCTCT	1380
50	GCGGGCACCA	CTCTGGAAGG	CTTCTGCGGG	GCCAAAGTCT	TGCTGAAGCG	GTCTGTGCGG	1440
	GCGGTGCTGA	GCGAGGACTC	TGCGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGAGCTCG	1500
	CTGGTGGGCG	TGCGGTGTGG	GGAATACAGG	GATGTGCTTG	ACCTGTCTTG	GAGCTCTCAT	1560
	GGCATTCCCT	TCCGTGGTGG	CCCAACCTCG	ACGGGCGAGT	CCTTGGCGCA	GGCGCCAGAG	1620
	CGTGGCTTGG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGCG	CACGTAGAGT	GGTGGTTTTG	1680
55	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCGAG	CGCTCAGCG	AGGGGGCGGA	1740
	GAGCTGCTCC	TGCTGGGTGT	AGGCAATGAG	GCGGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
	GGCAGCCCAA	AGCAATGTAT	GGTCTACTCG	GATCTCTCAG	ATCTGTTCAG	CCAAATCCCT	1860
	GAGCTGCAGG	GGAACTGTGT	CAGCCGGCAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
	CTGCTCTTCA	TGTTGGACAC	CTCTGCTTCA	GTAGGGCCCG	AGAAATTTGC	TCAGATGCAG	1980
60	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGAGGTGAC	ACAGGTCCGC	2040
	CTGGTGGTGT	ATGGCAGCCA	GGTGCAGACT	GCTTTCGGGC	TGGACACCAA	ACCCACCCGG	2100
	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGG	CCGGCTGGTT	2220
	GTCCCCAAAG	CTGTGGTGGT	GCTCAGAGGC	GGGAGAGGCG	CAGAGGATGC	AGCCGTTCCT	2280
65	GCCCCAAGAC	TGAGGAACAA	TGGCATCTCT	GTCTTGGTGG	TGGGGGTGGG	GCTGTCTCTA	2340
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGATTTCCC	TGATCCAGCT	GGCAGCTTAC	2400
	GCGGACCTGC	GATACCAACA	GGAGCTGCTC	ATTGAGTGGC	TGTGTGGAGA	AGCCAGGCAAT	2460
	CCAGTCAACC	CTCTCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGCGT	CCTGCAGAAAT	2520
	GGGAGCTACC	GCTGCAAGTG	TGGGATGGGC	TGGGAGGGCC	CCCACTGCGA	GAACCGTGAG	2580
70	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATTG	TTGAGAGGCC	CCTGAGGCAC	2640
	ATGGCTCCCG	TGCTAGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAGGGGCTG	2700
	GGCACTGAAA	TGCTGCTTAC	CTCTGGAAT	GTCTGTGCCC	CAGGTCTCTA	GAATGTCTCG	2760
	TTCCCGCCGT	GGCCAGGACC	ACTATTCTCA	CTGAGGGAGG	AGGATGTCTC	AATCTCAGCT	2820
	ATGCTGCTTA	GAGACAGGAA	AGCAGCTGAT	GTCAACCCCA	AACGATGTGT	TTGAAAAGTT	2880
75	TTGATGTGTA	AGTAATATCC	CACCTTCTGT	ACCTGTCTGT	CCTTGTGTAG	GCTATGTCTAT	2940
	CTGCCACCTT	TCCCTTGAAG	ATAAACAGAG	GGTCTGTAAG	ACTTAATTTT	AGCGGCTGTA	3000
	CGTTCCTTGT	CACACAATCA	ATGCTCGCCA	GAATGTGTGT	GACACAGTAA	TGCCAGCAG	3060
	AGGCCCTTAC	TAGAGCACTC	TTTGGACGGC	GAAGGCCACG	GCTTTTCAAG	ATGGAAGCA	3120
	GCAGCTTTTC	CACCTCCCCA	GAGACATCTT	GGATGCAITT	GCATTGAGTC	TGAAAGGGGG	3180
80	CTTGAGGGAC	GTCTGTGACT	TCTTGGCCAG	TGCTTTTGTG	GTGTGGAAGA	GACTTGGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGTGTGA	TGATGGGGGA	GGGGCTGAGT	3300
	TGTGATGGG	CCGAGTCTTG	GAGGGCCACG	TAAATCGGTT	CTGAGTCTGG	AGCAGTGTCC	3360
	ACCTGGAAGG	TCTTC					

A59 Protein sequence

Gene name: ESTs  
 Unigene number: Hs.157601  
 Protein Accession #: none found  
 Signal sequence: 1-17  
 Transmembrane domains: none found  
 VGM domains: 49-223; 341-518; 529-706  
 EGF domains: 298-333; 715-748  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLEAV CVFLFSRVPP SLPLQSVHVS KETICKISAA SKMMWCSAAV DIMFLDGSN 60
    SVGKGSFERS KHFALTCDG LDISPERVRV GAFQPSSTPH LEFPDSEFST QQEVKARIKR 120
    MVFKGGRRET ELAKYLLHR GLPGGRNASV PQILIIIVTDG KSGQDVALPS KQLKRGVTV 180
    FAVGVRFPRW EELHALASEP RGQHVLLAQ VEDATNGLFS TLSSSAICSS ATFDCEVEAK 240
    PCERTLEEM REFAGNAPCW RGSRETLAVL AAECPPFYSWK RVFLTHEATC YRTTCFPGCD 300
    90PCQNGGTC VPESLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDS SAGTTLDDGL 360
    RAKVVFKEFV RAVISEDRA RVGVATYSRE LLVAVPVGEY QDVDPDLVWSL DGIPFRGGPT 420
    LTGSALRQA ERGPGSAIRT GQDRPRRVV LLTSHSEDE VAGPARHARA RELLLLGVGS 480
    EAVRAELERI TGSPKRVVYV SDPQDLFNQI PELQKGLCSR QRPQCRQAL DLVFMLDTS 540
    SVGPENFAQM QSFVRSALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
    APYLCGVGSA GTALLHIYDK VMTVQRGAR GVPKAVVVLV GGRGAEDAAV PAQKLEKNGI 660
    SVLVVGQGVV LSEGLRLRAG PRDSLHVAA YADLRYHQDV LIENLCSEAK QPVNLCCKP 720
    CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSBCBVCVS QGWILETFLR HMAPVQEGSS 780
    RTPPSNYREG LGTEMVPTFW NVCAPGP
  
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A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTACAGG ATCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
    AAACCCCGTA TCCCATATGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTGG CGAGTATCAT CATTTGTGGT GTCTTCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
    CTGAGCTGTC CCTTGGGGGA GAGCAGAGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
    GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
    GGGAACTGGT TCTCTGCTCT TTTCGACAA CTTACAGAA CTTCTGCTGA GACAGCCTGT 420
    AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
    GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCTGCG GAACTCAAGT 540
    GGGCCCTGTC TCTCAGGCTC CCTGGCTTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
    AAGACCCGCC GTGGGGTGGG TGCGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
    AGCATCCAGT AGGACAAACA GCAGCTCTGT GAGGGGAGCA TCCTGGACCC CCACTGGGTC 720
    CTCAGGCGAG CCCACTGCTT CAGGAACAT ACCGATGTGT TCAACTGGA GGTGCGGGCA 780
    GGCTCAGACA AACTGGGCGAG CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
    TTCAACCCCA TGTACCCCAA AGACATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
    ACTTCTCTAG GCACAGTCTG GCGCATCTGT CTGCCCCTCT TTGATGAGGA GCTCCTCCTA 960
    GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAAG GAATGGAGG GAAGATGTCT 1020
    GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTACAGCA CACGCTGCA TGCAGACGAT 1080
    GCGTACCAGG GGGAGGTAC CAGGAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
    GACAGCTGCC AGGCTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGCTCATGT 1200
    GTGGGCATCG TTAGTGGGG CTATGGCTGC GGGGGCCGGA GCACCCAGG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGATCTTAC AATGTCTGGA AGGCTGAGCT GTAA
  
```

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

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1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSQDP LNSLDVKPLR KPRIPMTFR KVGIPYIIL LSLASIIIV VLIKVILDKY 60
    YFLCGQPLHF IPRKQLCDGE LDCPLGDEE HCVKSFPSGP AVAVRLSKDR STLQVLDSAT 120
    GWNFSACFDN FTEALAEAC EQMGYSSTPT FRAVEIGPDQ DLDVVELTEN SQELRMENSS 180
    GPCLSGSLVS LHLCLAGKSL KIPRVVGGEE ASVDSHPWQV SIQYDKQEVV GSSILDPRWV 240
    LTAABCFRKH TDVFNWVRV GSDKLGSPFS LAVAKIIIE FFMVYKDNM IALMKLQFPL 300
    TFGTVPKPC LFPEDEELTP ATPLNIIIGW FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
    AYQGEVTSKM MCAGIEPEGGV DTCQGDSSGP LMYQSDQNHV VGIVSWGTGC GGPSTPGVYT 420
    KVSAYLNWIV NWVKAEI
  
```

**A62 DNA SEQUENCE**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
CTGAGATCCT TGCCTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
AGACCCAGCT GTGCTCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCACT CTACCGGAAA CGGAGCCCAC 300
CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
CAGAGAAGCC AGCCGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG 420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTGGAGCAG CAACGAATGC 540
AACAAGCGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAGAATCA AGATTCTGCT 600
AACTCCTGCA CCAGCCCCGT CCTCTTCCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTAA 720
GGCTTAGAGA CAGAAACTTT AGCATTTGGG CCACTAGTGG CTCTAGCTC TAAATGTTTG 780
CCCGGCCATC CCTTTCCACA GTATCCTTCT TCCCTCCTCC CCGTCTCTCG GCTGTCTCGA 840
GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAAT 900
AAAGATTGTA AGACAGAGAG AGAAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCCCTCT GCCCTCTCTC CATTCGCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG 1020
TTTTTCCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080
TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAATAA AAAAAAATAA

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**A63 Protein sequence:**

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Protein Accession #: none found  
 Signal sequence: 1-22  
 Transmembrane domains: none found  
 C-type lectin domain: 47-156  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MASRSMRLLL LLSCLAKTV LGDIIMRPSG APGWFYHKSN CYGYFRKLKN WSDALELCQS 60
YGNAGHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLRSWSG 120
KSMGGNKHCA EMSNNMNFAT WSSNECNKRQ HFLLCKYRP

```

**A64 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

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1      11      21      31      41      51
|      |      |      |      |      |
GCGGAACACC GGCCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGSC 60
TCCCTGTGGG ACCTCTCGCG TCTCTCCCTC TTCTCCAGGT TTGCTGGCNG CAGTGGCGCG 120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGALT TCACCTGTGG GAAATGGCGAG ACAGTCCAGG 300
AAAGAGGTTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCGTGAAAAT GGCAGGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACT AAGATTTTCT 480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGCTCTGGCT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTGTT AATAAGCCAC TGGACCGGGA GGAATTTGCC AAGTATGAGC 600
TCPTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
TCATCGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
GTGTCTTAGA GGGATCTCTA CCAGTACTTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAGAAACCAA 840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
CCAGTGGGCT GGAACGGGAA AAAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGCTCCACC ACCACCGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAAATGCTC CAGATTTGAC CCCCAGAGT ACGAGGCCCA TGTCCTGAG AATGCAGTGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAAGC CCCCACCTCA CCAGCGTGGC 1140
GTGCCACCTA CCTTATCATG GCGGTGAGG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
CTGAGAGCAA CCAAGGCGATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCCCTT TTGTCTGAAG CTCCTCAACT 1320
CCACAGCCAC CATAGTGGTC CAGGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCACC 1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACCTGG GGAGCCTGTG TGTGTCTACA 1440
CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500

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5 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCAGTTTGTG AGGAACACCA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620  
 ATUGAAGCCC TCCACCACCT GGCACGGGAA CCTTCTGCT AACACTGATT GATGTCAACG 1680  
 ACCATGGGCC AGTCCCTGAG CCCCCTCAGA TCAACATCTG CAACCAAAGC CCTGTGCGCC 1740  
 ACCTGTCTGA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTCT CAGGCCGAGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACTTT TCTCTGCTG 1920  
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980  
 ATGTGGAATC CTGCGCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040  
 TCCTGGCTCT GCTGTCTCTC CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGGAGCC CTTCTTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GGAGTGTGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGCGGGCTAA ACAGACGCC ACAGCCCGGC CCTACGACAC CCTCTGGTG TTGACTATG 2400  
 AGGGCAGCGG CTCGAGCGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCTC TCCGACCAAG 2460  
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGGCTT CAAGAAGCTG GCAGACATGT 2520  
 ACGTGTGCGG GGAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTCAAGC 2580  
 20 CACAGAGCAT CTCCAGGGG TCTCAGTTCC CCTTCAGCT GAGGACTTCG GAGCTTGTC 2640  
 GGAAGTGGCC CTGCAACTT GCGGGAAGCA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCATG AAAACCTCTC 2760  
 CACCTGGGCC AGGGTTGCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAATA 2820  
 TGCTCAACCC TGTGTCCTGG GCTTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTATAT TTTTTTTTTT AATGCTATCT 2940  
 25 TCAGAACGTT AGAGAAAGTT CTTCAGAAAT GCAGCCAGA GCTGCTGGGC CCACTGGCCG 3000  
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTCT 3060  
 ATACTGAGT TGCCTAGGTT GCCCTTATT TTTTATTTTC CCTGTGTGCT TGCTATAGAT 3120  
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAATTTTTT TATTAAGAA A

**A65 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 35 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)  
 Cellular localization: plasma membrane

40 1 11 21 31 41 51  
 MGLERGPLAS LLLLLQVCNLQ CAASEPCRAV FREAEVTL EA GGAEQEPGQA LGKVFVGCPCG 60  
 QEPALPSTDN DDFTVANGET VQERRSLKER NPLKIPFSKR ILRRHKRDV VAPISVPENG 120  
 45 KGPFPQLNLQ LKSNKDRDTK IYYSITGPGA DSPPEGVFAV EKETGALLLN KPLDREBIK 180  
 YELFGEAVSE NGASVEDPMN ISILVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240  
 DDDDAIYTYN GVVAYSIESQ EPEDFDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300  
 TMDGDGDTT TAVAVVEILD ANDNAEMFDF QKYEARVPER AVGHVQRLT VTDLDAPNSP 360  
 50 AMRATYLLNG GDDGDHFTYT TPESNQGIL TTRKGLDFEA KMQHTLYVEV TNEAPFVLKL 420  
 PSTATIVVE VSDVNEAPVF VEPKVVVEVQ SGIPTEGEPVC VYTAEDPDKE NQKISYRILR 480  
 DEAGWLAMP DSGQVTAVGT LDREDEQFVR NNYEYVNLVA MDNGSPPTTG TGTLLLLTLD 540  
 VNDHGVPFEP RQITICNQSP VRHVLNITDK DLSHSTSPFQ AQLTDDSDIY WTAEVNEBEG 600  
 TVVLSLKKFL KQDTYDVHLS LSEDEGNKQL TVIRATVCDG HGHVETCPGP WRGGFILEVL 660  
 55 GAVLALLFL LNDVLRKK RKIKFPLILP EDDTRDNVFP YGEGGGGEDD QDYDITQLHR 720  
 GLEARFVVVL RNDVATITP TMYRPRPAN PDBIGNPIIE NLKAANTDPT APPYDITLVF 780  
 DYECSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMVGGGEDD

**A66 DNA SEQUENCE**

60 Gene name: ATPase, Ca++ transporting, type 2C, member 1  
 Unigene number: Hs.106778  
 Probeset Accession #: N51919  
 Nucleic Acid Accession #: AF189723  
 65 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51  
 ATGATTCCTG TATTGACATC AAAAAAGCCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60  
 ATTCTCCAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTATAGTCA TAGGCGAGCC 120  
 TTTCTAGGCT GGAATGAGTK TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180  
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTGGCTT CTGCACTCAT CAGTGTTTTA 240  
 ATGATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTATCAGTT 300  
 75 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360  
 CCAGAAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420  
 CAGGTGATGA CAGTTTGCCT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACCTTGTGTT 480  
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAAC GCCTTGTTC 540  
 AAGGTGACAG CTCTTCAGCG AGCTGCAACT AATGGAGATC TTGCATOGAG AAGTAACATT 600  
 80 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTTGTGTGAT TGGAAACAGG 660  
 GAAATATCTG AATTGCGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720  
 CCTCTGAGAG AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGTGATA 780  
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCTCTGA AATGTTTACT 840



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 15  
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 30

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ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTACACAGT 900
ACGCTAGCTTC TTGGTGTATT GAGATGGTGG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960
ATTGTTGAAA CTCTGGGCTG CTGTAATBTG ATTTGTTTCTG ATAAAACTGG AACACTGACG 1020
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
GGAGTTGGCT ATAAATCAAT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTTC 1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
ATGGGCTCTT ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGTCTT 1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTATGA AAGGTGCTTA CGAACAAATA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGACAGACT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACGC 1500
ATGGGCTCAG CGGGACTCAG AGTCTTCTCT TTGCTTCTG GTCCGTGAAT GGGACAGCTG 1560
ACATTCTCTT GCTTGGTGGG AATCATTTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACAACACTCA TTGCTCTCAG AGTATCAATA AAAATGATTA CTGGAGATTTC ACAGGAGACT 1680
GCAGTTGCAA AAGGTGCTTA TCTGGGATTG TATTCACAAA CTTCOCAGTA AGTCTCAGGA 1740
GAAGAATAG ATGCAATGGA TTTTCAGCAG CTTCACAAA TAGTACCAA GGTTCAGTA 1800
TTTTACAGAG GAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACCGT 1860
TCAGTTGTAG CCAAGCAGAG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGTGTCAGAC 1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG AAGGTGCTTA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040
AATAACATTA AAAATTTGCT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACITTA 2100
ATCTCATGGG CTACATTAAT GAACCTTCTT AATCTCTCA ATGCCATGCA GATTTTGTG 2160
ATCAATATTA TTATGGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCTATC GTAAACCTCC TCGCAACTGG AAGACAGCA TTTTGACTAA AAACCTGATA 2280
CTTAAATATC TTGTTCTCAT AATAATCATT GTTTGTGGGA CTTTGTTTGT CTCTCGCGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCA C ATGCTTTGTG 2400
TTTTTTGACA TGTTCATGCT ACTAAGTTC AGATCCAGA CCAAGCTCTG GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACATTA 2520
CTAGTTATTG ACTTTCTCTC GCTTCAGAA GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTTCTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
CTGAAGTAT GA
  
```

**A67 Protein sequence:**

Gene name:

ATPase, Ca++ transporting, type 2C, member 1

Unigene number:

Hs.106778

Probeset Accession #:

N51919

Protein Accession #:

AAF27813

Signal sequence:

none found

Transmembrane domains:

60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878

Pfam domains:

Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C

[744-889]

Cellular Localization: not determined

45  
 50  
 55  
 60

```

1 11 21 31 41 51
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHERRA FGNWNEFDIS EDEPLWKIKYI 60
SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQYRSEK SLEELSKLVP 120
PECHCVREBK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSIDES SLTGTTTPCS 180
KVTAPQPAAT NGOLASRSNI APMGTLVRCG KAGGVVIGTG ENSEFGRVFK MMQAEAPKT 240
ELQKSMIDLGL KQLSFYSEFI IGLIMLVGHL LKGLDILEMT ISVSLAVAAI PEGLEIVVTV 300
TLALGVMRMV KKRRAIVKLLP IVETLGCNV ICSDKTGTLT KNEMTVTHIP TSDGLEHART 360
GVQXNQFQEV IVDGDVVEGF YNPAVERIVE AGCVNDAVI RNNTLMGKPT EGALIALAMK 420
MGLDGLQDDY IRKAEYFPSS EQKNMAVCKV HRTQDRPEI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RDVYQKEKAR MGSAGLEVLA LASGPELQQL TELGLVGIID PFTGVKEAV 540
TTLASAGVSI KMTIGDSQET AVAIALSRLSL YSKTSQSVSG ESIDAMDVQQ LQIVPKVAV 600
PYRASPRHMK KIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGQTGT DVCKEADMI 660
LVDDDFQTIM SAIBEGRGYI NNKKNFVRPQ LSTSLAALTL ISLATGMNFF NFINAMQILM 720
INIIMDGPPA QSLGVSPVDK DVIRKPPRNW KDSILTKNLI LKILVSBIII VGTILFVFWR 780
ELRDNVITPR DTTMTPTCPV PFDMPNALS RSQTKSVFEI GLCSNRMFCY AVLGSIMQQL 840
LVYFPPLQK VFQTESLSIL DLLFLGLTSL SVCIVARLIK KVERSRKIQ KRVSTSSSF 900
LEV
  
```

**A68 DNA SEQUENCE**

Gene name:

bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number:

Hs.170195

Probeset Accession #:

BE616633

Nucleic Acid Accession #:

NM\_001719

Coding sequence:

123-1418 (underlined sequences correspond to start and stop codons)

75  
 80

```

1 11 21 31 41 51
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CTGCCCCCT 60
CTGCCACTCG GGGCGGTGCG GGGCCCGGAGC CCGGAGCCCG GTTAGCGCGT AGAGCCGGCG 120
CGATGCACAT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCTGGGCG CTCTGGGCAC 180
CCCTGTTCCT CTGCGCTTCC GCCCTGGCGG ACTTCAGCCT GGACAAAGAG GTGCACTCGA 240
GCTTCATCCA CGGCGGCTTC CGCAGCCAGG AGCGCGCGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCTAC CGCCCGGCGC CGCACCCTCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGCG GGGCCCGCG 420
GCCAGGGCTT CTCTACCTCC TACAAGGCCG TCTTCAGTAC CCAGGGCGCC CCTCTGGCCA 480
GCTGCAAGTA TAGCAATTTC CTCACGACG CGACATGGT CATGACCTTC GTCAACCTCG 540
TGAACATGTA CAAGGAATTC TTCCACCCAC GCTACCAACA TCGAGAGTTC CGGTTTGATC 600
TTTCCAGAT CCCAGAAGGG GAAGCTGTCA CGGCGCGCGA ATTCCGATC TACAAGGACT 660
  
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5  
10  
15  
20

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ACATCCGGG  ACGCTTCGAC  AATGAGACGT  TCCGGATCAG  CGTTTATCAG  GTGCTCCAGG  720
AGCACTTGGG  CAGGGAATCG  GATCTCTTCC  TGCTCGACAG  CCGTACCCTC  TGGGCTCCGG  780
AGGAGGGGCTG  GCTGGTGTIT  GACATCAGAG  CCACCAGCAA  CCACTGGGTG  GTCAATCCGC  840
GGCACAACCT  GGGCCCTGCAG  CTCTCGGTGG  AGACGCTGGA  TGGGCAGAGC  ATCAACCCCA  900
AGTTGGGGGG  CCGATTGGG  CGGCACGGGC  CCCAGAACAA  GCAGCCCTTC  ATGGTGGCTT  960
TCCTCAAGGC  CACGGAGGTC  CACTTCGGCA  GCATCCGGTC  CACGGGGAGC  AAACAGGCGA  1020
GCCAGAACCG  CTCGAAGACG  CCCAAGAACC  AGGAAGCCCT  GCGGATGGCC  AACGTGGCAG  1080
AGAACAGCAG  CAGCGACCAG  AGGCAGGCCT  GTAAGAAGCA  CGAGCTGTAT  GTCAGCTTCC  1140
GAGACCTGGG  CTGGCAGGAC  TGGATCATCG  CGCTGAAGG  CTACGCGGCC  TACTACTGTG  1200
AGGGGGAGTG  TGGCTTCCCT  CTGAACCTCT  ACATGAACGC  CACCAACCA  GCCATCGTGC  1260
AGACGCTGGT  CCACTTCATC  AACCGGAAA  OGGTGCCAA  GCCCTGCTGT  GCGCCACGCG  1320
AGCTCAATGC  CATCTCCGTC  CTCTACTTCG  ATGACAGCTC  CAACGTCATC  CTGAAGAAAT  1380
ACAGAAACAT  GGTGGTCCGG  GCGTGTGGCT  GCCACTAGCT  CCTCCGAGAA  TTCAGACCTT  1440
TTGGGGCCAA  GTTTTCTCG  ATCTCTCATT  GCTCGCCTTG  GCCAGGAACC  AGCAGACCAA  1500
CTGCGCTTTG  TTAGACCTTC  CCCTCCCTAT  CCCCACTTT  AAAGGTGTGA  GAGTATTAGG  1560
AAACATGAGC  AGCATATGTC  TTTTGATCAG  TTTTTCAGTG  GCAGCATCCA  ATGAACAGA  1620
TCCTACAGC  TGTGACGCA  AAACCTAGCA  GGAAGAAAA  ACAAACGATA  AAGAAAAATG  1680
GCCGGGCCAG  GTCATTGGCT  GGGAGGTCTC  AGCCATGCAC  GGAATGTTT  CCAGAGGTAA  1740
TTATGAGCGC  CTACCAAGCA  GGCCACCCAG  CCGTGGGAGG  AAGGGGGCGT  GGCAGGGGGT  1800
GGGCACATTG  GTGCTGTGTC  GAAAGGAAAA  TTGACCCGGA  AGTTCTGTGA  ATAAATGTCA  1860
CAATAAAACG  AATGAATG

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25  
30

A69 Protein sequence:  
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195  
Probeset Accession #: BE616633  
Protein Accession #: NP\_001710.1  
Signal sequence: 1-30  
Pfam domains: TGFb\_propeptide [37-281]  
Transmembrane domains: none found  
Cellular Localization: secreted

35  
40  
45

```

1 11 21 31 41 51
| | | | |
MHVRSRLRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQRRLS 60
ILGLEHRRPRP HLQCKHNSAP MFMLDLNLYM AVEBGGGPGG QGPSYFYKAV PSTQGPPLAS 120
LQDSHFLLTDA DMVMSFVNLV EHDKEFFHPR YHRRFRFDL SKIPEGEAVT AAEFRITYDY 180
IREREDNETF RLSVYQVLQE HLGREEDLEF LDRSTLWASE EGWLVPDITA TSNHWVWVPR 240
HNLLQLQSVL TLDGQSLNPK LAGLIGRHGP QNKQPFHVAF FKATEVHFRS IRSTGSKQRS 300
QMRSETPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSRF DLGWQDWIIA PEGYAAYYCE 360
GECAPFLMSY MNATNHAIVQ TLVVEFINPET VPKPCCAPTQ LNAISLVLYSD DSSNVILKKY 420
KRMVVRACGC H

```

Cervical

50

A70 DNA sequence  
Gene name: bone morphogenetic protein receptor IB (ALK-6)  
Unigene number: Hs.87223  
Probeset Accession #: AA250737  
Nucleic Acid Accession #: NM\_001203  
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

55  
60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
CGCGGGGCGC GGAGTCGGCG GGGCCCTCGCG GGACGCGGGC AGTGCAGAGA CCGCGGCGCT 60
GAGGACGCGG GAGCGCGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
GTGAAGAGAA AGGAAGATCA TTTCATGCCCT TGTGATATAA GGTTCAGACT TCTGCTGATT 180
CATACCAATT TGGCTCTGAG CTATGACAAAG AGAGGAACA AAAAGTTAA CTACAGCC 240
TGCCATAAGT GAGAAGCAAA CTCTCTGAT AACATGCTTT TGGGAGTGC AGGAAAATTA 300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCC TCCAAAGGTC 360
TTGCTTGTGA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
GACGGATATT GTTTCAGAT GATAGAAGAG GATGACTCTG GGTGCTCTGT GGTCACTTCT 480
GGTTGCTTAG GACTAGAAGG CTCAGATTTT CAGTGTGGGG ACCTCCCAT TOCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAANGACCT ACACCTTACA 600
CTGCCCTCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACACAG GGCTTTACTT 660
ATATCTGAGA CTGTCTGTAG TTTCCTCTTG GTCCCTATCA TATTATTTTG TTACTTCCGG 720
TATAAAGAC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
ATTCTCTCTG GAGAAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
TCAGGCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTGAGT GGTGAACAG 900
ATTGGAAGAG TGTGCTATGG GGAAGTTTGG ATGGGAAAGT GGCCTGGCBA AAGGTAGCT 960
GTGAAGATGT TCTTCAACAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGACA 1080
GGGTCTCTGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGTTTC CCTTTATGAT 1140
TATCTGAAGT CCAACACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTC 1200
AGTGGCTTAT GTCTATTACA CACAGAAATC TTAGTACTC AAGGCAAAOC AGCAATTGCC 1260
CATCGAGTC TGAAAGTAA AAACATTCTG GTGAAGAAA ATGGAACITG CTGTATTGCT 1320
GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGAGAT ACCACCTAAC 1380
ACTCGAGTTG GCACCAACG CTATATGCCCT CCAGAGAGT TGGACGAGAG CTGAAACAGA 1440
AATCACTTCC AGTCTTATAC CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
GTTGCTAGGA GATGTGATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620

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CGCCCCCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAA 1740  
 ACACITGCCA AATGTCCAGA GTCCAGGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800  
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCCAA AGACATCAA 1860  
 TAAGCATCCA CAGTACAGC CTGAACATC GTCCCTGCTTC CCAGTGGGT CAGACCTCAC 1920  
 CTTTCAGGA GCGACCTGGG CAAAGACAGA GAAGCTCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTTGTG GCGGAGAAA CCGTTGGTA ACTTGTCAA GATATGATGC AT

**A71 Protein sequence**  
 Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MLRSAGKLN VTKKEDGES TAPTPRKVL RCKCHHCPE DSVNNICSTD GYCFMIEED 60  
 DSGLPVVTSG CLGLEGSDFQ CRDTPIDRQ RSIECCERN ECKNDLHPTL PFLNDRFVD 120  
 GPIHRRALLI SVTVCSLLLV LIILFCYFRY KRQETPRYS IGLEQDETYI PPGESLFDLI 180  
 EQSQSGSGS GLPLLVQRTI AKQIQMVQKI GKGRYGEVNM GKNRGEKVAV KVPFTTEAS 240  
 WPRETIYDT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSSVS GLCHLHTEIF STQCKPALAH RDLKSKNILV KKNGTCCIAH LGLAVKFISD 360  
 INEVDLPENT RVGTRKRYMPP EVLDESINRN HFQSYIMADM YSFGILILNEV ARRCVSGGIV 420  
 EBYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECAHNHPAS 480  
 RLTALEVRKKT LAKMSSESQDI KL

**Bladder****A72 DNA SEQUENCE**

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 ATGTTACAGG ATCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60  
 AAACCCCTTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120  
 CTGAGCTTGG CGAGTATCAT CATTTGTGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180  
 TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240  
 CTGAGCTGTC CTTGGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CBAAGGGCCT 300  
 GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGGGCCACA 360  
 GGBAATCGST TCTTCGCTG TTTGAGAAC TTACAGAGG CTCTGCTGGA GACAGCCTGT 420  
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG OCCAGACCGA 480  
 GATCTGGATG TTGTTGAAT CACAGAAAC AGCCAGAGAG TTGCGATGCG GAACCTCAAT 540  
 GGGCCCTGTC TCTCAGGCTC CTTGGTCTCC CTGCACGTGC TTGCTGTGCG GAAGAGCCTG 600  
 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660  
 AGCATCCAGT AGCAACAACA GCACGTCTGT GGAGGGAGCA TCCTGACCCC CCACCTGGGTG 720  
 CTACAGGCGG GCTACAGCAG CAAACCCACT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780  
 GGCTCAGACA AACTGGGCGG CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840  
 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCCCTCTCA TGAAGCTGCA GTTCCCACTC 900  
 ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960  
 GCCACCCAC TCTGATCAT TGGATGGGGC TTACAGAGC AGAATGGAGG GAAGATGTCT 1020  
 GACATACTGC TGCAGCGGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080  
 GGTACACAGG GGGAGTCAC CGAGAAGATG ATGTGTGCGG GCATCCCGGA AGGGGGTGTG 1140  
 GACACCTGCG AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200  
 GTGGCATCG TTAGCTGGGG CTATGCTGCG GGGGGCCCGA GCACCCGAG AGTATACACT 1260  
 AAGGTCTCAG CTAATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

**A73 Protein sequence:**

Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPc domain: 204-429  
 Cellular Localization: plasma membrane/ER

1 11 21 31 41 51  
 MLQDFSDQPF LNSLDVKPLR KPRIPMETFR KVGIPPIIAL LSLASIIIVV VLIKVILDKY 60  
 YFLOGQPLRF IPKQKLCQGE LDCPLGEDEE HCVKSFPEGR AVAVRLSKDR STLQVLDSAT 120

GNWFSACFDN FTEALARTAC RQMGYSEKPT FRAVEIGPDQ DLDVVEITEN SQELMRNRS 180  
 GPCLSGSLVS LHCLACGKSL KTRPVVGEEZ ASVDSWFWQV SIQYDKQHVC GGSILDPHWV 240  
 LTAHCFRKH TIVFMKVRRA GSKLGSFSPS LAVAKIIIE FNFMYPRDND IALMKLQFPL 300  
 TFSGTVRPIC LFFFDSELTAT ATPLWIIGWG FTQNGGKMS DILLQASVQV IDSTRCNADD 360  
 AVQGEVTERK MCAGIPEGGV DTCQGDGGP LMYQSDQNHV VGIVSWGYGC GSPSTPGVYT 420  
 KVSAYLNWIY NVWKAL

**A74 DNA SEQUENCE**

Gene name: ESTs, Weakly similar to CGH7L collagen alpha 1(III) chain precursor [H.sapiens]  
 Unigene number: Hs.19322  
 Probeset Accession #: AA088458  
 Nucleic Acid Accession #: AA088458  
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
CTAGAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
GCCGCGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
CTGCGCCAGA GCAGAGCCAG GCGGACTTT GGGGCTGCAG GAGAGCCCGG CCCACTGGGG 240
CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTTGG GGGAGCTGCT GGCTGCAGCC 300
TGTGCGAGCC GGGCCCTGCC CCGTCTCTCC TCCGGGCCCC CCTGCCCTGC CCGTACGCTC 360
ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCATGCG TGAAGGAGCA GAACGAGCTC 420
CTCACCCAGG AGGTGACGCA GAGAGTGGAG CGCATCACGC AGCTGGAGCA GGAAGAGTGG 480
GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCGCTGAGCC AGCAGGACGG GGGACCTCTG 540
GATTTCACCT TCATCTAGTC CTGTGGGGCC GCGTGGGGCC CCAGGGCCAG CCGTGGCACTG 600
AGCCCTTCTGA GGGTGGGGCC CCGATCAGAC CCGCTCTCTC TGGCTGGAGA CCCCGGGCAG 660
GCCGAGGACG AGTCCCGGAG TGGGCGGCTT CCGCGGCCCC TTGCCAGATG GGCTCCCGAC 720
GCTTGGCCCC CGCTGGTCCC GCGACCGAGC GCTTGAAGTC GTTTGGCTTC TGCTTGTGTG 780
ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCG CTAAGTACTG CCGCTGTCTG 840
TGGACAGTGG GGTACCCCTC CATGAGTTAG GGTCCCGCCG TTTCAGCGGG TGCGGCCCTG 900
GGTCCCATCT TCAGGGAAG GCACTGCCCA GCGCAGGCTG CACTTCCAAC AACGGGACAG 960
AGAGGGGGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GAGACGGGCT 1080
GTAAGCGGGG GGTGCTGTGC TGGCTGGGGA GCGCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
CTGGCCAAAG CTGAGGAGCC CTGGCTGCG CCGATCGGCA GCGCGGCTGG GCGAGAGCTT 1200
GGGCTGTCTG TGCTCTCCAC AGACCCCTGG GTGATGGCTT TCCCGCTCTT GCGCGGGAGG 1260
TTGCCCCAGC TTGAGTCCCA CACAACATCC TGTGAGCTGG GCTCCCGAGG AGGGCCCCCA 1320
GACAGCTCCC AGCTCAGTCA TAGGCAAGGC CTGTTTCCCC GCACTCAGGA TTTCGAAGGC 1380
CTGGGCTCTT GCTCAACCCC CTTTGTCTTC ACGCCCGACC TGTCCCGAGG TTTCAGCTGG 1440
GAGAGGGCAC CTCCCTCAGC CARGGAAAGC GAGAACCCCC AGGTACAGG AGGAGGCTGG 1500
GGCAGGTCCC CTGGGTGTC ACTCCCTCAG CCGCTGCCCA GCGCCACTCC CGCTGGTGGT 1560
GGAGTAGGCA CTGGTGGGG GCGCTCTCTC AGCCCAAGCT GAGGGGTCCC AGTGTCAACA 1620
GAACCGAGGG CAGCGCAAG GCATGATGG GTTCTGCAGC CAGGGGCCCC CGATGCGGGG 1680
TCASTGTGTG TGGGGCGCAG GCGCTCCGAT GCGGGGTCAG TGCTTGGGGG GCGCAGGGCC 1740
CCCGATGGCG GGTCAAGTGG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT 1800
ACACTGTCCC ACAGAGCACC TGTCTCAGAG GAGGGGCCCC GGCAGGACGC GTGGCAACTC 1860
CCTTCCGAGC CCGAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920
TGCTGCACCT GGTCTCAGG GGTGTCCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980
GCCCTCTAC CCGAAGATG GAGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCTCTG 2040
ACCTCTCTGG CAGGAAGGG TGCAAGTCTT GAGGGCTCTG GCGCCACAGC CCCAGCACCC 2100
AGGTGGACTG CAGCGCAGT GGTGGGCCAG TGGCAGCCAG GGAGAAAGCC CCGCTCAGCA 2160
GGCTGGGGTC TGCCACCCAG GCGCTCCCA CGTCTGCTT TGAGGGTGCC TGCCATGCCC 2220
TGGGGGATCC CCGTATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
GGTGAATCTA TCAGGAGACC GCGCCATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340
GAGACAGGCT GGCACCTCGG GAAAAACTGC CTCTCAGCTT TGCTGTCTGG TGCAAGGTGA 2400
AAAGAAATAG GTCTCTCCAG TTTCAGCTT GAAATCAGGC TAGTGTAGTG CCGTGGAGAC 2460
CAGCAGGGGA GAATTTAAG GCGCCGGCTG GCAGGCTCTA GGTGGCTGGC AGAGGCACAT 2520
GCAGACCGTG CCGTGGAGCT GCGCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
GAGCAGCGTC CCGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCGAGT ACATACAGCT 2640
GCGTGACAC TGATGATACA CCGGAAATG TCTCAGGATG TTGAATGTG TCTTGGGGG 2700
CAGAAATGTC CCGAGTTGAG AATCTGCCCC AGAGGAACAC ACCACACCA GCGCTCAGGA 2760
TTTTGTGTTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGCTTACGCG 2820
CTGGAATCCC AGCACTTGA GCGCAGGAGT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
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**A75 DNA SEQUENCE**

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor  
 Unigene number: Hs.227948  
 Probeset Accession #: AB035089  
 Nucleic Acid Accession #: AB035089  
 Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

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25 A76 Protein sequence:  
 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor  
 Unigene number: Hs.227948  
 Probeset Accession #: AB035089  
 Protein Accession #: BAB21525  
 30 Signal sequence: none found  
 Transmembrane domains: none found  
 Serine Proteinase Inhibitor domain: 13-390  
 Cellular Localization: secreted

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45 A77 DNA SEQUENCE  
 Gene name: hypothetical protein FLJ13459  
 Unigene number: none found  
 Probeset Accession #: XM\_047266  
 Nucleic Acid Accession #: XM\_047266  
 50 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 55 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAGTGG CTGGGATTAC AGGTGTGAGC 60  
 CACCATGCCA GGCCTCTCTA ACCCTCTCAA GTCTGTTTTC TCATCTGCAA AACAGAGGTA 120  
 ATAGATCAG TATCTTCTTA ATGGAAGCAC CTGGACTACA TTTTCTTCAT TCATTGTTAT 180  
 CATAATGAG GACTAAAGCTG TCTCCGTTGG GGAGTTTGA ACCTAGACCT CATGTCTTCA 240  
 TGACGTCAIC ACTGCCCCAG GCCCAGCTGT GTCCCTACAC CAGCCCCAGC TGACGCATCT 300  
 60 TCTTTTCTG CCGTAGAGAA TGGTTACAT GCTTGGCGTG ATGCATCTGT GCCTTGCAG 360  
 ATCCTGGCGG GGCTGTGCCA AGCTGTGGC CTCCCTGCCC CTGAATACCG AGCCGCTGCT 420  
 GTCAAGGTGG GCACCAAGT CTCTCTGACA CCACCGAGGA CCTTCCCTCC AGGERTCTCT 480  
 TCACATGTGG ATTGACATCT TTCTCAAGA TGTGCTGCT CCACCCCCAG TTGACATCAA 540  
 GCCTCGGCAG CCAATCAGCT ATGAGCTCAG AGTTGTCTAT TGAACACCG AGGATGTGCT 600  
 65 TCTGGATGAC GAGATCCAC TCACCGGAGA GATGTGAGT GACATCTATG TGAAGAGCTG 660  
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGACGTT CACTTCAACT CCTGACTCG 720  
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT CCGCTTGAC TACCTGCCCA CGGAGCGGGA 780  
 GGTGAGCGTC TGGCGCAGGT CTGGACCTTT TGCCCTGGAG GAGGCGAGT TCCGCGAGCC 840  
 TGCAGTGTCT GTCTGTCAGG TCTGGGACTA TGACCGCATC TCTGCCAATG ACTTCTCTTG 900  
 70 ATCCCTGGAG TTGCAGCTAC CAGACATGGT GCGTGGGGCC CGGGGCCDGG AGCTCTGCTC 960  
 TGTGAGCTB GCGCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTGGCT GCGCGCGCT 1020  
 GAGGGGCTGG TGGCGGTAG TGAAGCTGAA GAGAGCAGAG GACGTGGAGC GGGAGGCGCA 1080  
 GAGGCTCTAG ATGAGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCAGAGGA 1140  
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCTTC ACGGCAAGG TGGAGGCAGA 1200  
 75 GTTGTAGCTG CTGACTGTGG AGGAGGCCGA GAAACGGCCA GTGGGGAAGG GCGGGAAGCA 1260  
 GCTGAGCTC GCGAGAACAC CCAGCGGCC CAAACTTCC TTCAACTGGT TTGTGAACCC 1320  
 GCTGAAGAAC TTGTCTTCT TCATCTGGCG CCGGTACTGG GGCACCTTGG TGCTGCTGCT 1380  
 ACTGTGTGCT CACACGCTCT TCTCTCTCT GATCTCTAC ACCATCCCTG GCGAGATCAG 1440  
 CCAGGTCAIC TTCCGTCCCC TCACAAAGTG ACTCTGCTG ACCTTGGACA CTCACCCAGG 1500  
 80 GTGCCAACCC TTCAATGCTT GCTCCTGAAA GTCTTTCTTA CCCATGTGAG CTACCCCGAG 1560  
 GTCTAGTGCT TCCCTGGAAT AAACCTATCA CAGCCACTG

A78 Protein sequence:  
 Gene name: hypothetical protein FLJ13459

Unigene number: none found  
 Probeset Accession #: XM\_047266  
 Protein Accession #: XP\_047266  
 Signal sequence: none found  
 Transmembrane domains: 291-313  
 C2 domain: 27-86  
 Cellular Localization: plasma membrane / ER

```

1      11      21      31      41      51
|      |      |      |      |      |
MMIDIFPDQDV PAPPFVDIKP RQPISYELRV VIWNTSDVVL DDENPLTGEM SSDIYVKSVM 60
KGLEHDKQET DVHFNLSLTGE GNFWNRFVFR FDYLPTEREV SVWRRSGPPA LEEAEFRQPA 120
VLVLQVMDYD RISANDFLGS LELQLPDMVR GARGPELCSV QLARNAGAPR CNLPRCRLR 180
GWWPVVLKE AEDVEREAQE AQAGKKRKQ RRRKGRPEDL EFTDMGGNVY ILTGKVEAEF 240
ELLTVEBAEK RVPVGRKQF EPLEKPSRFK TSPNWFVNPL KTFVFFIWR RYWRILVLLL 300
VLLTVFLLLV FYTIPQIISQ VIFRPLHK

```

#### A79 DNA SEQUENCE

Gene name: Homo sapiens mRNA; cDNA DKFp434K0322 (from clone DKFp434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Nucleic Acid Accession #: AL137708  
 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCCCTTCTGT CTGTCTCCTT GCTCTGCCCC 120
AGACTGGGGG GCTGCGAGAG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
ATGGCCTGGG CTGGGCCCTT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCGAGG 240
CTCTCTGTGG CAAGGAGAGG GAGGCCCCAA TGTGAGGAA CAGAGTCTCC TGGCTGGCTG 300
CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCTG 360
GGGTCACTGT AGGCCCATG TAGCACCTTG GTTCCCTGCG CTGTAGGTGA CAGGAGCCAG 420
CCGAGCCAGG TGCTGCTCCCT CCCAGGCCCT TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480
CGCCCGCCCC ACCTTCCCTTC CCACCCACAT GCCGAAGGCT GGCAGGCAG GCAGGTGGAC 540
GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGGAAATGTC TGGCGCTCC CAGCTGCACC 600
CTGCCCTTAC CTCCACCTCA TCCTCAGGCG CTGCGGCCCT GAGCCCTGCG 660
CAGGAATGCA CCTTAGCCCC AGGCCCTGCT AGTGAGCTCC GCGCAGAGCC AGCCCTGTCT 720
CTCCCGCCAT GACCTGCGAG ACCCTCTCTG GCTTCCAGT TCCGTGGGGT TGCACTGAA 780
ATGCTCCACC TGCAATGCTG GCAAACCATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGCT 840
AGAGGCAAGG AAGTGAATGG ACCGCAAGAG TGAGACCCCC AGGATGAGA TGGGACCCCC 900
AGGCAAGGCC GCGCTCCAGG GCGCCAGGAG AGAGAAGCAG GAGGGGAGAG AGCTTCTCTG 960
TGGAGGAGCG ATCTACAGT GGGGCGAAG GTGCTCTGAG GTCCGGTAA GGCAGGGACT 1020
AGGCTGCCCA GGCCTGCTCG GCTTGGCTGG GCTTGGGGCG TGCTGGAGG TGGCTGGGAG 1080
GCTGGGCTGG GGCAGCTAAG CTGGAGCTTT GGCAGGGTCC CAGAGCTTCC CTCCCTTCAG 1140
CTTCTGTCTG CACAGAACCC TGCCCTCTGG CCACCCCTGT CTGCTCTCTT GCCCTGGCAG 1200
ACCCAGCACT GGTGCTGTGT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC 1260
TCCAGCTGTA CCCAGCTTCC TGGGCGCTCT CTCCAAACC AGCAGGTAG AAGATGAGGG 1320
CACCAAGCAG TCTCTCCAG TGCCCGCGCC CCAGCTGCA CCACAGCTAT ACCTGGGCTT 1380
ATTCCAGAGC TTGTGCGCGG GACCCCTGTG GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440
GATAACCCAG CCAGATGGGG GCTGCACTGT TCCACAGATG CACTCAGCCT GGCCTTACCC 1500
CAGAGGCCCT GCTGGGCTCT CATTCGCGCG GCGCTTGGCG GCGGCGTCTT CTCTGCTTCC 1560
TGCTCTCTCT GTGCTGCTGT CTGCTGCTGT GCGCGCCACA GGAAGAGGCC CAGGGACAA 1620
GAGTCCGTGG GTCTGGGCGG TGCCCGCGCG ACCACCAACA CCCACTGCTT GTGGGCGGCG 1680
TCCTGTCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGCGAGCGA 1740
GGGAGTTTCA GCGCCAGGGA TGTTTAAACC CCACAGAGG CAGGGGCTTG AGGACCTTCC 1800
TGGCAGGAAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCTAT 1860
GGGCGGAGGG GAGCCACAGC GGGTCTCTGA GGAAGGCAGG GGGTACCCCA GATGCCAGGT 1920
TTTGGGTGGG TTTGGGCGGT CTCACAGAGC GAAGCCGAGC ATTGTGCTCT GTTGGGTGGC 1980
CTGGCTTGA GCGGGGGGGT CTGACCCAT GTCAITGCAAG GGTGCGCCGG GAGCCAGGGG 2040
CTCTGATGAG GCATGATGTC AGCACCCTCT GCCCTTGTTC CCAACTCACT CAGGTGCAA 2100
CCTGATGAG ATGGCCTTGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCTTCAAG 2160
CTCTCCCTGG AGTTGCACTT TGAAGCCAG GAGGTGAAGG GCGCGCTGCG GCAGGACCA 2220
CGGTTCTGG AGTTTCCGGA AAGGGTGAAG GGGGAAGGGC AGACCCCATG CCTGGGTGG 2280
TGGGAGCTG ACAGGGCAGG GCGCTTGGG TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340
GTGGGCTTGA GCGAGGCGAG CGACCTGAGG CTTGGGGGCA CCGTGGACCC CTATGCCCG 2400
GTCAGGTTCT CCACCCAGGC CGACACAGA CATGAGACAA AAGTGCACCG AGGCACGCTC 2460
TGCCCGTGT TTGACGAGAC CTGCTGCTTC CAGGTGAGTC AGGATGCTC GGTCTGGTGG 2520
GCTTGAAGCG GTGATGGGC CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGTCTGGGCA 2580
GCTGGGTGG CTTGAGCTAG GGCAGCAGGG CTTGGCTCAC GCGCTGCTCT CAGATCCCG 2640
AGGCGAGGCT GCGAGGGGCC ACCCTGCAAG TGCAGCTTTT CAATTTCAAG CGCTTCTGG 2700
GGCATGAGCC GCTCAGGCGG CTCCGTCTGC CACTGGGCAC CGTGGATCTG CAGCATGTT 2760
TGGGCACTG GTACCTGCTG GCGCGCGCGG CTGCCACTCA GGTGAGGTGC TGGTCAACC 2820
GCCACAGCCC AAGGCAGGC TGGCAGGGAC CCGCCCTAT GGGCCATCGG AAGACAGGC 2880
CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAATCTCG CCAGATCAC CCTCCCGGG 2940
TGAAGCCCTT CTGCTGCGCC ACAGCCCGAG CAGGTGGGG AGCTGTGCTT CTCTCTCGG 3000
TAGTGCCCA TACTAGGCGG GCTGACCGTG GTGGTCTGG AGGCTCGAGG CTGCGTCCA 3060
GGAATTCGAG AGCCCTAGCT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA TGGGAGAGG 3120
AGAAAGAAA CCAACAAAAA GGGCACGGCG GCCCCTACT TCAATGAGGC CTTCACCTTC 3180
CTGGTCCCTT TCAGCTAGGT CCAGATGTC GACCTGGTGC TGGCTGTCTG GAGCCGCGC 3240
CTGCCCTCC GAAGTGAAGC GTGAGGCAAG GTGCACTGG GTGCCCGGGC CTGGGCGAG 3300

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CCCTGACAG ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGGCCATTGC CCAGCGGCAC 3360  
 CCCTGCGGC CAGCCAGGGA GGTGGACCGC ATGCTGGCCC TGCAGCCCG CCTTGGCCCT 3420  
 CGCTTGCCT TGCCTCATC CTGAATGCAC CACATGCTC TGTCTCCCG CTGAGCCAG 3480  
 GCCTTGGCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCTT GCC

**A80 Protein sequence:**

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)  
 Unigene number: Hs.161031  
 Probeset Accession #: AL137708  
 Protein Accession #: CAB70885  
 Signal sequence: none found  
 Transmembrane domains: 69-85  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MGHPVPSPSA PAPAGTTAIF GLIPDLVAGT FCELWDSQEG CGDNPAKNGL QLSTDAISLA 60  
 STGPRWALI AGALAAGVLL VSCLLCAACC CRRHRKIKPR DKESVGLGSA RGTITTHLVR 120  
 SGLLTQSRE GLKSLQSPG QRGEFSPRDG LTPTEAGR

**A81 DNA SEQUENCE**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Nucleic Acid Accession #: X63629  
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51  
 | | | | |  
 GCGGAACACC GGCCTGCCCT CGCGGCAGCT GCCTCAGCCC TCTCTCTGCA GCCATGGGGC 60  
 TCCCTCGTGG ACCTCTCGCG TCTCTCTCC TTCTCCAGGT TTCTTGGCTG CAGTGGCGCG 120  
 CCTCCGAGCC GTCCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180  
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTTCAT GGGCTGCCCT GGGCAAGAGC 240  
 CAGCTTCGTT TAGCAGTGTAT AATGATGACT TCACTGTGGG GAATGGCGAG ACAGTCCAGG 300  
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCGATCCAAA CGTATCTTAC 360  
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAT GGCAGGGGTC 420  
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480  
 ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAAG 540  
 ABACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GAGAGATTGC AAGTATGAGC 600  
 TCTTTGGCCA CGCTGTGTCA GAGAAATGGT CCTCAGTGGG GAGCCCATG AACATCTCCA 660  
 TCATCGTAC CGACCAAGT GACCAACAGC CCAAGTTTAC CAGGACACC TTCCGAGGGA 720  
 GTGTCTTAGA GAGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780  
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840  
 AGGACCCACA CGTCAATTC ACCCGAGCAC AGGCAACATC AGCGTCATCT 900  
 CCAGTGGGCT GGCAGCGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960  
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GAGATCTCTT GATGCCAATG 1020  
 ACAATGCTCC CATGTTTGGC CCGAGAAAGT ACGAGGCCCA TGTGCTTGAAG AATGCAGTGG 1080  
 GCGATGAGGT GCGAGAGGCT AGCGTCACTG ATCTGGACGC CCGCAACTCA CCAGCGTGGC 1140  
 GTGCCACTTA CCTTATCATG GCGGTGAGC ACAGGGACCA TTTTACCATC ACCACCCACC 1200  
 CTGAGAGCAA CCGGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAAG GCCAAAACT 1260  
 AGCACACCTC GTACGTGAAA GTGACCAAGC AGGCCCTTTT TGTGCTGAAG CTCCCAACT 1320  
 CCACAGCCAC CATAGTGGTC CAGGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380  
 CTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GAGGCTGTG TGTGTCTACA 1440  
 CTGCAAGAA CCGCAACAAG GAGAATCAAA AGATCAGCTA CGCATCTCTG AAGAGACCCAG 1500  
 CAGGGTGGCT AGCCATGGAC CAGACAGTGG GCGAGGTCAAC AGCTGTGGGC ACCCTCGACC 1560  
 GTGAGGATGA GCATTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGACA 1620  
 ATGGAAGCCG TCCCAACACT GGCACGGGAA CCTTCTGCTT AACACTGATT GATGTCAAG 1680  
 ACCATGGCCC AGTCCCTGAG CCGCGTCAGA TCACCATCTG CAACCAAGC CCGTGTGGCC 1740  
 ACGTGTCTGA CATCAAGGAC AAGGACCTGT CTCCCAACAC CTCCCTTTTC CAGGCCAGC 1800  
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA GAGGAGAGGT GACACAGTGG 1860  
 TCTTGTCCCT GAAGAAGTTC CTGAGCAGG ATACATATGA CGTGCACCTT TCTCTCTCTG 1920  
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCGGGGCCAC TGTGTGGCAG TGCCATGGCC 1980  
 ATGTGAAAC CTGCTCTGGA CCTGGGAAG GAGGTTTCAT CTTCCCTGTG CTGGGGCTG 2040  
 TCTTGGCTCT GCTGTCTCTC CTGCTGGTGC TGTCTTTGTT GGTGAGAAAG AAGCGGAAGA 2100  
 TCAAGAGCT CCTCTACTC CCAGAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160  
 AAGAGGGGGG TGGCGAAGAG GACCAAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220  
 AGGCCAGGCC GAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280  
 TGTACCGTCC TAGGCGAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340  
 AGGCGGCTAA CACAGACCCC ACAGCCCGGC CCTAAGACAC CCTCTTGGTG TTGACTATG 2400  
 AGGGCAGCGG CTCCAGACGC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460  
 ACCAGATTA AGATTATCTG AACGAGTGGG CGAGCCGCTT CAAGAAGCTG GCAAGCATGT 2520  
 ACGGTGGCGG GAGGAGCAGC TGGCGGGCCT GCGTGCAGGG CTGGGGACCA AAGTTCAGGC 2580  
 CACAGAGCAT CTCCAGAGGG TCTCAGTTCC CCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640  
 GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700  
 TCTTAGCCT TTAGAGATGG AGGAATGTGG GCAGTTTGAAC TTGACGACTG AAAACCTCTC 2760  
 CACCTGGGGC AGGGTTGCTT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820  
 TGCTCAAOCC TGTGTCTCTG GCTTGGGCTT GCTGTGACTG ACCTACAGTG GACTTCTCT 2880  
 CTGGAATGGA ACCTTCTTAG GCTTCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940  
 TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCGG 3000  
 TCTCTGATTT CTGGTTTCCA GACCCCAATG OCTCCCATTC GAGTGGATCT CTGGTTTCT 3060  
 ATACTGATGT GCGCTAGGTT GCGCTTATT TTTTATTTC OCTGTGGGT TGCTATAGAT 3120  
 GAAGGGTGAAG GACAATCGTG TATATGTACT AGAAGTTTTT TATTAAGAA A

**A82 Protein sequence:**

Gene name: Cadherin 3, P-cadherin (placental)  
 Unigene number: Hs.2877  
 Probeset Accession #: X63629  
 Protein Accession #: CAA45177  
 Signal sequence: 1-24  
 Transmembrane domain: 659-675 (second underlined sequence)  
 Cellular localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MGLPRGPLAS LLLQLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
    QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKTFPSKR ILRRHKRDWV VAPISVPENG 120
    KGFFPQRINQ LKSNKORDYK IFYSITGPGA DSPFEGVFAV EKETGMWLLN KPLDREBIK 180
    YELFGHAVSE NGASVEDFMN ISIIVTQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
    DEDDAIYTYN GVVAISHSQ EPKDPHDLMF TIRRTGTIS VISSGLDREK VPBYTLTIQA 300
    TDMDGDSITT TAVAVVILLD ANDNAPMFDQ QKYBAHVPEH AVGEHVQRLT VTDLDAFNSP 360
    ANRATYLMG GDDGDHFTIT THPESNQGIL TTRKGLDPEA KNQHTLYEVV TNEAPFVLKL 420
    PTSTATIVVH VEDVNEAFVF VFPKVVVEVQ EGLTGEPCVC VYTAEDPDKE NQKLSYRILR 480
    DPAGWLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540
    VNDHGVPEEP RQITICNQSP VRHVLANITDK DLSPTSPFQ AQIATDDSDIY WTAEVNEBGD 600
    TVVL6LKKFL RQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGVETCPGP WKGGFILPVL 660
    GAVLALLPLL LVLLLVLRKK RKIKEPLLLP EDDTRDNVYF YGEGGGGEED QDYDITQLHR 720
    GLEARPEVVL RNDVAPTIIP TMYRPRPAN FDEIGNFILE NLKAANTDPT APPYDTLLVF 780
    DYEGSGSDAA SLSSLTSAS DQDQDYDYLN EWGSRFKILA DMVGGGEDD
  
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**A83 DNA SEQUENCE**

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Probeset Accession #: F07953  
 Nucleic Acid Accession #: NM\_016334  
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCCAGCGTG CTGTGGCCTC 60
    GGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTACACTTC GCCATGAGTT TCCTGATCGA 120
    CTCACGATC ATGATTACCT CCCAAACT ATTTTGTGA TTGGGTGGC TTTCTTCAT 180
    GCGCAATGG TTTAAGACT ATGAGATACG TCAGTATGTT GTACASGGA TCCTCTCGT 240
    GAGTTTGCA TTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
    GAATAGCAGC TCCCGTTATT TTCACGGA AAATGAACCTG TCGTAATTC TGCTGATCCT 360
    GGTITTCATG GTGCCCTTTT ACATGSCCTA TTTTATGTG AGCAATATCC GACTACTGCA 420
    TAAACAACGA CCGCTTTTTC CCGTCTCTCT ATGCGTGACC TTTATGTATT TCTTCTGGA 480
    ACTAGGAGAT CCGCTTTCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
    CATCAGCCGG GTTGTGTGTA TTGGAGTGAC TCTCAGGCT CTCTCTCTG GATTTGGTGC 600
    TGTCACCTGC CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
    TCTAGCCCTG GAACGCGGAC TGCTGCAAAAC CATGGATATG ATCATAAGCA AAAAGAAAG 720
    GATGGCAATG GCACGAGAGAA CAATGTTCCA GAAGGGGGA GTGCATAACA AACCATCAGG 780
    TTTCTGGGGA ATGATAAAAA GTGTACCAC TTCAGCATCA GGAAGTGAAG ATCTTACTCT 840
    TATTCAACAG GAAGTGGATG CTTTGGGAAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
    TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAGG GGAATATTT 960
    TAAITTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGCTTACCAT 1020
    CAATATTGTT TTTGATCGAG TTGGGAAAC GATCTCTGTC ACAAGAGGCA TTGAGATCAC 1080
    TGTGAATTAT CTGGGAATCC AATTTGATGT GAAGTTTGG TCCCAACACA TTTCTTCTAT 1140
    TCTTGTGGA ATAATCATCG TCACATCCAT CAGAGGATG CTGATCACTC TTACCAAGTT 1200
    CTTTTATGCC ATCTCAGCA GTAAGTCCTT CAATGTCTAT GTCTGTCTAT TAGCAGAT 1260
    AATGGGATG TACTTTGTCT CCTCTGTGCT GCTGATCGA ATGAGTATG CTTTGAATA 1320
    CCGCACCATA ATCACTGAAG TCCTTGGAGA ACTGCACTTC AACTTCTATC ACCGTTGTT 1380
    TGAATGTATC TTCTGTGTA GCGCTCTCTC TAGCATACTC TTCTCTATTT TGGCTCACAA 1440
    ACAGGCACCA GAGAAGCAAA TGGCACCCTG AACTTAAGCC TACTACAGAC TGTAGAGGC 1500
    CAGTGTGTTT AAAATTAGA TATAAGAGGG GGGAAAAATG GAACCAAGGC CTGACATTTT 1560
    ATAAACAAC AAATGCTAT GTAGCATTT TTACCTTCA TAGCATACTC CTTCCCTCTC 1620
    AGGTGATCT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAATCAAG 1680
    ACATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CAGAGAGGAG 1740
    CCAGAAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800
    TGAGCCAAAC ACCTAGGATT TCCGTTTAA GGTTCACATG GAAAGGTTA TAGCTTGGC 1860
    TTGAGATTGA CTCATTAAAA TCAGAGACTG T
  
```

**A84 Protein sequence**

Gene name: putative G-protein coupled receptor  
 Unigene number: Hs.16085  
 Protein Accession #: NP\_057418.1  
 Signal sequence: none found  
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402.  
 Cellular Localization: plasma membrane

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1      11      21      31      41      51

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	MSFLIDSSIM	ITSQILFFGF	GWLFFMRQLF	KDYBIRQYVV	QVIFSVPFAF	SCIMFELIIF	60
	ELLGLVNSSS	RYPHWKNMLC	VILLILVFMV	PFYIGYFIVS	NIRLLHKQRL	LFSCLMLWTF	120
5	MYFFWKLQDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYFLRN	180
	VTDLDLLE	RRLQYMDMI	ISKKRRMAMA	RRTMFQKGEV	HNKPSGFWGM	IKSVTTSASG	240
	SENLTLLQOE	VDALBELSRQ	LPLETADLYA	TKERIEYSKT	PKGKYFNLFG	YFFSIYCVWK	300
	LFMATINIVP	DRVGKTDVPT	RGIEITVNVL	GIQFDVKFWS	QHISFILVGI	IIVTSIRGLL	360
	ITLTKEFFYAI	SSSKSSNVIV	LLLAQIMGMV	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
10	FYHRNFDVIF	LVSLALSSILF	LYLAHKQAPE	KQMAP			
	<b>A95 DNA SEQUENCE:</b>						
	Gene name:			TTK protein kinase			
	Unigene number:			Rs.169B40			
15	Probeset Accession #:			M86699			
	Nucleic Acid Accession #:			NM_003318			
	Coding sequence:			1026-3551 (underlined sequences correspond to start and stop codons)			
20	1	11	21	31	41	51	
	GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACCT	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	COGCTCCCG	GGTTCAAGCG	ATTCTCCTGC	120
	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAATAATTTT	180
	CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
25	ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAAACTG	300
	TGCTGGCTGT	ATTCCTTTTT	TGTTGTTGGA	TTTTTGAAAC	AGGGTCTCCC	TTGGTCCGCC	360
	AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATAACC	TCCACTCCT	GGTTTCAAGT	420
	GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	GCGTGCACCA	CCACACCCCG	480
	CTAATTTTTG	TATTTTTATT	AGAGACAGGG	TTTCACCATG	TTGGCCAGGC	TGTTCTCAAA	540
30	CTCCTGGACT	CAAGGATCC	GCCTGCCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACCATG	CCTGACCTTA	TAAATCTTAA	GTCAATTTTT	CTGGTCCATT	TCATCCTTAG	660
	GGTCCCTACA	ACCAATCTGC	ATTAGCGGCT	ACAATAATCC	TTAATTCAT	GATTTCACAA	720
	AGGAAGATGA	AGTGATTGAT	GATTAGAAA	GGGGAAGTAG	TAGCCCACT	GCACACTCCT	780
	GGATGATGAT	CCTAATATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
35	TTTGGTTTAA	ATTAATTTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTGATGTGA	900
	ATGTAGAGCT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCCCAG	960
	TGCAGTTTTT	GGTAAAGATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
	CCATAAGGAA	CAAGTGAGA	GACATTAANA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
40	AACTAAGCTT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGAAGCT	GTAAACCAAA	1140
	TTATGATGAT	GGCAACAGAC	CCAGAGGACT	GGTTGAGTTT	GTGCTCAAA	CTAGAGAAAA	1200
	ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATGTAT	TGGTCCGTAC	AGTCAAGCAA	1260
	TTGAAGCGCT	TCCCCAGAT	AAATATGGCC	AAATGAGAG	TTTGTCTAGA	ATTCAAGTGA	1320
	GATTGTCTGA	ATTAAAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAAATG	1380
45	CCAGAGCAAA	TGCAAGAAA	TTTGCTTTTG	TTCAATATAT	TTTGTACAAA	TTTGAACCTG	1440
	CACAGAGTAA	GTCTAAAAAA	AGTAAACAA	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAA	1500
	TACCACTAGA	AATGCTGGAA	ATTGCCCTGC	GGAAATTTAA	CTTCCAAAA	AAGCAGCTGC	1560
	TTTCAAGGGA	GGTAAAGAA	AATTTATCAG	CATCTACGGT	ATTAAGTGGC	CAAGAATCAT	1620
	TTTCCGGTTC	ACTTGGGCAT	TTACAGATA	GGACAAACAG	TTGTGATTCC	AGAGGACAGA	1680
	CTACTAAAGC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAATATAGGT	1740
50	ACCGGATTC	ATTGAGACAA	CTAAACAGTC	ATGCCCATTT	GGAGAGTCC	GAAGAGTCC	1800
	CAGTTAACTT	TCTAAATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTGTACCTTT	1860
	GTTTTATGAA	GTCTTCTGCT	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTA	CCTGGATCTA	1920
	AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAATTTTAA	GTCTGTTCRA	AATAGTCAAT	1980
	TCAAGGAACC	TCGTGGTGTG	GATGAAGAAG	GTTCGAACT	TATTTATTCT	GATTCAATTA	2040
55	CCCTGAGTAC	TAAACGGA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
	AAGAACCAGA	GGTTCAGAG	AGTAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
	GTATTAACCA	GAATCTGTCT	GCATCTTCAA	ATCACTGGCA	GATTCGGGAG	TTAGCCCGAA	2220
	AAGTTAATAC	AGAGCAGAAA	CATACCACCT	TTGAGCAACC	TGTCTTTTCA	GTTCACAAAC	2280
60	AGTCACCACC	ATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTTGT	AAGACACCRA	2340
	GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTTAGAAC	TCCAGTTGTA	AGAATGACT	2400
	TTCCACCTGC	TTGTCAAGTG	TCAACACCTT	ATGGCCAAAC	TGCTGTTTTC	CAGCAGCAAC	2460
	AGCATCAAT	ACTTGCCACT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
	ATGAATGCAT	TTGGTTTAAA	GGAGAATTT	ATTCATATAT	AAAGCAGATA	GGAGTGGAG	2580
65	GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAGAAACA	GATATATGCT	ATTAATATG	2640
	TGAACCTTGA	AGAAGCAGAT	AACCAAACCT	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
	TGAATAAACT	ACAACACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAATCAACGG	2760
	ACCAGTACAT	CTACATGGTA	ATGGAGTGTG	GAATATTTGA	TCCTAATAGT	TGCTTTAAAA	2820
	AGAAAAATC	CMTGATCCA	TGGGAACGCA	AGAGTTACTG	GAATAATATG	TTAGAGGCAG	2880
70	TTACACAAAT	CCATCAACAT	GGCATTTGTT	ACAGTATCTT	TAAACCAAGT	AACTTTCTGA	2940
	TAGTTGATGG	AATGCTAAG	CTAATTGATT	TTGGGATTGC	AAACCAATG	CAACAGATA	3000
	CAACAAGTGT	TGTTAAAGAT	TCTCAGTTTG	GCACAGTTAA	TTATATGCCA	CCAGAAGCAA	3060
	TCAAGATAT	GTCTTCTCTC	AGAGAGAATG	GGAAATCTAA	GTCAAGATA	AGCCCAAAA	3120
	GTGATGTTTG	GTCCCTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCATTTT	3180
	AGCAGATAT	TATTCAGATT	TCTAATTTAC	ATGCCATAT	TGATCCTAAT	CATGAATTTG	3240
75	AATTTCCGGA	TATTCAGAG	AAAGATCTTC	AAGATGTGTT	AAAGTGTGTT	TTAAAGAGGG	3300
	ACCCAAACA	GAGGATATCC	ATTCCTGAGC	TCCTGGCTCA	TCCATAATGT	CAAAATCAAA	3360
	CTCATCCACT	TAACTCCATG	GCCAAGGGAA	CCAATGAAGA	AATGAATAT	GTCTCGGCC	3420
	AACTTGTTGG	TCTGAATCT	CCTAATCTCA	TTTGAAGAC	TGCTAAACT	TTATATGAAC	3480
	ACTATAGTGG	TGGTGAAGT	CATAATCTCT	CATCTCCCAA	GACTTTTGAA	AAAAAAGGG	3540
80	GAATAAATG	TATTCAGATT	ATTCGTAATG	TCAGATAGGA	GGTATAAAT	ATATTGGACT	3600
	GTATACCTTT	TGAATCCCTG	TGGAAATCTA	CATTTGAGAA	CAACATCACT	CTGAAGTGT	3660
	ATCAGCAACA	AAAATCCAGT	GAGATTATCT	TTAAAGAAA	ACTGTAAAA	TAGCAACCAA	3720
	TTATGCACT	GTATATATG	TAGACTTGT	TTCTCTGTT	TATGCTCTG	TGTAATCTAC	3780
	TTGACATCAT	TTTACTCTTG	GAATAGTGGG	TGGATAGCAA	GATATTTCTA	AAAAACTTTG	3840

TAAATAAAGT TTTGTGGCTA AAATGA

**A86 Protein sequence:**

Gene name: TTK protein kinase  
 Unigene number: Rs.169840  
 Probeset Accession #: M86699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

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1      11      21      31      41      51
|      |      |      |      |      |
15  MNKVRDIKKN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MANNPEDWL SLLLLLEKNS 60
    VPLSDALLNK LIGRYSQAIE ALPPDKYQON ESPARIQVRF AELKAIQEPD DARDVFMAR 120
    ANCKKFAEVH ISFAQFELSQ GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKQLLS 180
    EEEKNLBSAS TVLTAQESFS GSLGHLQNRN NSCDNRQQT KARFLYGENM PPQDAEIGYR 240
    NSLRQTNKTK QSCPPGRVPV NLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGRSKP 300
    SGNDSCELRN LKSVQNSHPK EPLVEDERKS ELIITDSITL KNTKESLLA KLEETKEYQE 360
    PEVPESNQKQ WQAKRKSECI NQNPASSENH WQIPELARKV NTSQKHITFE QPVFVSXQS 420
    PPISTSKWFD PKSTICKTPSS NTLDVYMSCF RTPVVKNDFF PACQLSTFYG QPACFQQQH 480
    QILATPLQNL QVLASSANE CISEVKGRYS ILKQIGSGGS SKVFOVINEK KQIYAIKYVN 540
    LEEADNQTLN SYRNEIAYLN XLQHSBDKII RLYDYETDQ YIYMVMECGN IDLNSWKKK 600
    KSIDPWERKS YWKNMLEAVH TIHQHGYVHS DLKPNFLIV DGLMKLIDFG IANQMPPDTT 660
    SVVKDSQVGT VNYMPPPAIK DMSSERENK SKSKISPKSD VMSLGCLLYY MTYGTTPFQQ 720
    IINQISKLEA IYDNEHTEF PDIPKDLQD VLKCKLRDP KQRIPIPELL AHPYVQIQTH 780
    FVNQMAKQTT EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGSEHNSSS SKTFEIKRKG 840
    K
  
```

**A87 DNA SEQUENCE**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719  
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
40  GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCOCT 60
    CTGCCACCTG GGGCGGTGCG GGGCCGGAGC CCGGAGCCCG GTAGCGCGT AGAGCCGCG 120
    CGATGCACTT GGCCTCACTG CGAGCTGCGG GCGCGCACAG CTCTGTGGCG CTCTGGGCAC 180
    CCTGTTCCTT GCTGGGCTCC GCCCTGGCGG ACTTCAGCCT GGACAAACGAG GTGCACTCGA 240
    GCTTCATCCA CGGGCGCTTC CGCAGCCAGB AGCGGGCGGA GATGACGCGC GAGATCCTCT 300
    CCAATTTGGG CTGGCCCAAC GCGCCGCGCC CGCACTTCCA GGGCAAGCAC AACTCGGCAC 360
    CCAATGTCAT GCTGGAACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCG 420
    GCCAGGGCTT CTCTACCCCT TACAAGGCCG TCTTCAGTAC CAGGGGCCCC CCTCTGCCCA 480
    GCCTGCAGTA TAGCCATTTC CTCACCGAGC CCGACATGGT CATGAGCTTC GTCAACCTCG 540
    TGGAAACATG CAAGGAATTG TTCCACCCAC GCTACACCCA TCGAGAGTTC CGGTTTGATC 600
    TTTCCAGAT CCACAGAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
    ACATCCGGGA AGCCTTCGAC AATGAGACGT TCCGGATCAG GCTTTATCAG GTGCTCCAG 720
    AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGGTACCCCT TGGGCCCTCG 780
    AGGAGGGCTG GCTGGTGTIT GACATCACAG CCACCAACAA CCACTGGGTG GTCAATCCGC 840
    GGCACAACCT GGGCCCTGCG CTCTCGGTGG AGACGCTGGA TGGGAGAGC ATCAACCCCA 900
    AGTTCGGCGG CTTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
    TCTTCAGGC CACGAGGTC CACTTCGCA GCATCGGTG CACGGGAGC AAACAGCGCA 1020
    GCCGAACCG CTCCAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
    AGAACAGCAG CAGCGACCAG AGGCAGGCTT GTAGAGCA CGAGCTGTAT GTCAGCTTCC 1140
    GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTACGCGGCC TACTACTGTG 1200
    AGGGGAGTGT TGCCTTCCCT CTGAACCTCT ACATGAACGC CACCAACCAAC GCCATCGTGC 1260
    AGACGCTGGT CCACCTCATC AACCCGAAA CGGTGCCCCA GCCCTGCTGT GCGCCCAAGC 1320
    AGCTCAATGC CATCTCCGTC CTCTACTTGG ATGACAGCTC CAAGCTCATC CTGAAGAAAT 1380
    ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
    TTGGGGCCAA GTTTTCTTGG ATCTCCATT GCTCGCTTGG GCCAGGAACC AGCAGACCAA 1500
    CTGCTTTTGG TGAGACCTTC CCTTCCCTAT CCGCAACTTT AAGGTGTGA GAGTATTAGG 1560
    AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG CGAGCATCCA ATGAACAAGA 1620
    TCTTACAGC TGTGACGGCA AAACCTAGCA GSAAAAAA ACRACGCATA AAGAAAAATG 1680
    GCGGGCCAG GTCATTGGCT GGAAGTCTC AGCCATGCAC GGACTGGTIT CCAGAGGTAA 1740
    TTATGAGGCG CTACAGCCA GGCACCCAG CGTGGGAGG AAGGGGGCTT GGCAGGGGT 1800
    GGGCAGATTG GTCTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
    CAATAAAAAG AATGAATG
  
```

**A88 Protein sequence:**

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Protein Accession #: NP\_001710.1  
 Signal sequence: 1-30  
 Pfam domains: TGF $\beta$  propeptide [37-281]  
 Transmembrane domains: none found  
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
5  MHVRSLSRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRLRSQE RREMOREILS 60
   ILGLPHRPRP HLQKHNHSAF MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
   LQDSHFLIDA DMVMSFVNLV BEDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
   IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGMVLFDTA TSNHWVUNPR 240
   HNLGLQLSVE TLDGQSINPK LAGLIGHGSP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
   QNRSKTPKNQ BALHMANVAE NSSSDQROAC KIKHELYVSPR DLGWQDWILA PEGYAAYYCE 360
10  GECAFLNSY MNATNHAIVQ TLVHPINPET VFKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
   RNMVVRACGC H

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**A89 DNA SEQUENCE:**

```

15  Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Nucleic Acid Accession #: AC012478
   Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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20      1      11      21      31      41      51
|      |      |      |      |      |
   ATGCGCGCCG TGCCCGCTGCC CGCCCCCGCTC CTGCCCGCTGC TGCTGCTGCG GCTCCTGGCC 60
   GCTCCGCGCG CCGCGCGCCAG CAGAGCCGAG TCGCTCTCCG CGCCGTGCGC CGAACCCGAG 120
25  CGGAGTCCGC GGCACCCGCC CGGCCCGGGG CCGGGGAACA CCACCCGGTT TGGGTCTGGG 180
   CGCGCGGGCG TCCAGCGCAG CTCACGCTCC AACAGCAGTG GCGACGCTT GGTGACCCGC 240
   ATTTCCATCC CTCTCCGCGA CCTACCCACC CTCACGGCAG CGGTGATCGT GCGTTTCCGC 300
   TTTACCAACC TCCTCATCGC CTGCTGCTGC CTGCGCTCT TCAGGTGCGG AAGAGAGTTA 360
   AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGA AATGGCGCCA 420
30  CTAAATGAAG AGGATGATGA AGATGAGGAC TCACAGTAT TCGACATCAA ATACAGAGTG 480
   TCCTTGCCGG CTGCTAGTGA ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
   GTGCCCCACC CTCTCATCTT CGACATGAC CTTCACGCAA GATGCACTGG AAGGCTGAT 600
   GGTGGAATCA GACCTGGTAA AACCTGTTTC CCAGCTGCTT GGCATCTCTT GGAAGTGTG 660
   TCAGCTGCAA CCTGGGCTGT GAAGGACTGG ACCTGGAGAC CCTCTTGGCT CGGAGGTGTT 720
35  GAAACCAAAA CGAAGCTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTG AGGCATCTGC 780
   TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840
   TTTGGGCATC CCTTTAAAGT GCGCCCTACT TCTACTCCCC ATGGTTTTCG ACAAATGCAG 900
   CTGARTCTCA TGGAAAGCTT GGATTCCTCT GCCTTACGCA GAACACCCG GGTCCATCTT 960
   GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
40  CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCTTTTACAC ACAAAACCATG 1080
   AGTACCTTGG CTCTGGATGT TTTCTGTGGT GCGCGCCAGC GGGGCACTTT TTGTGAGGAC 1140
   AGAGCAGTGA CTTTAACTCT CCAGGTTAGC TCTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
   GCGCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
   ACCCATCTCT TCAGGTGTGC TCGTTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
45  AGGGTGTTC GCGGTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
   TGCCTTTTGG TTTTGAAAGT TCTGTGTAGG CGCCATCTCT ACCTTGACCT CTTCTACAAA 1440
   ATCTGTCTCC CTTCTTAAAGT CGTGGAAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
   GTCCTTGGGT CATTTGAGCA GAGCCACCAA AAGGCAGCTG CTGCCACCGG GGAGCCTGTC 1560
   AAACGAGGCG CAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
50  GCGAACCTGC AGCAATTCOC AGATACCCAA GGCCAGGAAG GCCACGTGA GATGTCTACT 1680
   CACCTTGAGG GAGACTTGGG TGGGGTGGCA AATTCTTATT TGGAGGAAGA GGGTTTCCAG 1740
   GATGGCAGAT GGCAGAGAT GGTCTGTATG TCTGAGGAAG GCCACCTAG TTTGACAGGA 1800
   TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT 1860
   TCCCCCGGAC AGCCCCGTGT TCTGTCCAGG CCCTGA

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**A90 Protein sequence:**

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60  Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Protein Accession #: PGENESH predicted
   Signal sequence: 1-27
   Transmembrane domains: 94-115, 448-469
   Cellular Localization: not determined

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65      1      11      21      31      41      51
|      |      |      |      |      |
   MRAVPLPAFL LFLLLALLLA APAARASRAE SVSAPNPEPE RESRPPPGPG PGNTTFPGSG 60
   AAGGGSSSSS NSSGDALVTR ISILLRDLFT LKAAVIVAF FTLILLIACL LRVFRSGKRL 120
70  KTRKYDIIT TPAERVENAP LNEEDDED D STVPDIKYRV SLPAALRRQL PGQYLLTVP 180
   VPPFFILID LPARCSGRPD GGIRPQKTCF PAWHPVESW SAATWGVKDW TNKPSCVGGV 240
   ETKTNMYKT PAPSCVSGIC SDCEWQARFH VTMLLLLEP FGHFFKVPPT STPHGRQLQ 300
   LNLMEKLDSS ALRNTRAPS ARCLPLVIAE MAARSDLEFN PWHFSTATGS PIKTLYTQTM 360
   STLGLDVFCG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHRL RLLRBCPPLS 420
75  THFVRLARD ARGQASLTCR RVFRPRQBL HGGGSAQTAT CLVLKILLR RHPHLDLFYK 480
   ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHGEFV KRGPSCQLTR HTCPGWGIT 540
   ANLQTIPTDQ GQGGFRREIVT HPGGDLGVA NFYLEEGEFQ DGRQCKNVM SEEGPPSLTG 600
   CERLTGSHH SESHKSWSYL SPKQPLFLSR P

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**EMING****A91 DNA SEQUENCE**

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   Gene name:      G protein-coupled receptor 64
   Unigene number: Hs.184942

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Probeset Accession #: AA435577  
 Nucleic Acid Accession #: NM\_005756  
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5  
 10  
 15  
 20  
 25  
 30  
 35  
 40  
 45  
 50  
 55  
 60  
 65  
 70  
 75  
 80

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1      11      21      31      41      51
|      |      |      |      |      |
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTCTCGAA 60
CTGCGCGTCA GGATGGTTTT CTCTGTCAAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
GTTTACTCGA CGTTCAGAT ATTCCTTGTC ATCATTTGTC TTCATGTCGT TCTGGTAACA 180
TCCCTGGAAG AAGATACTGA TAATTCAGT TTGTCAACCAC CACCTGCTAA ATTATCTGTT 240
GTCAATTTTG CCCCCTCTCT CAATGAGGTT GAAACACACA GCCTCAATGA TGTTACTTTA 300
AGCTTACTCC CTTCACACGA AACAGAAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
GCTTCAGGCG TCAACCCCA GAGAAATATC TGCAATTTGT CATCTATTTG CAATGACTCA 420
GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCAGAAAT 480
CAACATATAA CGAATGGCAC CTAACTGGA GTCTCTGCTC TAAGTGAATT AAAACGCTCA 540
GAGCTCAACA AAACCTTGCA AACCTAAGT GAGACTTACT TTATAATGTX TGCTACAGCA 600
GAGGCCCAAA GCACATTAAT TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660
TGCTCTCAAA TAGCCCTTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
TCTGTACAGA TCCCTGCCCC TTCTTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACBTGGCC CACCATTFTT TCCAGSCCAA 840
TCCATCCGAG TGGTGCTCTG GGCCACTGTG CTTTCCCAGG TCCCACAAAG TACCTCTTTT 900
GCTGAGCTTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
CAACCCCTTT CACCCAGGCC TTCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC 1020
CCACAGCTTC AAACGATCTC TTCCCTATG CCCCACACCC ATGCTCCCGG CACCCCACT 1080
CCTGTGAAAG CCTCATTTTC CTCTCCACC GTGTCTGCCC CTGGAATGT CAACACTACC 1140
AGCGCACCTC CTGTCCAGAC AGACATCTTC AACACCAGCA GTATTCTGA TCTTGAGAAC 1200
CAAGTGTGTC AGATGGAGAA GGCTCTGTCC TTGGGCGGCC TGGAGCTTAA CCTGCGAGGA 1260
GAAATGATCA ACCAAGTCAG CAGACTCTCT CATTCGCCGC CTGACATGCT GGCCTCTCTG 1320
GCTCAAGATG TGTCTGAAAT AGTGGATGAC ATTGGCTTAC AGCTGAACCT TTCAACACG 1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TTCACACAAA CTACCTTTGT GGCCCAAGAC CCTGCAATTC TTCAGGTTTC TCTGAAACCC 1500
CAAGCTCTCT AGAACAGTAT TGGCACAATT ACTCTTCTT CATCGCTGAT GAATAATTTA 1560
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTTTTGA AACACCTGCT 1620
TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680
GTTGCAAACT TGACCGTTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
AACCOCAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGGT 1800
GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAG ACAGGAGATT GAATGAAACC 1860
ATCTGTACCT GTAGCCATCT AACAGCTTC GGCGTTCTGC TGGACCTATC TAGGACATCT 1920
GTGCTGCTG CCAATAGAT GGCTCTGAGC TTCAATACAT ATATTGGTTG TGGGCTTTCA 1980
TCAATTTTTT TGTCAGTTCAC TCTTGTAAOC TACATAGCTT TGTAAAAGAT CCGGAGGGAT 2040
TACCTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCTGGTCTTC 2100
CTCCTGACT CGTGGATTCG TCTGTATAAG ATGCAAGGCC TCTGCTATC AGTGGCTGTA 2160
TTCTCTCAT ATTTCTCTT GTCTCTATC ACATGGATGG GCCTAGAACG ATTCATATG 2220
TACCTGGCCC TGTCTAAAGT ATTTAACTAC TACATCCGAA AATACATCCT TAAATCTGCG 2280
ATTGTGCGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCTGACTAT ATCCCAGAT 2340
AACTATGGGC TTGGATCTTA TGGGAATTC CCCAATGGTT CACCGGATGA CTCTGCTGG 2400
ATCAACAACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTCTGTGT GATATTTTTG 2460
CTGAAGTCA GCATGTTTAT TTGTGCTCTG GTTCAGCTCT GTCCGAATTA AAGAGAGAG 2520
CAACTGGGAG CCGAGCGAAA AACCAATATT CAAGACCTCA GGAGTATCGC TGGCTTTACA 2580
TTTTTACTCG GAATAACTTG GGGCTTTGCC TTCTTGGCT GGGGACAGT TAACGTGACC 2640
TTTATGTATC TGTTTGCCAT CTTTAATACC TTACAAGGAT TTTTCAATT CATCTTTTAC 2700
TGTGTGGCCA AAGAAAATGT CAGGAAGCAA TGGAGCGGT ATCTTTGTTG TGGAAAGTTA 2760
GGCTGGCTG AAAATTTCTGA CTGAGTAAA ACTGCTACTA ATGTTTAAA GAAGCAGACT 2820
GTAAACCAAG GAGTGTCCAG CTCTTCAAT TCTTTACAGT CAAGCAGTAA CTCCACTAAC 2880
TCCACACAC TGCTAGTGAA TAATGATTGC TCAGTACAG CAAGCGGAA TGGAAATGCT 2940
TCTACAGAGA GGAATGGGTT CTCCTTTAGT GTTCAGATG GAGATGTGTG CCTTCAGAT 3000
TTCACTGAAA AACGACATAT GTTTAAGCAG AAGGAAGATT CCTGCAATGG GAAGGGCGT 3060
ATGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
CTTCTCTTA AAATCAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180
CACATGTGA GATGTATGAA AATCACTCA TTTTATTCTC GGCACATCT GGAGAAGCAT 3240
AAGCTAATTA AGGCGGATGA TTATTATTAC AAGAGAAAC CAGACATTA CACCTGGTT 3300
TTTAGACATT TCTGATTTGG TTCTTATCT TTCAATTTAT AAGAGGTTG GTTTTAAACA 3360
ATACACTAAG AATGACTCCT ATAAAGAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
TTTAAAGAGG CTAAGTTATC TTGATAACA TCATATAAAG CAACTGTTGA CTTCAGCCTG 3480
TTGGTGAGTT TAGTTGTGCA TGCCCTTGGT GTATATAAGC TAAATCTIAG TGACCCATGT 3540
GTCAAAAAAT TTACTTCTAC ATTTTITGT ATTTATTTTC TACTGTGTA ATGTATTCCT 3600
TTGTAGAAAT ATGGTTGTTT TGCTCACTGT GATAATTCAG AAAATCCTTG CTGCTTCCG 3660
AAATCCTTAA GCTCCTTTT GAGATGATAT AGGATGTGAA ATACAGAAAC CTGAGTGAAA 3720
TCAGAAATA ATGATCCGAG CAGACTGAG AAAATGTGAG CAGACAGTGC CACAGTTAGC 3780
TCATACAGTG CTTTGTAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
TGGGTCAATG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
GTGACGAGCC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCGCAT 3960
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
AGAGGATGA ACTGTCTATC AGACCATGTG TCAGGAAAAT TGTGAACGTA GATGAGGTAC 4080
ATACACTGCC GCTTCTCAAA TCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140
CTTCTCTTAA AAAGGTACAT ATATATGAAA AAAATCATA TTGCGTTCT TAAAAAGCA 4200
ACTGATAGGT ACATTGTGTA TTGTATGAC TGGTACACTC TGGCCAGACC AGAGCTATAA 4260
TTGTTTTTAA AATGTGTCTT GAAGAATGCA CAGTGACAG GGGAGTAGCT ATTGGGAACA 4320
GGGAACCTGC CTACACTGCT ATTTGTGCTA CATGTATGGA GCCTTGATTG CTCCTAGTTA 4380
TATACAGGGT CTATCTTGCT TCTACCTTAC ATCTGCTTGA GCAGTGCCCT AAGTACATCC 4440
TTATTAGGAA CATTTCAAAC CCTTTTAGT TAAGTCTTTC ACTAAGGTT TCTTGATAT 4500
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTAGTG 4560
CTGACTGTGC TTTGCAATAT TTCTTTCTG ATTTATTTAA TTTCTGTGA TTTATATGTT 4620

```

AAAATCAAAA ATGTTAAAAAT CAATGAAATA AATTGTCAGT TAAGA

### A92 Protein sequence

Gene name: G protein-coupled receptor 64  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLTSLLEE	DTDNSSLSP	PAKLSVVSFA	60
PSSNEVETTS	LNDVTLSLP	SNETKTKIT	IVKTFNAGSV	KPQRNICNL	SICNDSAFFR	120
GEIMFYDKE	STVPQNHIT	NGTLTGVLSL	SELKRSSELNK	TLQTLSEYF	IMCATAEAQ9	180
TLNCTFTIKL	NNTMNAACAT	AALERVKIRP	MEHCCCSVRI	PCPSSPEELG	KIQCDIQDPI	240
VCLADHPRGP	PPSSSQSIPV	VPRATVLSQV	PKATSPAEP	DYSPVTHNVP	SPFISIQPLS	300
PQPSAPIASS	PAIDMPQSE	TISSPMPQTH	VSGTPPPVKA	SFSSPTVSAP	ANVNTTSAPP	360
VQTDIVNTSS	ISDLENQVLQ	MEKALSLGSL	EPNLAGEMIN	QVSRLLHSEF	DMLAPLAQRL	420
LKVVDIDGLQ	LNFSTNTISL	TSPSLALAVI	RVNASSFNIT	TFVAQDPANL	QVSLSTQAPE	480
NSIGTITLPS	SLMNNLPARD	MELASHVQFN	FFETPALFQD	PSLENLSLIS	YVSSSVANL	540
TVRNLTNVT	VTLRHNPSQ	DELTVRVCFW	DLGRNGGRGG	NSDNGCSVD	RRINETICTC	600
SELTSPGVLL	DLSTSVLPA	QMMALITITY	IGCGLSIFL	SVTLVYIAF	EKIRRDYPSK	660
ILQLCAALL	LNLVFLDS	NIALYKMQGL	CISVAVFLHY	PLLVSTFWMG	LEAPFMXIAL	720
VKVENTYIRK	YILKFCIVGW	GVPVAVVTII	LTISPNDYGL	GSYGKFPNGS	PDDFCWINNN	780
AVFYITVVG	FCVIFLLNVS	MFIVVLVQLC	RIKIKKQLGA	QRKTSIQDLR	SIAGLTFLG	840
ITMGFAFFAN	GFNVNFMVL	FAIENTLQGF	FIFIFYCVAK	ENVRKQWRRY	LCCGRLRLAE	900
NSDWSKTATN	GLKKQTVNQS	VSSSNSLQS	SSNSTNSTTL	LVNDCSVHA	SGNGMASTER	960
NGVSFSVQNG	DVCLRDFTGK	QHMFNEKEDS	CNGKGRMALR	RTEKRGSLHF	IEQM	

### Fibrosis

### A93 DNA SEQUENCE

Gene name: RGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CCGCAGAGGA	GCCTGAGCCA	GGCTAGCCAG	GGCGCCCCCA	GGCCCTCCCC	AGGCCGCGAG	60
CGCCCTGCCC	CGCGTGCTTG	GCCTCCCCTC	CCGAGACTGCA	GGGACAGCAC	CGCGTAACCTG	120
CGAGTGGGAGC	GGAGGACCCG	AGCGGCTGAG	GAGAGAGGAG	GCGCGCGCTT	AGCTGCTACG	180
GGGTCCGCGC	GGCGCCCTCC	CGAGGGGGGG	TCAGGAGGAG	GAAGGAGGAC	CGGTGCGAGA	240
ATGCTCTGCG	CGTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
GGGAACGGCG	CGACTGCGG	GCATCACGGG	TTGTTAGCAT	CGGCACGTCA	GCCTGGGGTC	360
TGTCACATG	GAACATAACT	GGCCTGCTGC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
TGTGAGCTA	CATGCGAACC	TGGATGTAA	TTTGGTGAAT	GCGTGGGACC	AAACAAATGC	480
AGATGCTTTC	CAGATACAC	CGGAAAACCC	TGCACTCAAG	ATGTGAATG	GTGTGGAATG	540
AAACCCCGGC	CATGCCAACA	CAGATGTGTG	AATACACAG	GAAGCTACAA	GTGCTTTTGC	600
CTCAGTGGCC	CAATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATC	660
ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCTT	GTGTCCATCC	720
TCAGGACTCC	GCCTGGGCCC	AAATGGAAGA	GACTGTCTAG	ATATTGATGA	ATGTGCTCTC	780
GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGGGAAG	CTACTACTGC	840
AAATGTCACA	TTGGTTTCGA	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
AATGAATGTA	CTATGGATAG	CCATACGTGC	AGCCACCATG	CCATATGCTT	CAATACCCAA	960
GGGTCTTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
ATCCCTGAAA	ATTCTGTGAA	GGAAATCTCT	AGAGCACCTG	GTACCATCAA	AGACAGAAATC	1080
AGAAAGTTTC	TTGCTCACAA	AAACAGCATG	AAAAAGAAGG	CAAAAATTAA	AAATGTTACC	1140
CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
ATAGTTTCCA	GAGGCGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAAATGAAGA	GAAATGAAA	1260
GAGGGGCTTG	AGGATGAGAA	AAGAGAGGAG	AAAGCCCTGA	AGAAATGACAT	AGAGGAGCGA	1320
AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGTGAATT	CGGCTGATT	1380
CTGGTCCAAA	GGAAAGCGCT	AACITCCAAA	CTGGAAACATA	AAGATTAA	TATCTCGGTT	1440
GACTGCGACT	TCAATCATGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
TGGAATCTCG	CTGATCGAGA	TAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGGCA	1560
GGTCACAAGA	AAGACATGG	CCGATTGAAA	CTTCTCTTAC	CTGACCTGCA	ACCCCAAAGC	1620
AACITCTGTT	TGCTCTTGA	TTACCGGCTG	GCCGGAGACA	AAGTGGGGA	ACTTCGAGTG	1680
TTTGTGAAA	TAGCTGAAA	TGCCCTGGCA	TGGGAGAAGA	CCACGAGTGA	GGATGAAAAG	1740
TGGAAGACAG	GGAAATTC	GTGTATCAA	GGAACTGATG	CTACCAAAAG	CATCATTTTT	1800
GAGCAGAAC	TGCGCAAGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
TCAGGCTTAT	GTCCGATAG	CCTTTATCT	GTGGATGACT	GAATGTTACT	ATCTTTATAT	1920
TTGACTTTGT	ATGTCAGTTC	CCGTGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCAAT	1980
TAGAATTAT	TAGCTGAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTAT	AAGATGCTTT	2040
TCTGTATATA	GATATGCCAA	TATTGCTTT	AAATATCATA	TCACTGTATC	TTCTCAGTCA	2100
TTTCTGAATC	TTTCCACATT	ATATTATATA	ATATTGAAAT	GTCACTTTAT	CTCCCTCTCT	2160
CAGTATATCT	GATTTGTATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTAGAAAA	2220
TAGAAAAAAA	AGCAGAGAGA	AATGTTTAAC	TGTTTGAATC	TTATGATACT	TCTTGGAAAC	2280
TATGACATCA	AGATAGACT	TTTGCCTAAG	TGGCTTAGCT	GGGTCTTCA	TAGCCAAACT	2340
TGTATATTTA	AATCTTTTGT	AATAATAATA	TCCAAATCAT	CAAAAAAAA	AAAAAAA	

**A94 Protein sequence:**

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

1	11	21	31	41	51	
MPLPWSLALP	LLLSNVAGGF	GNAASARHNG	LLASARQPGV	CHYGTKLACC	YGWRRNSKGV	60
CEATCEPGCK	FGECVGNKC	RCFPGYTGCT	CSQDVNRCGM	KPRPCQHRCV	NTHGSIKFC	120
LSGHMLMPEA	TCVNSRTCAM	INCQYSCEDT	EEGFPQCLCP	SGLRLAPNGR	DCLDIDECAS	180
GKVICPYNRR	CVNTFGSYTC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SEHANCFTNQ	240
GSFKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KILLAHKNSM	KKKAKIKNVT	300
PEPTRTFTPK	VNLQPFNYEB	IVSRGNSHNG	GKKGNSEKMK	EGLRDEKREE	KALKNDIER	360
SLRGDVFEPK	VNEAGEFGLI	LVQRKALTSK	LEHKDLNISV	DCSPNHGICD	WKQDREDDFD	420
WNPADRIDAI	GFYMAVFLA	GHKKDIIGRLK	LLLPDLQPOS	NFCLLFYVRL	AGDKVQKLRV	480
FVKNNSNALA	WEKTTSEDEK	WKTGKIQLYQ	GTDATKSIIF	EAERGKSKTG	ELAVDGVLLV	540
SGLCPDSLLS	VDD					

**GLIOBLASTOMA****A95 DNA SEQUENCE**

Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Nucleic Acid Accession #: none found  
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1	11	21	31	41	51	
AGCAACGACG	CGGGCGAGCG	GGAGCGGGCG	CGCGCCCATG	TGGCTGCTGG	GGCGCTGTGG	60
CCGTCTGTCT	AGCAGCGCCG	CGGAGAGCTA	GCTGCTCCCT	GGGAACAAC	TCACCAATGA	120
GTGCACATCA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	CGCGCTGGCA	180
GTGTGACGGG	CTGCCCTGACT	GCTTCGACAA	GAGTGATGAG	AAGGAGTGCC	CCAAGGCTAA	240
GTGGAATGT	GGCCCAACCT	TCTTCCOCTG	TGCCAGCGGC	ATCCATTGCA	TCATTGGTCC	300
CTTCCGCTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCTCTCG	CTTTGCTCCA	CGCCCGCTTA	CCACTGCAAG	AACCGCTCT	GTATTGACAA	420
GAGCTTCTTC	TGCGATGGAC	AGAATAACTG	TCAGACAAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTCTCTCA	GAAACCGGCA	GTGGGACAGT	GTGTGTGACT	TCAGAGAAC	AACITGTGTA	540
TTACCCGAGC	ATCACCTATG	CCATCATCGG	CAGCTCCGTC	ATTTTGTGTC	TGGTGTGGCC	600
CCTGCTGGCA	CTGGTCTTGC	ACCACGAGCG	GAAGCGGAAC	AACCTCATGA	CGCTGCCGCT	660
GCACCGGCTG	CAGCAGCTTC	TGCTGTCTGC	CGCGCTGGTG	GTCTGGGACC	ACCCGCCACA	720
CTGCAACATC	ACCTACGACG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCTCTG	GAGTATGGCT	CCCCACCTCT	CTACTCGGAG	GCTTGTCTGG	ACCAGAGGCC	840
TGCGATGTAT	GACCTTCCCT	CACCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACCTGCCC	CCCTACCGCT	CCCGGTCCGG	GAGTGCCAAC	AGTGCCAGCT	CCGAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACGAG	CCACAGCCCG	GGGCAAGCTG	GCCCCAGGGA	1020
GGGCACTGCT	GAGCCACGAG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTATATCCA	AAGTCCATAT	GGGTAAATCT	GCTCTGACTT	GTGCGCATTC	TAACAATTGG	1140
TGCTCATGGG	AAGCTCTTAT	AGCACCTGTA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACATATCTC	GCATTCCTCT	CCTCCCCCAG	ACTTCAGAGA	TGTTTTCTCG	GCGTCTCAGT	1260
TGACATGATC	TGTTGTGGGT	CTTTCTGTGC	AGGTCACTCT	TCCCTTGGGA	CCCGAGATCA	1320
CACCTCATTT	TTTCAATTTA	TTCTGTTTCT	GTGGAGAGAG	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGAGGAGAG	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTTGGGGA	TTTGGGTTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCACGTGATG	GTCAACCCCG	CAAAAAAATT	CCATTGAGGC	1560
ATCAAAACCT	GCTTTGCACA	ATCTTATTGG	ATGCCCCCGG	TTGAGCAGAG	TCAGTGGCCA	1620
AAGAAAACCT	TGGACGTGAG	TAACACCCCT	CAGCAGTCCG	AACGTTATTT	TGGTTTGTGG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATCTGCGCTT	TAGAAATTTG	CCCAAGAAATG	1740
CTCATCTGGA	GAGCTTTCCT	CAGCAGCATA	TATCATCAGC	CTCATCCTAA	AATAGGCCAGG	1800
GAGCCCTCTC	CATGAGTTTA	TCCAAGTTCT	CAGCTCTCTA	AATGCAGGCT	GCCAGAGACC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACTTAC	CTGTTTCTCG	GACTGTCAAC	CTCCAGCTGT	1920
ACCTGCCCGY	AGCCAAGGAA	TGAGGACCTA	ACTTGAATGG	GCCCAAGATC	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCCAAC	CCAGCCCTGT	CTTGTCTATT	CATGAGCAGT	CAACTCTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAAAGT	CTTTTACCT	GTGCATTTGG	ACTTGAGGAC	2100
ACTGGTTTCT	ATCAAGGCTG	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCCGTGGCTC	2160
CTGCACTGTG	CACGCTCTCT	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGTC	AGGCTCTCTC	CAACATCCCA	GTAGTTTCTC	CTCTGAGACA	CATGGGCAAG	2280
AGACAAATTT	GAGTCAAGAT	TTTCCATTGG	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAACACAGT	TGTTTGTGTT	TTCCCTTCTA	GTTAAGGGAC	TATTATATAT	GTATAGGAA	2400
AGCTGTCTCT	TTTTTTGTGTT	TTCCCTTAAAC	AAGGTCCAAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCTTTGC	CCCGCTGAGC	CCCGTGATAA	CAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTTGTGC	ATTGTTGTCAC	TTTGAAGTTA	TTATTTATCA	AGTTCTTGAA	GGAGAGAGAA	2580
AGAGGGACTC	CTCTCTCCCT	CCGTGTATAG	TCTCTATGTT	TGTGCTAGTT	TTCTTTTTTT	2640
TTCTCTGTGT	CCAGTCAGCC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAAAACTGT	2700
AGGTGTTGTT	TGGCAAGAAA	CCACACTGAC	TGNTAGAGGG	TAAATAGGAA	CCAGGTAGAG	2760
CCACTCCGGG	CAGCTGTCTAC	CCATTGAGAA	CTTCTTCCG	CAGCTGAGAA	AATGTTTCACT	2820
AACCTGTGTT	ACGCTAATTA	AAACAGAGCC	TGCAGGAAGT	GGGCTAAGG	TGCTTTCAG	2880



5 TGATCCTGTT CTGTAGACTT TCTTTCTTT TTTAACCAG ATCCAAAGGA TGTACAGAA 2940  
 AAGCTAGCCA CTGGTATTTT GTTTGTGTTA AAAAAAAGAA GAAAGAAAGA AAGAAAGAAA 3000  
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060  
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 TGATTTTITT AATGAATGTT TTTAAAAATA TATAAATAGC ACACCAANGC GGCAGGGTIT 3420  
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 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAACCTG 3720  
 GAAAGCTTGT GTGTGCTTGC TTTTGTGTGT TGTGTAGGCT TGTGTTTGT TTTTAAATT 3780  
 TTATACITTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAWG GWTMTAMARM 3840  
 AAMMAAAAC AWWTGTTGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCACTTCGGG 3900  
 TGGGCGCGCG GGGCCCACTG AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAG 3960  
 20 GAAACCTTGG CCAAGAAAAA GGTGCGGAGA ATTCTCCAC CCAAAAAA ACGCCCGGG 4020  
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G 4080

25 A96 Protein sequence:  
 Gene name: ESTs  
 Unigene number: Hs.293616  
 Probeset Accession #: AW043782  
 Protein Accession #: none found  
 30 Signal sequence: 1-17  
 Transmembrane domains: 169-191  
 LDLa domains: 28-66, 70-108, 112-149  
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51  
 MWLLGLPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNNG RCIPGAWQCD GLEDCDFKSD 60  
 EKECKPARKK CGPTFFPCAS GIHCILIGFR CNGFEDCFDG SDENCINNP LECSTARYHC 120  
 40 KNGLCIDKSF ICQGNHCQD NSDEKSCBS QBPSSQVVFV TSENQLVYYP SITTYAIGSS 180  
 VIFVLVALL ALVLHQRKR NNLMTLFVHR LQHPVLLSRL VVLDHPHHCN VTYNVMNGIQ 240  
 YVASQABQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PFYRSRSGSA 300  
 NSASSQAASS LLSVEDTSES PQQPFQPGST AEPRDSEPSQ GTRSV

#### 45 LUNG

50 A97 DNA SEQUENCE  
 Gene name: putative GPCR, Weakly similar to dJ365012.1  
 Unigene number: Hs.256897  
 Probeset Accession #: BE001836  
 Nucleic Acid Accession #: BE001836  
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 ATGGGCGTCA AATCTTTTTC CTTCACACT GGGAAATGATG GGCTAGACCC AGACCCCAATC 60  
 ATGTTAAGTA TGTATAGGAT CAGTGCCCA GCTGGTGTGG AAGACAGTGG GGTCACTACTG 120  
 GGTTAGAGCC CACATAGCAC TAAAGTCTT CAACATGCAA TTAGAAGCTC AATGTTGAC 180  
 60 GGGAAATATG TTCACTCTAA AAAAGATGTT TCTATTAGAA TTTACTTACT CTTCATGAA 240  
 AACATAGATG CTTCCTCTTT CTTGATTAGT GATGGCCATC AGTTAACCCA AGTGCACTCA 300  
 GAGAGTCAA ATTCTGACAC AATCCAGCAA GTAACATATA AAACATGATG CCCAGTCGAA 360  
 GAATATCAGC TGTCTCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAG AGATTGAGA 420  
 AATTTCTGTA AGCTCTTGAA GCCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480  
 65 AGAGCAAAGG CTACCAAGCA CTGCAACAGC CTGAATGGAG TCCTGCACTG TACCTGTGAA 540  
 GACAGCTACA CTTGGTTTCC TCCCTCATGC CTTGATCCCC AGAAGTGTCT CTTTCAACAG 600  
 GCTGGAGCAC TCCCAAGCTG TGAATGTCT CATCAACACC TCAGCCAGAG TGTCAATTC 660  
 TGTGAGAGAA CAAGATTG GGGCACTTTC AAAATTAAATG AAAGGTTTAC AATGACCTT 720  
 TTGAATTCAT CTTCGCTAT ATACTCCAAA TATGCAATG GAATGAAAT TCAACTTAAA 780  
 70 AAAGCATATG AAAGAATTCA AGGTTTGGAG TCGGTTGAGG TCACCCATT TCGAAATGGA 840  
 AGCATCGTTC CTGGGATGTA AGTTGTTGGC TCCAGCAGTG CATCTGAAT GCTGTACGCC 900  
 ATTGAACTAT TTGCGAGAA GGCTAAGACA GCCCTTCACA AGCTGTTTCC ATTAGAAGAC 960  
 GGCCTTTCA GAGTGTCTGG AAAAGCCAG TGTAAATGACA TTGCTCTTGG ATTTGGGTCC 1020  
 AAGGATGATG AATATACCTT GCCTGCAGC AGTGGCTACA GGGGAACAT CACAGCCAG 1080  
 75 TGTGATCTCT CTGGGTGGCA GGTCAACAG GAGACTGTGT TGCTCTCTCT GCTTGAAGAA 1140  
 CTGAACAGTA ATTTCAATAT GATTGAGGC AATGCCACTG AGGCAGCTGT GTCACTCTTC 1200  
 GTGCAAAATC TTTCTGTCT CATTCGGCAA AACCATCAA CCACAGTGGG GAATCTGGCT 1260  
 TCGTGTGTGT CGATCTGAG CAATATTCA TCTCTGTAC TGGCCAGCCA TTTCAGGGTG 1320  
 TCCAATCAA CAATGAGGTA TGTATCAGT ATAGCTGACA ATATCTTATA TTCAGCTCA 1380  
 80 GTACCAACT GGCAGTCTT ACTGCGGAA GAAAGTATG CCAGCTCAG GTFACAGAG 1440  
 ACATTAGAAA ACATCAGCAC TCTGTGCTT CCGACAGCTC TTCTCTGAA TTTTCTCGG 1500  
 AATTCATTG ACTGGAAGG GATTCCAGTG AACAAAGCC AACTCAAAAG GGGTTACAGC 1560  
 TATCAGATTA AATGTGTCT CCAAAATACA TCTATTCCA TCAGAGGCCG TGTGTTAATT 1620  
 GGGTCAGACC AATTCAGAG ATCCCTTCCA GAAACTATA TCAGCATGSC CTCGTGACT 1680  
 CTGGGGAACA TTTCAACCGT TTCCAAAAT GGAATGCTC AGGTCAATGG ACCTGTGATA 1740

5  
10  
15  
20

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TCCACGGTTA TTCAAAACTA TTCCATAAAT GAAGTTTTC TATTTTTTTC CAAGATAGAG 1800
TCAAACCTGA GCCAGCCTCA TTGTGTGTTT TGGGATTTC GTGATTTTGA GTGGAAAGAT 1860
GCAGGCTGCC ACCTAGTGAA TGAAACTCAA GACATCGTGA CGTGCCAAATG TACTCACTTG 1920
ACCTCCTTCT CATATTGAT GTACCTTTT GTCCCTCTA CAATCTTCCC CGTTGTAAAA 1980
TGGATCACCT ATGTGGGACT GGGTATCTCC ATTGGAAGTC TCAITTTATG CCTGATCATC 2040
GAGGCTTTGT TTTGGAAGCA GATTAAAAAA AGCCAAACCT CTCACACACG TCGTATTTCG 2100
ATGGTGAACA TAGCCCTGTC CCTCTTGATT GCTGATGCTC GGTTTATTGT TGGTGCCACA 2160
GTGGACACCA CGGTGAACCC TTCGGGAGTC TGCACAGYTG CTGTGTTCTT TACACACTTC 2220
TTCTACCTCT CTTGTTTCTT CTGGATGCTC ATGCTTGGCA TCCTGCTGGC TTACCGGATC 2280
ATCCTCGTGT TCCATCACAT GGGCCAGCAT TTGATGATGG CTGTTGGATT TTGCTGGGT 2340
TATGGGTGCC CTTCTATTAT ATCTGTGATT ACCATTGCTG TCACGCCAAC TAGCAATACC 2400
TACAAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAACC ACTCCTGGCT 2460
TTTGTGTGCC CTGCACTGGC TATTGTGGCT GTGAACCTCG TTGTGGTGGT GCTAGTTCTC 2520
ACAAAGCTCT GGAGGCCGAC TGTGGGGAA AGACTGAGTC GGGATGACAA GGCACCATC 2580
ATCCGCGTGG GGAAGAGCCT CCTCATTCIG ACCCTCTGCT TAGGGCTCAC CTGGGGCTTT 2640
GGAATAGGAA CAATAGTGA CAGCCAGAAT CTGGCTTGGC ATGTTATTTT TGCTTTACTC 2700
AATGCATTCC AGGCATTTT TATCTTATGC TTGGGAATAC TCTTGGACAG TAAGCTGCGA 2760
CACTTCTGCT TCAACAAGTT GTCTGCCTTA AGTCTTGGGA AGCAAACAGA AAGCAAAC 2820
TCATCAGATT TATCTGCCAA ACCCAATTC TCAAAGCCTT TCAACCCACT GCAAAACAAA 2880
GGCCATTATG CATTTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940
GCTCAAATG AATAA

```

**A98 PROTEIN SEQUENCE**

25  
30

```

Gene name: putative GPCR, Weakly similar to dJ365012.1
Unigene number: Hs.256897
Protein Accession #: none found
Signal sequence: 1-17
Pfam domain: 7tm_2 [561-820]
Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789
Cellular Localization: plasma membrane

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35  
40  
45  
50

```

1 11 21 31 41 51
| | | | |
MHALLLCFVS LMGASGLSL QSPVEBYQL LQVTRYDSKE KRDLRNLFLK LKPLPLWSRG 60
LIRIIRAKAT TDGNSLNGVL QCTCEDSYTW FPFSCIDPQN CYLHTAGALP SCECHLNLS 120
QSVNFCERTK IWGTFKINER PTNDLLNSSS AIYSKYANGI EIQLKKAYER IQGFESVQVT 180
QFRNGSIYAG YEVVSSSSAS ELLSAIERVA EKAKTALHLK FPLEDGSFRV FGKAQCNDIV 240
FGFGSKDDEY TLPSSSGYRG NITAKCESSG NQVIRETCVL SLLBELNMF SMIVGNATEA 300
AVSSFVQNL S VIKRQNPSTT VGNLASVVSI LSNISLSLA SRFVSNSTM EDVISIADNI 360
LMSASVTNWT VLLREKYAS SRLLETLENI STLVPPTALP LNFVRKPIDW KGIFVNSQL 420
KRGYSYQXKM CPQMTSIPR GRVLIGSDQF QRSLPETIIS MASLTGLNLL FVSENGNAQV 480
NGFVSTVIQ MYSTNEVFLF FSKIESNLQ PHCVFWDPSH LQWMDAGCHL VNETQDIVTC 540
QCIIHLSFSI LMSFPVPSII FPFVKNITVY GLGISIGSLI LCLIEALFW KQIKKSQTS 600
TRRICMVNIA LSLIADVWF IVGATVDTTV NPSGVCTAAV FTFHFFYLSE FFMMLGLIL 660
LAYRIILVFH RMAQHLMAV GFCLGYGCP L IISVITIAVT QPSNTYKRD VCNLWNSGS 720
KPLLAFFVPA LAIVAVNFVV VLLVLTKLWR PTVGERLSD DEATITRVGK SLLILTPLLG 780
LWNGFGIGTI VDSQNLAMHV IFALLNAPQV RTVTITYCIV K

```

**A99 DNA SEQUENCE**

55

```

Gene name: putative G-protein coupled receptor
Unigene number: Hs.16065
Probeset Accession #: F07953
Nucleic Acid Accession #: NM_016334
Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

```

60  
65  
70  
75  
80

```

1 11 21 31 41 51
| | | | |
AGCACCTGGG AAAAGGCAGA CGGTGTGAGG GGGCCTGTGG CCCAGCGTG CTGTGGCCTC 60
GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTGTGGA TTTGGGTGGC TTTTCTTCAT 180
GCGCCAAATG TTTAAAGACT ATGAGATAGC TCAGTATGTT GTACAGGTGA TCTTCTCCGT 240
GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
GAATAGCAGC TCCGTTTATT TYCACTGGAA AATGAACCTG TCGTAATTC TGCTGATCCT 360
GGTTTTCATG GTGCCTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
TAACAACAAG CTGCTTTTTT CCGTCTCTCT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
ACTAGGAGAT CCGTTTCCCA TTCTCAGCCC AAAACATGGG ATCTATATCCA TAGAACAGCT 540
CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTTCTTCTCTG GATTTGGTGC 600
TGTCACCTGC CCACTACACT ACATGCTTCA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
TCTAGCCCTG GAACGGGAGC TGCTGCAAC CATGGATATG ATCATAAGCA AAAAGAAAG 720
GATGCAATG GCACGAGAA CAATGTTCGA GAAGGGGGA GGCATAACA AACCATCAGG 780
TTCTGGGGGA ATGATAAAAA GTGTTACCA TTAGCATCA GGAAGTGAA ATCTTACTCT 840
TATTCAACAG GAAGTGGATG CTTTGGAGA ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
TGATCTATAT GCTACCAAG AGAGAATAGA ATACTCCAAA AOCITCAAGG GGAATATTT 960
TAATTTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
CAATATTGTT TTTGATCGAG TTGGGAAAAC GGATCCCTGC ACAAGAGGCA TTGAGATCAC 1080
TGTGAATTAT CTGGGAATCC AATTGATGT GAAGTTTGG TCCCAACACA TTCTCTCTCA 1140
TCTTGTGGA ATATCATCG TCACATCCAT CAGAGGATTC CTGATCACTC TTACCAAGTT 1200
CTTTTATGCC ATCTCTAGCA GTAACTCTC CAATGTCTAT GTCTGTCTAT TAGCACAGAT 1260
AATGGGCATG TACTTGTCT CCTCTGTGCT GCTGATCGA ATGAGTATGC CTTAGAAATA 1320
CGCACCATATA ATCACTGAAG TCCTTGAGA ACTGCAGTTC AACTCTCATC ACGTGTGGIT 1380
TGATGTGATC TTCTGTGCTA GCGCTCTCTC TAGCATACTC TTCCTCTATT TGGCTACAAA 1440

```

	ACAGGACACCA	GAGAAGCAAA	TGGCACCTTG	AACCTAAGCC	TACTACAGAC	TGTTAGAGGC	1500
	CAGTGGTTTC	AAAATTITAGA	TATAAGAGGG	GGGAAAAATG	GAACCAAGGC	CTGACATTTT	1560
	ATAAACAAAC	AAATGCTAT	GGTAGCATTT	TTCACTTCA	TAGCATACTC	CTTCCCCCTC	1620
5	AGGTGATACT	ATGACCATGA	GTAGCATCAG	CCAGAACATG	AGAGGGAGAA	CTAACTCAAG	1680
	ACAATACTCA	GCAGAGAGCA	TCCCGTGTGG	ATATGAGGCT	GGTGTAGAGG	CGAGAGGGAG	1740
	CCAAGAAACT	AAAGGTGAAA	AATACACTGG	AACCTCTGGG	CAAGACATGT	CTATGGTAGC	1800
	TGAGCCAAAC	ACGTAGGATT	TCCGTTTAA	GGTTCACATG	GAAAAGGTTA	TAGCTTTGCC	1860
	TTGAGATTGA	CTCATTAAAA	TCAGAGACTG	T			
10	<u>A100 Protein sequence</u>						
	Gene name: putative G-protein coupled receptor						
	Unigene number: Hs.16085						
	Protein Accession #: NP_057418.1						
	Signal sequences: none found						
15	Transmembrane domains: S-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446						
	Cellular Localization: plasma membrane						
	1	11	21	31	41	51	
20	MSFLIDSSIM	ITSQILFFGF	GNLFFMRQLF	KDYBIRQYVV	QVIFSVTFAF	SCTMFELIIF	60
	EILGVNLSSS	RYFRHKNMNC	VILLILVFMV	PFYIGYFIVS	NIRLLHKQRL	LFSCLLWLTF	120
	MYFFWKLGGP	EPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYFLRN	180
	VTDTLILALE	RRLLQITMDMI	ISKKKRMAMA	RRTMFQKGEV	HNKPSGFMGM	IKSVTTESAS	240
	SENLTLIQQE	VDALKEELSRQ	LFLETADLYA	TKERIEYSKT	FKGRYFNFLG	YFYSIYCVWK	300
25	IFMATINIVP	DRVGKIDPVT	RGEITVNYL	GIQFDVKFWS	QELSFILVGI	IIVTSIRGLL	360
	ITLTFFPFAI	SSSKSSNVTV	LLLAQIMGMX	FVSSVLLIRM	SMPLRYRTII	TEVLGELQPN	420
	FYHRWFDVIF	LVSLSSILF	LXLAHQAPE	QKMAP			
30	<u>A101 DNA SEQUENCE</u>						
	Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]						
	Unigene number: Hs.19322						
	Probeset Accession #: AA088458						
	Nucleic Acid Accession #: AA088458						
35	Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)						
	1	11	21	31	41	51	
40	GCCCTTGGAC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
	CTGAAGAAAA	AGGAGCTGGA	GCAGGAGAA	GAGGTGCTGC	TGCAAGGTTT	GGAGATGATG	120
	GGCGGGGGCT	CGACTTGGA	CCAGCAGCAG	CTGCACACGAG	TGCAGGAGCG	CCAGCCCGCC	180
	CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTTCAG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTGC	CCAGAGTACA	AGAGGTGGCC	CGGTGCTGGG	GGAGCTGTCT	GGCTGCACCC	300
	TGTGCCAGCC	GGGCCCTGCC	CCCGTCTCTC	TCCGGGCCCC	CCTGCCCTGC	CTTGACGTCC	360
	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGACTC	420
45	CTCACCCAGG	AGGTGACCGA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAGTCTG	480
	GCGCTCAITA	AGCAGCTGTT	TGAGGCCCGC	GCCTTGAGCC	AGCAGGACCG	GGGACCTCTG	540
	GATTCCACCT	TCATCTGATC	CTTGTGGGCC	GGGTGGGCC	CCAGGGCCAG	CTTGCACTC	600
	AGCCCTTCGA	GGGTGGGGCG	CCCATCGCAC	CCACCTCTCT	TGGCTGBAGA	CCCCCGGCG	660
	GCCAGGCGAC	AGTCCCGGAG	TGGGCCTCTT	CTGCGGCCCC	TGCGCAGATG	GGCTCCCGAG	720
50	GCCTGCCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTTCGGCTC	CTGGTTGCTG	780
	ACATGGGCTG	GGGCTCTCTT	TGAGTCCGCA	TAGTCCGCG	CTACTACTGG	CCGCTGTCTG	840
	TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCGCCG	TTTCCAGCGG	TGCGGCCCTG	900
	GGTCCCATCT	TCAGGGAAG	GCACCTGCTA	CGCCAGGCTG	CACCTCCAC	AACGGGCAGC	960
	AGAGGGCGCG	GGGGCGCTCC	GACGCGGGTC	CAGGGCGAGC	TTCCCGCTCA	ACCAGGGCAC	1020
55	CAGGACGAGG	TGGCTGTAGC	TGGACCGGAC	GGAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAGCGGGG	GGTGCTTGCC	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTCCG	ACTTCAGGTT	1140
	CTGGCCAGCG	CTGAGGAGCC	CTGGCTGCAG	CGGATCGGCA	CGCCGGGTGG	GGGAGAGCTT	1200
	GGCCTGCTAT	TGGCTCCGAC	AGACCTTGGG	GTGATGGCTT	TCCCGCTCTT	GGCGGGGAGG	1260
	TGCGCCGAG	TTGAGTCCCA	CACACATCC	TGTGAGCGTG	GCTCCCGAGG	AGGGCCGCTA	1320
60	GACAGCTCCC	AGGCACGTCA	TAGGCAAGGC	CTGTTTCCCG	CGACTCAGGA	TTTCCAGGCG	1380
	CTGGGGTCTC	GCTCACCCCC	CTTGTCTCTC	ACGCCGAGCC	TGTCCCGAGG	TTTCAGCTGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAGC	GAGAACCCCG	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCGTGCCCA	GGCCCACTCC	CGTGGTGTCT	1560
	GGAGTACGCA	CTGGTGGGGG	GGCCCTGCTC	AGCCCACTCT	GGAGGGTCCC	AGTGTACCCA	1620
65	GAAACAGGGG	CAAGGCAACA	GCATCGATGG	GTTCTGCAGC	CCAGGGGCCG	CGATGGGGGG	1680
	TCAGTGTGTG	TGGGGCGCAG	GGCCTCGGAT	GGCGGGTCAG	TGCCTGGGGG	GGCGAGGGCC	1740
	CCCGATGCGG	GGTCAGTGGG	TGGGGGGCGC	AGGGCCCGCT	CGTGTCCAGG	GCACCTTGGT	1800
	ACACTGTCCC	ACAAGGCACC	TGTCTCAGAG	GAGGGCGCCT	GGCAGGCAGC	GTGGCAACTC	1860
	CCCTCCGGAG	CCAGCTCCCA	TGCTAACCTG	CCCAAGCAG	CCCCACAGCA	CCACATTCCC	1920
70	TGCTGCACCT	GGTCTGCAGG	GGTGTCCGAG	GACAGGCCCA	AGTCAGGCCA	GCATGCAGCT	1980
	GCCCTCTCTC	CTTGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCGCTG	2040
	ACCTCTCTGG	CAGGAAGAGG	TGCAGGTCTT	GAGGGCTGCT	CCCCACAGCG	CCAGCAGCTC	2100
	AGGTGAGCTG	CAGCGCAGTG	GGTGGGCCAG	TGGCAGCCAG	GGAGAAGCCC	CCGCTCAGCA	2160
	GGCTGGGGTC	TGCCACCCAG	GGCCTCCCCA	CGTCTGCCCT	TGAGGGTGGC	TGCCATGGCC	2220
75	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AGGCAGGAGA	CAGACAGATG	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGAGACC	GCCCAACATG	AGCTGGAGCC	CGCAGCTGAA	GGGGAAGTGT	2340
	GAGACAGGCT	GGTACCTCCG	GAAAGAACTG	CTTTACAGCT	TGGTGTCTCC	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAAGTG	CCCTGGAGAC	2460
	CACGAGGGCA	GAAATTTAAG	GCCCGGCTG	GCAAGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
80	GCAGACCCCT	CCTGGAGCCT	GCCCTAGGAC	GCTGGGGCGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CCTGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAAGT	ACATACAGCT	2640
	GGGTGCACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTA	TCCTTGGGGG	2700
	CAGAAAGTGT	CCCAATTTAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTGTGTGTG	ATCAAGTTCC	AAGGAAAGG	AACATCTCAG	CCGGGCGTGG	TGGTTCAAGC	2820

5 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880  
 CCCCATCTCT ACBAAAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940  
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000  
 TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060  
 AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

# A102 DNA SEQUENCE

10 Gene name: TMPS83a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Nucleic Acid Accession #: AB038157  
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51  
 | | | | |  
 ACCGGGCACC GGACGGCTCG GGTACTTTCC TTCTTAATTA GGTTCATGCC GTGTGAGCCA 60  
 GGAAGAGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGCC CTACTATCTC TTCCTGGTGG 120  
 CCATCTACAT TTTTGGGACT CGGGAATATG GAGGTAGAGG TGGAGGCCGA GCCGGATGTC 180  
 AGAGGTCCTG AAATAGTCCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240  
 TCATTCCGAT CGCTTTTTCG CCTTGATGAT TTGAAATAAA GTCCCTGTGC ACCAGATGCA 300  
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360  
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTOGACTGC 420  
 TCAGGGAGAT ACAGATGTGG CTCTATCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480  
 GGAATCTCCG ATTGCAAGAA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540  
 AATGCCGTGC TCGTGGGTGG CACAGCTGCT TCGTGAAGA CCAATGTGTC CGATGACTGG 600  
 AAGGGTCACT AGCAAAATGT TGCTGTGCCC CAACTGGGTT TCCCAAGCTA TGTGAGTCA 660  
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720  
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780  
 TGTGCTCTCG GCCACGTGGT TACCTTCGAG TGCACAGCCT GTGCTCATAG AAGGGGCTAC 840  
 AGCTCAGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900  
 CTTGAGTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACBCCCTC GTGATCATC 960  
 ACTGCTGCAC ACATGTTTTA TGACTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020  
 CTAGTTTCCC TGTGGACAA TCACBCCCA TCCCACTTGG TGGAGAGAT TGTCTACCAC 1080  
 AGCAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GCGCGGGCCA 1140  
 CTACCGTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTTCCC 1200  
 GATGGAAAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGAAGCC 1260  
 TCCCTGTGCC TGAACCAAGC GGCCGTCCCT TTGATTCCA ACAGATCTG CAACCACAGG 1320  
 GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTCGG CGGGCTACCT GACGGGTGGC 1380  
 GTGGACAGCT GCGAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440  
 AAGTTAGTGG TACGACCCAG CTTTGGCATC GGCTGGCAG AGGTGAACAA GCTGGGGTGG 1500  
 TACACCCGTG TCACCTCTCT CCTGGACTGG ATCCACAGAC AGATGGAGAG AGACTAAAA 1560  
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620  
 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680  
 TTCGGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAACTT 1740  
 CAAGCTGCTT TTTGTTTTTT GGTGGAGTCT CGCTCTGTGG CCCAGGCTGG 1800  
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCTCCGCTT CCCTGTGTC AGCGATTCTC 1860  
 TTGCTCAGC TTCCCGAGTA CTTGGGACCA CAGGTGCCCG CCACCAACCC CAACTAATTT 1920  
 TTGTATTTT AGTAGAGCA GGGTTTACC ATGTTGGCCA GGTCTCTCTC AAACCCCTGA 1980  
 CCTCAATGA TGTGCTGCTT TCAGCTTCCC AAGTGTCTGG GATTAAGAGC ATGGGCCACC 2040  
 AGGCTAGCG TCAAGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAGCA GCAACTTGCA 2100  
 AGGGCGGCTT TTCCACTGG TCCATCTGCT TTTCTCTCCA GGGGTCTGTC AAATTCCTG 2160  
 ACAGATAGC ACCTCAAGTG ACCTCAAGTG CAAGGCCACC AACAGCCTCT CAGAAAAGAC 2220  
 GCACCAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCATCTCTA GGGACCAAGAA 2280  
 CCAAAACCAC CCTTCTTACT TCCAAGACTT ATTTTCACAT GTGGGAGGT TAATCTAGGA 2340  
 ATGACTGTT TAAGGCTTAT TTTCATGAT TCCTGTAGC ATTGTGTGCT TGACGTATTA 2400  
 TTGTCCTTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460  
 AAAAAA

# A103 Protein sequence:

65 Gene name: TMPS83a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51  
 | | | | |  
 MGENDFPAVE APFSFRLFLG LDDLKISFVA PDADAVAAQI LSLPLKFFP IIVIGIIALI 60  
 IALAIGLGIH FDCSGKYRCR SBFKICIELIA RCDGVSDCKD GEDEYRCVRV GQNAVLLQVF 120  
 PAASWKTMCB DDMKGYANV ACAQLGPPSY VSSDNLRVSS LEGQFREBPV STIHLPLPDK 180  
 VTALHESVYV REGCASHGVV TLQCTACGHR RGYSSRIVGG NMSLLQWPNW QASLQFQGYE 240  
 LCGGSVITPL WITTAARCVY DLYLPSKWTI QVGLVSLIDN PAPSHLVEKI VYHSKYKPKR 300  
 LGNDIALAKL AGPLTFNEMI QPVCLPNSRZ NFPGKVCWT SGWGATEDGA GDASPVLNHA 360  
 AVPLISNKIC NHRDVGII SPSEMLCAGYL TGGVDSQCGD SGGPLVCQR RLWKLVGATS 420  
 PGIGCAEVNK PGVITRTVTSF LDNIHQMER DLKT

**A104 DNA SEQUENCE**

Gene name: Homo sapiens G protein-coupled receptor (H077175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM\_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
10  ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCTCTGG GGGCACCAGC CAACGCCCTCC 60
    GCGTGGCCGG GCTGTGGCGC CAACGCCCTG GACGGCCAGC TCCCTTCCGC GCGGGCCGTG 120
    GAGCCCTGGC TCGTACCGCT CTCTTTCGGC GCGCTGATGC TCGTGGGCTT GGTGGGGAAC 180
    TCGCTGGTCA TCTACGTCAT CTGCGGCCAC AAGCCGATGC GGACCCGAC CAACCTTCTAC 240
15  ATCGCCAAAC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300
    CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT CGTCAACTAC 360
    ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
    TGTGACGTGA CGGTGTTCCC GTTGGCGGCC CTGCAACGCC GCACGCCCGC CTGGCGCTG 480
    GCGTGCAGCC TCAGCACTG GGTAGGCTCT GCGCGCGTGT CTGCGCGGCT GCTCGCCCTG 540
20  CACCGCTCTG CACCCGGGCC GCGCGCTTAC TGCAGTGAAG CCTTCCCGAG CCGCGCCCTG 600
    GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGTGCGGCT GCTCGCCACC 660
    TCGCGCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGGTGGC CCOCGCGCCC 720
    GCGGATAGCG CCCTGCAAGG SCAGGTGCTG GCAGAGCGCG CAGGCGCGCT GCGGGCTAAG 780
    GTCTCGCGCG TGGTGGCGGC CGTGGTCTCT CTCTTTCGCG CCTGCTGGGG CCOCATCCAG 840
25  GTCTTCTCTG TGTGCGAGCC GCGGGCGCCC GCGGGCTCTC GGCACCCAG CAGCTAGGCC 900
    GCGTACGCGC TTAAGACTGT GCGTCACTGC ATGTCTTACA GCAACTCTGC GCTGAACCCG 960
    CTGCTCTACG CCTTCTGGGG CTGCACTTTC CGACAGGCTT TCGCGCGGCT CTGCCCCCTG 1020
    GCGCGCGCGC GCGCGCGCGC CCGCGGCCGG CCGCGACCCT CCGACCCGCG AGCCCCACAC 1080
    GCGGAGCTGC ACCGCGCTGG GTCCACCCCG GCGCGCGCGA GCGCGCGAGC GCCAGGGAGC 1140
    AGTGGGCTGG CGCGCGCGCG GCTGTGCGCT CTGGGCGGAG ACAACGCCCC TCTCTGA

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**A105 Protein sequence**

Gene name:

Homo sapiens G protein-coupled receptor (H077175), mRNA  
Hs.208229

Unigene number:

AI819198

Protein Accession #:

none found

Signal sequence:

7tm\_1 [59-323]

Pfam domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282  
plasma membrane

Transmembrane domains:

Cellular Localization:

```

1      11      21      31      41      51
|      |      |      |      |      |
45  MHTVATSGEN ASWGAANANAS GCPGOGANAS DGPVPSPEAV DANLVPLFFA ALMLLGLVGN 60
    SLVIVVICRH KPMRTVINFY IANLAATDVT FLLCCVPFTA LLVPLGHWL GDFNCKFVNY 120
    IQQSVQATC ATLTAMSVDR WYTVFPLRA LRRRTPLRAL AVSLGHWGS AAVSAPVLAL 180
    HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACTAAMLRH LGRVAVRPAP 240
    ADSALQQQVL AERAGAVRAK VSRLLVAAVL LPAACWGPFIQ LFLVLQALGP AGSWHFRSYA 300
50  AYALKTMAHC MSYSNSALNP LLYAFILGSHF RQAFERKVCPC APRFRFRPRR PPSDFPAAEH 360
    AELHRLGSHF APARAQKFGS SGLAARGLCV LGEDNAPL

```

**A106 DNA SEQUENCE**

Gene name:

Integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM\_062214

Coding sequence:

680-2990 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
60  CCCAGAGCGG CCTCCCCCTG TTGCTGGCAT CCCAGCTTC CTCCCTGACC AGCCAGGACG 60
    CTGCGGACTT GCTTTTSCCC GCTGCTCGCG AGACGGGGCT GCAAGCTGC AACTAATGGT 120
    GTTGGCTTCC CTGCCACCTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180
65  TCCCTCGAC CTGCGCGCGG TACCTTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
    TAGGCTGCTT TCCCCCCAG CTTCGGGCTT TGTFTGGGTT TGATTGTGTT TGGCTCTTCG 300
    CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGAGGA GAACCAAAAG CTCTTTTCTT 360
    TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCT GCGGGGCTCT 420
    TGGCCGTGGA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCGGGGAG 480
70  GCGCGTAGGG GCCCTGAGAT GCGAGCGGCT GCCCGGGCCC GCTTAAGTGC AOCGCTTGCT 540
    CCGAGCGCGG GGGTCCGCTT GCTAGGCTTG CGGAAACGCT CCTAGGACA CTGCGCGCGG 600
    GCGCGGAGGG TCGCCCGGGA GGCGGAGCCC GCGTCCGGAA GGCAGCCAGG CCGCGGGGCG 660
    GGGCGCGGCT GTTTGTCATT ATGTGCGGCT CGGCCCTGCG TTTTITTTACC GCTGCTTTG 720
    TCTGCTTGCA AAACGACCGG CGAGGTCCCG CCTGTTTCTT CTGGGCGAGC TGGGTGTTT 780
75  CACTTGTCTT TGGAGTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGACAGAT 840
    CCTGTGCGAG GTTCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTCAA GAGGATTCTA 900
    TTTAGGTTGG ATCAAGAGT GAACGTGTG ATATGTGTTT CAATTTAATA AGCAAGGCT 960
    GCTCAGTTGA TTCAATAGAA TACCATCTG TGCATGTTAT AATACCCACT GAAATGAAA 1020
    TTAATACCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAGCTA 1080
80  ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCTGTT GGATCTTTAT TATCTTGTG 1140
    ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTAT 1200
    CTAGAAAATG GCAATTTTTC TCCGTTGACT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260
    AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTACT 1320
    ACAATTTAGA CTGATGCGCT CCCCATGGAT ACATCCATGT GCTGTCTTGT ACAGAGACA 1380
    TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACAG 1440

```

5 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560  
 GCAAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACAACTGCT 1620  
 ACGTCAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680  
 ACACACACAT TAATGTGATC TTGTGAGTTC AAGGAAACAC ATTTTCATTG TATAAGGATC 1740  
 TTCTACCCCT CTGTCCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800  
 ATAATTTGGT AGTGGGAAGC TATCAGAAGC TCATTTCAGA AGTGAAAGTT CAGGTGGAAA 1860  
 ACCAGGTACA AGGCATCTAT TTAAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920  
 CAGGCATGGA AGGATGCGGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980  
 10 TTCAATGTAA AAAATGTGAT GTACACAGGAG GAAAAAATA TGCAATAATC AAACCTATTG 2040  
 GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCTG TGTGAGGACA 2100  
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTCCTAGT 2160  
 GTGATGAGAA TAAATGTCAAT TTGATGAAG ATCACTTTTC TTCTGAGAGT TGCAAGTCAC 2220  
 15 ACAAGGATCA GCCTGTTTGC AGTGTGCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280  
 ACAAAATTAA GCITGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340  
 CATATCACCA TGGAAATCTG TGTGTGAGG ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 TCAATTCAAA GGGCCAAAGT TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520  
 20 GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCGCACTGTG TATACAGCCT 2580  
 GCAAGGAAAA CTGCAATGAT ATGCAATGCC TTCACTCTCA CAATTGTGCT CAGGCTATAC 2640  
 TTGATCAGTG CAAACCTCA TGTCTCTCA TGGAAACACA GCATTATGTC GACCAAACTT 2700  
 CAGAATGTTT CCGCAGCTCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACTT 2760  
 TCTTGATTGG GTGCTTAAA GTCCCTGATCA TTAGACAGGT GATACTACAA TGGATAGTA 2820  
 25 ATAAATTTAA GTCTCTATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATTC 2880  
 TGCAAAATGT CTGCAAGAAA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAGATTTT 3000  
 TTAAACACTT AATGGGAAAC TGGAAATGTT AATAATTGCT CCTAAAGATT ATAAATTTAA 3060  
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGTTGTG ACACTCGAAC 3120  
 30 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGTTGTA GCACTTTACT GTAATATATA 3240  
 ACTTATTATG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300  
 TACCTGTTAT CCGTACGCTT CCGAGAGAGA ACAAATGCTG GAGAGAGTPT AGCATTGTGT 3360  
 CACTACAGG GTACAGTAAT CCGTGCACAG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420  
 35 TATATTCTAA GGTTCGCAAA CACTTCAACA GTTGGTGGT GAATAGACAA GAACAGCTAG 3480  
 ATGAATAAAT GATTCGTGTT TCACCTTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540  
 AAAGATTATT GCTTTTAAA GTGTGTAGTT TTATGCAATG GTGTTTATGG TTGCTTATT 3600  
 TTGTGAGATG GATACATAT TCTCTCTTT GCCTTTATGT TTTGTTTCT 3660  
 40 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAAT GCTAAGTTAC 3720  
 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTAAAGGCT 3780  
 GAATGTTAA

**A107 Protein sequence:**

45 Gene name: Integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 Signal sequence: 1-39  
 50 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 TNF domain: 54-469  
 Cellular Localization: plasma membrane

55  
 1 11 21 31 41 51  
 60 MCGBALAFT AAFVCLQNDR RGPASFLWAA WVPSLVLG LG QGENDRCASS NAASCARCLA 60  
 LGPECGWCVQ EDFISGGRS ERCDIVSNLI SKCCSVDSIE YPSVHVIIPT ENBINTQVTP 120  
 GEVSIQLRPG AEANFMLKVH PLKKYFVDLY YLVDVSAAMH NNIEKLNSVG NDLSRKMAFP 180  
 SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDVNLDCMP PHGYIEVLSI TENITEFEKA 240  
 VHRQKISGNI DTPGGFDAM LQAAVCESHI GWRKEAKRLI LVMTDQTSIL ALDSKLGLIV 300  
 VPNDGNCHLK MNVYVSTTM EHPSLGQLSE KLIDNNINVI FAVGQKQFHW YKDLLEPLFG 360  
 65 TIAGBIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAI CPDG SRKPGMSGCR 420  
 NVTSENDEVL NVTVTMKKCD VTGGKNYAI KPIGFNETAK ITHRNCSQ CEDNRGPKGK 480  
 CVDETFLDSK CFQCDENKCH FDEQPFSSBS CKSHEDQFVC SGRGVCVCGK CSCHKIKLSE 540  
 VYGYKECKDD FSCPYHHGNL CAGHGCEEAG RCQCPSQWEG DRQCPSAAAA QHCVNSKQV 600  
 CSGRGTCVCG RCECTDERSI GRFCEHCPTC YTACKENMNC MQCLHPENLS QAILDQCKTS 660  
 70 CALMEQOHYV DQTECFSSP SYLRIFPFIIF IVTFILGLLK VLIIRQVILQ WNSNKIKSSS 720  
 DYRVASAKKD KLILQSVCTR AVTYREKPE ETKMDISKLN AHETFRCNF

**A108 DNA sequence**

75 Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
 ATGCTGTCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60  
 GGAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC 120  
 GACCGGGAGA GCGAGAGCCG GCCGGAGGCT GCCCGGCTCC TGTGGGACCG CGCTGCAGCC 180  
 GGGGAGGCGG AGAAGGGGAA CCGGGCGGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240

5	CGCGGGCCGC	CGCCAGCTGG	GCAGGCTCCC	GGGACTGOGG	CTGGGGGCGC	GCAGGACCCCT	300
	CGCCTGCGTC	CTGGACGTTT	CCGGGGGAGG	GTCCGATTGC	CAGTGAAACC	TCCAGAGGCT	360
	TCCGACGAC	AGCCCCGGGG	GCCTTCTGAC	TGCATCCCGA	GATTTCCATC	AGCGAGTGCA	420
	ACTCATAAGG	CAGTCCCTAA	GGGACCCGGG	CCACCCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCTGGAC	CTAGGGCCCG	GCCTCGTCGC	CTCCTGGGCG	TCCGCGCAGA	GGGAGTGCC	540
	CCCGCGGAA	AGCGCGCGG	GACAGTCAST	GACBAGGCC	GGGGTCCGCC	GGGGCCAGA	600
	CTTCTGGAG	ACCCTCTG	GCTCTGGA	GACGCGCTGT	CCGCGCCAG	GGTGGTGCCA	660
	TGTGGGGCG	TGCGCGCTCG	TCCGTCTCCT	CATCTGGAA	CBCCGCTTCG	CTCCTGCAGC	720
10	TGCTGCTGGC	TGCGCTGCTG	GCGCGGGGG	CGAGGGCCCA	GCGCGAGTA	CTGCCACGGC	780
	TGGCTGGACG	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCCGAGCG	CTTGGACGGC	840
	GGCGAGCCCA	CCATCTGCTG	CGCGAGCTGC	GCGTTGCGCT	ACTGCTGCTC	CAGCGCCGAG	900
	GGCGCGCTGG	ACCAGGGCGG	CTCGACAAAT	GACCGCCAGC	AGCGCGCTGG	CGAGCCTGGC	960
	CGCGCGGACA	AAGACGGGCC	CCGACGGCTC	GGCAGGGCTT	CATGCTCTAG	GGGTACCCAA	1020
15	GGAGACGGCG	AGGGTGGGCC	CCDACCCTGT	AGGGCTTGGC	AGCGGTGCTC	CCCTGAAGGC	1080
	TCCCCGAAG	AGTCCCGCTT	CTCAGGGCT	TTCCCGGGCG	TGCTGCCCGC	TGCCAGACGC	1140
	CGCGGATTCC	CATCTTCTCC	ACCGGGCGGC	CCCTCTCCCG	TGCGAGCGCC	CGCCTTGCC	1200
	ATCTACGTGC	GCTTGGCTCC	TGTTGGCTCC	GCTTGGCTCC	CCCTTATCAT	CTTGGGTCC	1260
	CTGGTGGCAG	CCTGTTGCTG	CAGATGCTCT	CGGCTTAAGC	AGGATCCCCA	GCAGAGCCGA	1320
20	GCCTCAGGGG	GTAACCGCTT	GATGGAGACC	ATCCCATGTA	TCCCTAGTBC	CAGCACTCC	1380
	CGGGGTCTGT	CGTACGCGCA	GCTGCCAGTT	CCAGCTCCAG	CGCCAACTCC	CGCCAACTCC	1440
	GGGGCCCGGG	CGCCCCCAAC	AAGTTCACAG	ACCAACTGTT	GCTTGCCTGA	AGGGAACCATG	1500
	AACAACGTGT	ATGTCAACAT	GCCACGAAT	TTCTCTGTGC	TGAACCTGTA	GCAGGCCACC	1560
	CAGATTGTGC	CACATCAAGG	GCAGTATCTG	CATCCCCCAT	ACGTGGGGTA	CACGGTGCG	1620
25	CAGACTCTG	TGCCATGAC	AGCTGTGCCA	CCCTTCTATG	ACGCGCTGCA	GCTTGGCTAC	1680
	AGCAGATTTC	AGTCCCGCTT	CCCTCACACC	AACAGTGAAC	AGAAGATGTA	CCGAGCGGTG	1740
	ACTGTATAAC	CGAGAGTCA	TGGTGGGTTT	CTTACAGTAA	GGGAGACGAA	GGCAGGGGTG	1800
	GATCTCGAG	GTTGGAAGTCC	GCACATCTCG	GTTGATTTTA	TGGCAGGATT	CCTTGGATG	1860
	GCTTCATTTC	CCCCCAGACT	GTATGAAAC	ATCTCGAAT	TAGCATTTCT	GGATATGTTT	1920
30	CATCCAGGGT	ATCATTTGAT	TATGATGAA	AACCGGCTCT	AGCTGGAGAT	GACTGTGATG	1980
	TGCTGATGG	GCTGTATACA	AATGCTTGAG	TCCGAAAGTG	CCTTGAGATA	TGGTTGACGA	2040
	AAGAATTTTA	TAAACTGATA	AATTAAGGAT	TTTATTTATG	TGTTTATTTA	TATTTCTTTT	2100
	TGTTGTTGA	CTGCACAGGA	TCAAATGCC	TGTTATCTCC	CTTTACTGCG	GACTTTTFTT	2160
	TTTTTTTTTT	TTTTTTTTTA	TCAGACAGGG	TCCTGCTCTG	TGCCCCAGGC	TGGAGTGCG	2220
35	TGGTGCGATC	TGGGCTCACT	GCAACTTCAG	CTCTCTGGAT	TCAGSCAACA	CTCCTGCCCT	2280
	AGCCTCCAC	GTTGGCTGGGA	TTACAGGTGC	CTGCCCCCAT	GGCTAAATTT	TTGTATTTTT	2340
	TGTAGAGATG	GGGTTTCAAC	ATGTTGGCTG	GGCTGGTCTC	ACTCTCTGTA	CTCAAGCAA	2400
	TCCTGCTGTC	TCAGCTCCCG	AAAGTGGCTG	GATTACAGGC	GTTAGCCACC	GCCCCAGCC	2460
	TGAGCCFTTT	TTTTTTCTA	ATGCATCCAA	GGTTAAGGGG	AAGAGCGAAA	TAACAGGACT	2520
40	ATTCTAAAG	GAAACCTGTT	TGAACCTGTT	GAGATCAGTC	ATCAGTCTCA	GTATTCACCA	2580
	GGCACACCTT	AATTTCAATG	TAAAAAGATA	TATATATTTT	GTCTATTTTT	GTGCTTTTGG	2640
	GGGCTTATTT	TGTGCTTTTT	TACCTTATGT	AGAGATCTTA	TTACAAGGTG	ATTTTCTACA	2700
	TTAAAAAGAG	ACTGAATAA	ATTGTATAT	TACTTAACCTA	ATGAAGACAT	TTCAAGACTC	2760
	TGGATGATT	TGAATCTTCA	AGTAGTAGGT	GGTATAGTCA	TAAACCAATT	CATCCCCCTC	2820
45	TTGATTGTAT	CTTAATTTTC	TGGCTTTAAG	GTGACATCTG	AGAGGTAAATG	CATCTTTTTC	2880
	TATATTGAAA	TCATAAACA	TCACCCGCTG	CTTCTCTGAG	TTACTTTTAA	TTTTGCGCTG	2940
	TGGTATGGT	TTGGGCTTTC	CTTCTGTTTG	GTTTTCAGAG	CCCATGCTCT	ATATAGTCTC	3000
	GAGTCAAGT	AATTTCTATA	CTTGTAAATG	AAGATCAGTA	TTCTGCTCTA	GATCTGATAA	3060
	AAAAATTTTC	TGTCCTTAGT	TATAAAATTT	CAAGAAATG	TGTTACAAAG	ATACTTAGTA	3120
50	TAGCTCTCTA	GCCATACCTT	GAGACTTGGG	ATGAAATTTA	AACAGATAC	GATTACTTTT	3180
	GCAGATCA	AGGCTTTTTA	TACTCTTGT	ATCAAAATGG	CTTATTTTTC	AGGCACTAAG	3240
	GATTTGTAG	AGAAAGCTT	TTCAACGAAG	GATTGCTTTT	CTTCTCCAC	ACGTGCTCTG	3300
	ATTCTCTCTA	TCCTTACAGC	CTCAACAGGC	ACTGTATTCA	TGCGCAATGT	TCCAAATAT	3360
	CAATTCAG	TGAATTTAT	TGTGTGTTCT	TTACTTTATAT	AAAAAAGAT	AATCTTAAGG	3420
55	ATGTGCAAGT	ACATTTCCAA	CTGCTAGCAC	AACCAATAT	TTGTAATTA	ACAARTCGCT	3480
	GTATGATATG	GTCTTCTACA	CATTTATGTC	TATAGATATC	TATCGATCAT	CTTCTATTC	3540
	TGTTTCATGA	CTGAATAATG	TAAACCAAGT	GTTGGCAATT	GGTATCATCA	ATGATACTCA	3600
	TTTTTAAATA	ACCAAGGCA	GGGAAATATC	ATTTTACTTA	TAAATAATA	TTTTATGATG	3660
60	TGAAAAAA	AAAAAA	AAAAAA				

**A109 Protein sequence**

Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

70	1	11	21	31	41	51	
	MLSGFLMSPS	TQHRAYTFG	GKKLPWEASI	GAHTSRGRGS	DRERBSRPEA	AGLLMDRAAA	60
	GEAEKGNRGE	PPAWIRAQQQ	PRPPFAGQAP	GTAAAGCAQDP	RLRPGRSRGR	VRLPVKPFPEA	120
75	SGRQPRGSPD	CIPRFPSSA	THKAVPKGTG	PPAEDGDGLG	APGPRARRRR	LLGVAAEGSG	180
	PRGRGRTVS	DEARGSPGPR	LLGRFPALSG	DALSAPRVVP	CGALAARPSF	HPGTPLRSCS	240
	CCWLRCWRNS	RGPSGEYCHG	WLDAGQVWRI	GFQCPFRFDG	GDATICCGSC	ALRYCCSSAE	300
	ARLDQGGCDN	DRQQAGGEPG	RADKDGPRRL	GRASCLRGTO	GDGEGAPPVV	RAWQRCSPFG	360
	SPKGRQLLRA	FPGLLEPRARE	RGFSSSPRGG	PSPLQRPALF	IYVFLIVGSG	VVFVAFIILGS	420
80	LVAACCCRCI	RPKQDPQQR	APFGNRLMET	IFMIPSASTS	RGSRRQSSST	AASSSSSANS	480
	GARAPPTRSQ	TNCCLEPGTM	NNVYVMPMTN	FSVINCQOAT	QIVPHQGGYL	HPFYVGYTVQ	540
	HDSVPMTAVP	PFMDGLQPGY	RQIQSPFPHT	NSEQKMPAV	TV		

**A110 DNA SEQUENCE:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Nucleic Acid Accession #: AA487468  
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

```

1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCTCTCTA CTCGTACAG TTCTCTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAAGAG GCCTCTCTAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCCTGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
   CAAATGAAG  AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
   GAAACCACTG ATAAGANTTT ATCACCCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
   GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTACCC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAGT CAAATTTCAT 600
   GAAGAAAACC TCTGGCACAT TGACAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
20 TTACTATTTA GTTTTATTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTPTTAA 720
   TCTGAAAAAA AAAAAAATAA AAAAAAATAA

```

25 A111 Protein sequence:  
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
 Unigene number: Hs.100686  
 Probeset Accession #: AA487468  
 Protein Accession #: none found  
 Signal sequence: 1-23  
 Transmembrane domains: none found  
 Cellular Localization: secreted

30

```

35 1      11      21      31      41      51
   |      |      |      |      |      |
   MMLHSALGLC LLLVTVSENL AIAIKKEKRP PQTLSRQWGD DITWVQTYEE GLFYAOKSEK 60
   PLMWIHELED CQYSQALKKV FAQNEIQEM AQNKFIHLNL MHSTEDKNLS PDGQYVPRIM 120
   FVDPSTLVRA DIAGRYSNRL YTYEPEDLEL LIENMKALR LIQSEL

```

40

A112 DNA SEQUENCE  
 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Nucleic Acid Accession #: NM\_016425  
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

```

50 1      11      21      31      41      51
   |      |      |      |      |      |
   ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCBC 60
   AAAACCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
   CTGAGCCTGG CAGATATCAT CATGTGGTGT GTCTCATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGAAGTTC CTTTGGGGGA GGAAGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
   GCAGTGGCAG TCCGCCCTCTC CAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
   GGGAACTGAT TCTCTGCTG TTTGACACAC TTACAGAAAG CTCTGCTGA GACAGCCTGT 420
   AGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
   GGGCCCTGTC TCTCAGGCTC CTTGGTCTCC CTGCACGTGC TTGCTGTGG GAAGAGCCTG 600
   AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
   AGCATCCAGT ACACAAACA GCAAGTCTGT GAGGGAGACA TCCCTGGACC CCACTGGGTC 720
   CTACCGGCAG CCCACTGCTT CAGGAACAT ACCGATGTGT TCAACTGGAA GGTGGGGCA 780
   GGCTCAGACA AACTGGGCAG CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCAITGAA 840
   TTCACCCCAA TGATACCCAA AGACAAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
   ACTTTCCTAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCCACCCCTC TCTGGATCAT TGGATGGGGC TTACGAAAG AGAATGGAGG GAAGATGTCT 1020
   GACATACTGT TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
   GCCTACCAGG GGGAAAGTCAC CAGAAAGATG ATGTGTGCAG GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCGAGG AGTATACACC 1260
   AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

```

75 A113 Protein sequence:  
 Gene name: Homo sapiens type II membrane serine protease mRNA  
 Unigene number: Hs.63325  
 Probeset Accession #: AA411502  
 Protein Accession #: NP\_057509  
 Signal sequence: none found  
 Transmembrane domains: 31-53  
 LDLa domain: 54-94  
 Tryp\_SPC domain: 204-429  
 Cellular Localization: plasma membrane/ER

80



1	31	21	31	41	51	
MLQDFSDQRP	INSLDVKPLR	KPRIPMETFR	KVGIPRIIAL	LSLASIIIVV	VLIKVILDKY	60
YFLCGQPLHF	IPRKLCDGE	LDCPLGEDZE	HCVKSFPEGP	AVAVRLSKDR	STLQVILDSAT	120
GNWFSACFDN	FTEALAEIAC	RQMGYSSEKPT	FRAVEIGPDQ	DLDVVEITEN	SQELMRNNS	180
GPCLSGSLVS	LBCLACGKSL	KTPRVVGGEE	ASVDSNFWQV	SIQYDKQHV	GGSLDPHNV	240
LTAACHFRKH	TDVFNWVKRA	GSDKLGSFPS	LAVAKIIIE	FNPMPYKDN	IALMGLQFPL	300
TFSGTVRPIC	LPFFDEELTP	ATPLNIIIGW	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
AYQGEVTERK	MCAGIPBBGV	DTCCGDSGGP	LMYQSDQWNV	VGIVSWGYGC	GGPSTPGVYT	420
KVSAYLNWIV	NVWKAEL					

**A114 DNA SEQUENCE:**

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: M86699  
 Nucleic Acid Accession #: NM\_003318  
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
CAATGGCACA	ATCTCAGCCT	ACTGCACCTT	CCGCTCCCG	GGTTCACGCG	ATTCTCCTGC	120
CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACATAATT	180
CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTGTGTC	AGGCTGGTCT	TGAACCTCTG	240
ACCTCAGGTS	ATCCACITGC	CTTGGGCTCC	CAAAAGTGCTA	GGATTACAGC	CGTGAACCTG	300
TGCCCTGGCTG	ATTTCTTTTT	TGTTGTGGGA	TTTTTGAAC	AGGGTCTCCC	TTGGTCCGCC	360
AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATATAAC	TCCACCTCCT	GGTTTCAAGT	420
GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	GCCTGCAAC	CCACACCCCG	480
CTAATTTTGT	TATTTTATT	AGAGACAGGG	TTTCACCATG	TTGGCCAGGC	TGTTCTCAAA	540
CTCTGGGACT	CAAGGGATCC	GCCTGGCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
AGTCACCATG	CCTGACCTTA	TAAATCTTAA	GTCTTTTCTT	CTGGTCCATT	TCTTCTCTAG	660
GGTCTCTACA	ACAAATCTGC	ATTAGGCGGT	ACAAATATCC	TAACTTCTAT	GATTCACAAA	720
AGGAAGATGA	AGTGATTCT	GATTTAGAAA	GGGGAAGTAG	TAAAGCCACT	GCACACTCCT	780
GGATGATGAT	CCTAAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
TTTGTGTTAA	ATTAAATTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTGATGTGA	900
ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTCCCCCAG	960
TGCAGTTTTC	TGTAGAAATG	GAATCCGAGG	ATTAAAGTGG	CAGAGAATTG	ACAATTGATT	1020
CCATAATGAA	CAAAAGTGAGA	GACATTAATA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
AACTAAGCTT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAAGT	GTAAACCAAA	1140
TTATGATGAT	GGCAAGCAAC	CCAGAGGACT	GGTTGAGTTT	GTGCTCAAAA	CTAGAGAAAA	1200
ACAGTGTTC	GCTAAGTGT	GCTCTTTTAA	ATAAATGTAT	TGGTCCGTAC	AGTCAAGCAA	1260
TTGAAGGCT	TCCCCAGAT	AAATATGACC	AAAATGAGAG	TTTGTCTAGA	ATTCAAGTGA	1320
GATTTGCTGA	ATTAAAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAAATG	1380
CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTTCAATATC	TTTTGCACAA	TTTGAAGTGT	1440
CACAGGTTAA	TGTCAAAATA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
TACCCTCTAGA	AAATGCTGAA	ATTGCCCTGC	GGAAATTTAA	CCTCCAAAAA	AAGCAGCTGC	1560
TTTCAGAGGA	GAAAGAGAG	AAATTTATCAG	CATCTACGGT	ATTAACTGCC	CAAGAATCAT	1620
TTTCCGTTTC	ACTTGGGCT	TTACAGATA	GGAAACAACAG	TTGTGATTCC	AGAGGACAGA	1680
CTACTAAGTC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAGAGTGCA	GAATAGGTT	1740
ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCATTT	GGAAAGATCC	1800
CAGTTAAGCT	TCTAAATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCT	GTGTGACCTT	1860
GTTTTATGAA	AAGACAAACC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
AACTAAGTGG	AAATGATTCC	TGTGAATTAA	GAATTTTAAA	GTCTGTTCAA	AAATAGTCATT	1980
TCAAGGAACC	TTTGGTGTCA	GATGAAAGAA	GTCTGTAAGT	TATTATTACT	GATTCATATA	2040
CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAGAGATATC	2100
AAGAACCCGA	GGTTCCAGAG	AGTAACCCGA	AACAGTGCCA	AGCTAAGAGA	AGTCAGAGT	2160
GATTAACCA	GAATCCCTGC	GCATCTTCAA	ATCACTGGCA	GATTCGGAG	TTAGCCCGAA	2220
AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGAGCAACC	TGCTTTTTCA	GTTCACAAAC	2280
AGTCACCAAC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
GCAGCAATAC	CTTGGTAAAG	TACATGAGCT	GTTTTAGAAC	TCCAGTTGTA	AAGAAATGACT	2400
TTCCACCTGC	TTGTCAAGTG	TCAACACCTT	ATGGCCCAAC	TGCCCTTTTC	CAGCAGCAAC	2460
AGCATCAAT	ACTTGCCTAT	CCACTTCAAA	ATTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
ATGAATGCAT	TTCCGTTAAA	GGAAGAATTT	ATTCCATATT	AAAGCAGATA	GGAGTGGAG	2580
GTTCAGCAA	GGYATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAATATG	2640
TGAATTAAGA	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	COGGAACGAA	ATAGCTTATT	2700
TGAATAAAT	ACAACAACAC	AGTGATAAGA	TCAATCCGCT	TTATGATTAT	GAATCACCG	2760
ACCAATACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAAA	2820
AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAATAATATG	TTAGAGGCAG	2880
TTACACAAT	CCATCAACAT	GGCATTGTTT	ACAGTATCT	TAAACAGGCT	AACTTTCTGA	2940
TAGTTGATGG	TAATGCTAAG	CTAATTGATT	TTGGGATTGC	AAACCAATATG	CAACCAAGTA	3000
CACCAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAGCAAA	3060
TCAAGATAT	GTCTTCTCTC	AGAGAGAAAT	GGAAATCTAA	GTCAAAGATA	AGCCCCAAAA	3120
GTGATGTTTG	GTCCCTTAGGA	TGTATTTTGT	ACTATATGAC	TTAAGGGAAA	ACACCATTTT	3180
AGCAGATAAT	TATACGATT	TCTAAATTAC	ATGCCATAAT	TGATCCCTAAT	CATGAAATTTG	3240
AATTTCCCGA	TAATTCAGAG	AAAGATCTTC	AAAGTGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
ACCCAAAACA	GAGGATATCC	ATTCCTTGAGC	TCTTGGCTCA	TCCATATGTT	CAAAATCAAA	3360
CTCATCCAGT	TAAACCAATG	GCCAAAGGGA	CCACTGAAGA	AATGAATAT	GTTCCTGGGC	3420
AACTTGTTGG	TCTGAATCT	CCTAACTCCA	TTTGAAGAGC	TGCTAAAAGT	TTATATGAAC	3480
ACTATAGTGG	TGGTGAAGT	CATAATCTTT	CATCTCCCAA	GACTTTTGAA	AAAAAAGGG	3540
GAAAAAATG	ATTTCGAGT	ATTTCGAGT	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
GTATATCTCT	TGAATCCCTG	TGGAAATCTA	CATTTGAAGA	CAACATCACT	CTGAAGTGT	3660
ATCAGCAAAA	AAAATTCAGT	GAGATTATCT	TTAAAAAGAA	ACTGTAAAAA	TAGCAACCAAC	3720

TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAACTCTAC 3780  
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATCTTA AAAAAGCTTTG 3840  
 TAAATAAAGT TTTTGGGCTA AATAGA

# A115 Protein sequence:

Gene name: TTK protein kinase  
 Unigene number: Hs.169840  
 Probeset Accession #: MB6699  
 Protein Accession #: NP\_003309  
 Signal sequence: none found  
 Transmembrane domains: none found  
 Protein Kinase Domain: 510-775  
 Cellular Localization: cytoplasmic and nuclear

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1      11      21      31      41      51
|      |      |      |      |      |
MNXVRDIKMK FKNEDLIDEL ELNKKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS 60
VPLSDALLNK LIKRYSOAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120
ANCKKPAFVH ISPAQFELSQ GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180
EKKKNLBSAS TVLTAQSFSS GSLGHLQNRN NSGDSRGQTT KARFLYGENM PPQDARIQYR 240
NSLRQTNTKX QSCFFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPKSKP 300
SGNDSCELRN LKSVQNSHFK EPLVSDKSS ELIITDSITL KNTLESSLLA KLEETKEYQE 360
PEVPSNQKQK WQAKKKSECI NQNPAASSNH WQIPELARKV NTEQKHITFE QPVFSVSKQS 420
PPISTSKWFD EKSIKCTPSS NTLDDYMSCF RTPVVXNDFF PACQLSTPYG QPACFQQQOH 480
QILATPLQNL QVLASSANE CTSVKRIYS ILKQIGSGGS SKVPQVLNEK KQIYAIKYVN 540
LEBADNQILD SYRNEIAYLN KLQGHSDKII RLYDYRITDQ YIYMVMCEGN IDLNSWLKKK 600
KSIDPWRRKS YWNKMLRAVH TTHQHIVLES DLKPFANFLIV DGLMLKIDFG IANQMOPDTI 660
SVVKDSQVGT VNYNPPPAIK DMSSSRENGK SKSKISPKSD VWSLGCILYI MTYGTTPFQQ 720
IINQISKLHA IIDPNHEIEF PDIEKDLQD VLKCCLEKRP KQRISIPELL AHFYVQIQTH 780
FVNQMAKGTI BEMKYVLGQL VGLNSPNSIL KAAKTLRYRY SGGSSEHSSS SKTFEKKRGK 840
X

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## OVARIAN

### A116 DNA SEQUENCE

Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Nucleic Acid Accession #: NM\_001508  
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCAGCCCTA TTCTGGTGTG CCTGATCATC 120
TTCTGTATGG GCTTCTGGGG GAACAGCGCC ACCATTGGGG TCACCCAGGT GCTGCAGAA 180
AAGGAGTACT TGCAAGAGGA GGTGACAGAC CACATGGTGA GTTGGCTTG CTGGACATC 240
TTGGTGTTC TCATCGGCAT GCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC 300
ACGTCCAGCT ACACCTGTGC CTSCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360
GCTACGCTGC TGACGCTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCAOCC 420
TTGAGGTACA AGCTGTGTGC GGGACCTTGC CAGGTGAAGC TGCTGATTTG CTTCGTCTGG 480
GTCACTCTCG CCTGTGTGGC ACTGCCCTTG CTGTTTGCCA TGCGTACTGA GTACCCCTTG 540
GTGAACGTGC CCAGCCACCG GGTCTCTACT TGCAACCGCT CCAGCACCGG CCACCACGAG 600
CAGCCCGAGA CTTCCATAT GTCCATCTGT ACCACCTCT CCAGCCGCTG GACCGTGTTC 660
CAGTCAGCA TCTTCGGGCG CTTCGTGTGT TACCTGTGG TCCTGTCTTC CTAGCCCTTC 720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGCTCGCTT GGCCGGGGGC 780
ACGCGGCTTC CACAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
ACCATCATCT TCTGAGGCT GATTGTGTG ACATTGGCGG TATGCTGGAT GCCCAACGAG 900
ATTGAGAGGA TCATGGCTGC GGCCAAACCC AAGCAGGACT GGAGGAGGTC CTACTTCGGG 960
GGGTACATGA TCTCTCTCCC CTCTCGGAG ACCTTTTCT ACCTCAGCTC GGTCTCAAC 1020
CGCTCTCTGT ACACGGTGTG CTGCGAGCAG TTTCGGCGGG TGTTCTGTGA GGTGCTGTGC 1080
TGCCGCTGT GCTGCGAGCA CGCCAACCC GAGAAGCGCC TGCGGTACA TGCGCACTCC 1140
ACCAACGACA GCGCCGCTT TGTGACGCG CCGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
TCTGCAAGGA GAAGTGAAG GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
TCTAAGTCCC AGTCAATGAG TCTCGAGTCA CTAGAGCCCA ACTGAGCGGC GAAACGAGCC 1320
AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

```

### A117 Protein sequence:

Gene name: G protein-coupled receptor 39  
 Unigene number: Hs.85339  
 Probeset Accession #: AA349893  
 Protein Accession #: NM\_001508, NP\_001409  
 Signal sequence: none found  
 Pfam domains: 7tm\_1 [72-172, 224-344]  
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342  
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MASPSLPGSD CSQIIDHSIV PEFEVATWIK ITLILVYLII FVMGILGNSA TIRVTQVLQK 60

```

KGYLQKEVTD BMVSLACSDI LVEFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120  
 ATLLHVLTLF FERYIAICHP FRYKAVSGFC QVKLLIGFVW VTSALVALPL LFAMGTETPL 180  
 VNVPSHRGLT CNRSSTRHHE QPETSNNMIC TNLSSRWTVF QSSIFGAEVU YLVVLLSVAF 240  
 MCNNMMQVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCHMPNQ 300  
 IRRIMAAAKP KHDWTRSYFR AYMILLFPSE TFFYLSSVIN PLLYTVSSQQ FRFVFQVLC 360  
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEFQ 420  
 SKSQSLSLSE LEPNSGAKPA NSAAENGFOE HEV

**A118 DNA sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.87223  
 Probeset Accession #: AA250737  
 Nucleic Acid Accession #: NM\_001203  
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 CGCGGGGCGC GGAGTCGGCG GGGCTTCGCG GGACGCGGGC AGTGGCGAGA CCQCGGCGCT 60  
 GAGGACGCGG GAGCGGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTCTCTAGAT 120  
 GTGAAAGGAA AGGAAGATCA TTTCATGCTT TGTGATAAAA GGTTCAGACT TCTGCTGATT 180  
 CATAACCAAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTCACAGCC 240  
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TCGGAAGTGC AGGAAATTA 300  
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360  
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCACCAATAT TTGCAGCACA 420  
 GACGATATT GTTTCACBAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480  
 GGTTCCTTAG GACTAGAGG CTGAGATTTT CAGTGTCCGG AACTCCCAT TCCTCATCAA 540  
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTACA 600  
 CTGCTCCAT TGAATAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCCTTACTT 660  
 ATATCTGTGA CTGTCGTAG TTTGCTCTTG GTCCCTATCA TATTAATTTG TTACTTCCGG 720  
 TATAAAGGAA AGCAACGATC ACCTCGATAC AGCATTTGGT TAGAACAGGA TGAACCTTAC 780  
 ATTCTCTCTG GAGAAATCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840  
 TCAGGCTTCC CTCTGCTGCT CCAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAACACG 900  
 ATTGGAAGAG GTGCTATGCG GGAAGTTTGG ATGGGAAGT GGCCTGGCHA AAGGTAGCT 960  
 GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020  
 ACAGTGTGTA TGACCAACCA AAACATTTTG GGTTCATPG CTGCAGATAT CAAAGGACA 1080  
 GGTCTCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140  
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTCT 1200  
 AGTGGCTTAT GTCAATTTACA CACGAAATC TTTAGTACTC AAGGCAACCC AGCAATTGCC 1260  
 CATCGAGATC TGAAGAATGA AAACATTTCT GTGAAGAAA ATGGAACCTG CTGTATGTCT 1320  
 GACCTGGGCC TGGCTGTGTA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380  
 ACTCAGATGT GCACCAAAAG CTATATGCTT CCAGAAAGT TGGACGAGAG CTGGAACAGA 1440  
 AATCACTTCC AGTCTGCTAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CCTTGGGAG 1500  
 GTTGTAGGGA GATGTGTATC AGGAGGTATA GTGGAAGAT ACCAGCTTCC TTATCATGAC 1560  
 CTAGTGCCCA GTGACCCCTC TTAIGAGGAC ATGAGGAGGA TTGTGTGCAT CAGGAAGTTA 1620  
 CGCCCTCTAT TCCCAAAACG GTGGAGCAGT GATGAGTGTG TAAGGCAGAT GGGAAACTC 1680  
 ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740  
 ACACCTGCCA AAATGTGAGA GTCCCAAGGAC ATTAACTCT GATAGGAGAG GAAAAGTAA 1800  
 CATCTCTGCA GAAAGCCAA CAGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860  
 TAAGCATCCA CAGTACAGC CTTGAACATC GTCCCTCTTC CCAGTGGGTT CAGACCTCAC 1920  
 CTTTCAGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980  
 TCTGTTGTA GCGGAGAAA CCGTGGGTA ACTTGTCAA GATATGATGC AT

**A119 Protein sequence**

Gene name: bone morphogenetic protein receptor IB (ALK-6)  
 Unigene number: Hs.72472 / Hs.87223  
 Probeset Accession #: AA250737 / U89326  
 Protein Accession #: NP\_001194  
 Signal sequence: 1-13  
 Transmembrane domains: 128-144  
 PFAM domains: activin\_receptor [30-111], protein kinase [204-491]  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MLRSAGKLN VETKKGEGES TAPTPRPKVL RCKCHEHCPS DSVNNICSTD GYCFTMIERD 60  
 DSGLPVVTSG CLGLESGDFQ CRDTPIPHQR RSIECCTERN ECKDLHPTL PFLKRDVFD 120  
 GPIHRRALLI SVTVCALLLV LILFCYFRY KQETRPYRS IGLQDETYI PGESLEDLI 180  
 EQSQSSGSGS GLPLLVQRTI AKQIQMVKQI GKGRYGEVVM GKNRGEKVAV KVFFTTESAS 240  
 WPRETEYYQT VLMRHENILG FLAADIKGTG SWTQLYLTID YHENGSLYDY LKSTTLDAKS 300  
 MLKLAYSVS GLCHLHTEIF STQGKPAIAH RDLKSKNIV KINGTCCIAI LGLAVKFISD 360  
 TNEVDIPFWT RVGTIKRYMP EVLDESLENH HFQSYIMADM YSFLILWEV ARRCVSGGIV 420  
 EBYQLPYHDL VPSDPSYEDM REIVCIKRLR PSFPNRWSSD RCLRMGKLM TECWAHPAS 480  
 RLTLALRVKTY LARMSQSQDI XL

**A120 DNA SEQUENCE**

Gene name: LIV-1 protein, estrogen regulated  
 Unigene number: Hs.79136  
 Probeset Accession #: U41060  
 Nucleic Acid Accession #: NM\_012319.2  
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	CTCGTGGCGA	ATTGCGGCAG	AGACCGCGTG	TTGCGGCGTG	GTAGAGATT	CTCGAAGACA	60
	CCAGTGGGCG	CTGTGGGAAC	CAAACCTGCG	CGCGTGGCGG	GGCCGTGGGA	CAACGAGGCC	120
5	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCCCTG	ACCTTTGCCC	180
	TCTCTGTAC	AAATCCCCTT	CATGAACATA	AAGCAGCTGC	TTTCCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATTA	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAATATA	TTCTTTGTCA	GTGAAGGGT	360
	TCAGAAATTT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AGAATCCAT	ATACACCATG	420
10	ACCAAGACCA	TCATCTCAGC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCAGACCATG	480
	AGCATCACTC	AGACCACGAG	CATCACTCTG	ACCATGATCA	TCATCTCTAC	CATAATCATG	540
	CTGCTTCTGG	TAAATAAAG	CGAAAAGCTC	TTTGCCCGAG	CCATGACTCA	GATAGTTTCA	600
	GTAAAGATCC	TAGAAACAGC	CAGGSGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGA	660
	GAAGGAATGT	CAAGGACAGT	GTTAGTGCTA	GTGAAGTGAC	CTCAACTGTG	TACAACACTG	720
15	TCTCTGAAGG	AACTCAGTTT	CTAGAGACAA	TAGAGACTCC	AAAGCTTGGG	AAACTCTTCC	780
	CCAAAGATGT	AGCAGCTCC	ACTCCACCCG	GTGTCACTC	AAAGAGCCCG	GTGAGCCGGC	840
	TGGCTGATGG	GAATAACAA	GAATCTGTGA	GTGAGCCCGG	AAAGGCTTTT	ATGTATTCCA	900
	GAACACAAA	TGAATATCT	CAGGAGTGTT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
	GCAATGGCAT	CCAGGTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
20	TCACCAAAAT	TGATGCTAGA	TCTTGTCTGA	TTCAATACAG	TGAAAGAAGG	GCTGAAATCC	1080
	CTCCAAAGAC	CAATTCATTA	CAATAGCCT	GGGTGGTGG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTTCTT	GTCTCTGCTG	GGGTTATCT	TAGTGCTCT	CATGAATCCG	GTGTTTTTCA	1200
	AAITTTCTCT	GAGTTTCTCT	GTGSCACTGG	CCGTTGGGAC	TTTGTGTTGG	GATGCTTTTT	1260
	TACACTTCTT	TCCACATCTT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
25	CAATGGAAAT	GAAGAAGGAG	CCACTTTTCA	GTCTCTCTGT	TTCTCAAAAC	ATAGAAGAAA	1380
	GTGCTTATTT	TGATTCACAG	TGAAGGGGTC	TAAACAGCTC	AGGAGGCCCTG	TATTTTCATGT	1440
	TTCTTGTGTA	ACATGTCTCT	ACATGTATCA	AACAATTTAA	AGATAAGAAG	AAAAGAATAT	1500
	AGAAAGAAAC	TGAATATGAT	GATGATGTGG	AGATTAAGAA	GCAGTTGTCC	AAGTATGAAT	1560
	CTCAACTTTT	AACAAATGAG	GAGAAAGTAG	ATACAGATGA	TCGAACTGAA	GGCTATTTAC	1620
30	GAGCAGACTC	ACAAGAGCCC	TCCCACTTTG	ATTCCTAGCA	GCCTGCGATC	TGGAAGAGAG	1680
	AAGAGGTGAT	TACTGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCAACACCA	TCATGATCAT	TCCATCATCA	CCACCAACCA	AACCAACCAT		1860
	CTCAGACTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCGGC	GTGCCCACCT	1920
35	TGGCCTGGAT	GGTGATAATG	GGTGATGGCC	TGCACAAATT	CAGCGATGGC	CTAGCAATTG	1980
	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAGTAC	TTCTGTGTCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GGTGACTTTG	CTGTTCTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CTTTTATAAT	GCAATGTCTG	CCATGCTGGC	GTATCTTGGA	ATGGCAACAG	2160
	GAATTTTCAT	TGGTCTTTAT	GCTGAAAATG	TTTCTATGTG	GATATTTTGA	CTTACTGCTG	2220
40	GCTTATTCAT	GTATGTGTCT	CTGGTTGATA	TGGTACCTGA	AAATGCTGCAC	AATGATGCTA	2280
	GTGACATGAG	TGGAGACCCG	TGGGGGTATTT	TCTTTTATCA	GAATGCTGGG	ATGCTTTTGG	2340
	GTITTTGGAAT	TATGTTACTT	ATTTCCATAT	TGGAACATAA	AAATCGTGTG	CGTATAAAT	2400
	TCTAGTTAAG	GTTTAAATGC	TAGATAGTCT	TAAAAGTTTG	TCATAGTTTC	AGTAGGTCAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
45	TTGTATTGAA	TATGTCTGTC	TGTTACAAAG	TCAGTTTAAAG	GTACGTTTAA	ATATTTAAGT	2580
	TATTCTATCT	TGGAGATAAA	ATCTGTATGT	GCAATTCACC	GGTATTACCA	GTTTATTATG	2640
	TAAACAGAGG	ATTGCGCATG	ACATGTTCTG	TATGTTTCAG	GGAAATATGT	CTTTAATGCT	2700
	TTTTCAGAA	CTAACACAT	TATTCCTATA	CTGGATTTTA	GCTCTCTGAA	GAATGCTGAG	2760
50	TGTTTAGGAA	TAGAAATGTG	CATGAGCCCT	AAAATACCAA	GAAAGCTTAT	ACTGAATTTA	2820
	AGCAAGAGAA	TAAAGAGAGG	AAAGAGAGAA	TCTGAGAAAT	GGGAGGCGAT	AGATTCTTAT	2880
	AAAAATCAAA	AAATTTGTGT	TAAATTAGAG	GGGAGAAATT	TAGAAATTAAG	TATAAAAAGG	2940
	CAGAAATAGT	ATAGAGTACA	TTCAATTAAC	ATTTTGTCTA	GGATTATTTC	CCGTAAAAAC	3000
	GTATGAGACA	CTCTCAATTA	CTAATTAGTG	TACATTTAAC	TTTGTATTAAT	ACAGAAATCT	3060
	AAATATATTT	AATGAATTTA	AGCAATATAC	ACTTGACCAA	GAAATTTGAA	TTTCAAAATG	3120
55	TTCTGTGGGG	TTATATATCA	GATGAGTACA	GTGAGTAGTT	TATGTATCAC	CAGACTGGGT	3180
	TATTGCCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTCGGT	ACCTGGTTTA	3240
	CAAAATATAT	AGAGTAGTAA	AACTTTGATA	TATATGAGGA	TATTAATACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTCAGAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTTG	3360
60	GAGCAATTTG	CTTTATATAC	GGTACTGTAG	CCATACATAG	CCTGCTCTGT	GCATTTCTTA	3420
	GATGTTTCTT	TTTACACAA	TAAATTCCTT	ATATCAGCTT	G		

**AL21 PROTEIN SEQUENCE**

Gene name:

Unigene number:

Protein Accession #:

Signal sequence:

Pfam domain:

Transmembrane domains:

Cellular Localization:

LIV-1 protein, estrogen regulated

Hs.79136

NP\_036451

1-21

Zip[591-743]

330-346, 352-368, 427-444, 663-679, 688-703, 730-745

plasma membrane

	1	11	21	31	41	51	
	MARKLSVILI	LTFALSVTNP	LEELKAAAFP	QTEKISPFW	BSGINVDLAI	STRQYHLQQL	60
	FXYRGNNNL	SVGSRKLLQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHER	HSDHEHSDH	120
75	RHSDHDS	HNHHAAGKN	KRKALCPDH	SDSSGKDPN	SGKGARPE	HASGRNVKD	180
	SVSASVTST	VNTVSEGT	PLETISTPRP	GKLFPPKDVSS	STPFSVTSKS	RVSRLAGRKT	240
	NEVSVEPRKG	FMSYRNTMEN	PQBCFNASKL	LTSHGMIQV	PLNATEPNYL	CPALINQIDA	300
	RSCLHTSEK	KAEIIPKTYG	LQIAWVGFI	AISTISFLSL	LGVILVPLMN	KVFKEFLLSF	360
	LVALAVGTLG	GDVFLHLLPH	SHASHHSES	HEEPAMEMKR	GPLFSELSSQ	NIEESAYFDS	420
80	TWBLTALGG	LYPMFLVERV	LTLIKQFDK	KKNQKKPEN	DDVSEIKKQL	SKYESQLSTN	480
	REKVDYDDRT	EGYLADSDQE	PSHFDSQQA	VLEEEBVMIA	HAHPQEVYNE	YVPRGCKNKC	540
	ESHEHDTLGG	SDDLIEHHHD	YHHLHHHHH	QNHHPHSHSQ	KYSREELKDA	GVATLAWMI	600
	MGDLHNFSD	GLAIGAAFTG	GLSSGLSTSV	AVFCHLPHF	LQDFAVLLKA	GMTVKQAVLY	660
	NALSAMLAYL	GMAITGIFIGH	YAENVSMHIF	ALTAGLFMYV	ALVDMVPEML	HNDSDEHGS	720

RMGYFFLQNA GMLLFGGIML LISIFERKIV PRINT

5 A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Nucleic Acid Accession #: NM\_015507  
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

10  
 15  
 20  
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1	11	21	31	41	51	
CCGCAGAGGA	GCCTCGGCCA	GGCTAGCCAG	GGCGCCOCCA	GCCCTCTCCC	AGGCCGCGAG	60
CGCCCTGTC	GCGGTGCTTG	GCCTCCCTTC	CCAGACTGCA	GGGACGACAC	CCGGTAACCTG	120
CGASTGGAGC	GGAGGACCCG	AGCCGCTGAG	GAGAGAGGAG	GCGGCGGCTT	AGCTGCTACG	180
GGGTCCGGCC	GGCGCCCTCC	CGAGGGGGGC	TCAGGAGGAG	GAAGGAGGAC	CCGTGCGAGA	240
ATGCTCTGCG	CCTGGAGCCT	TGCGCTCCCG	CTGCTGCTCT	CCTGGGTGGC	AGGTGGTTTC	300
GGGAACGCGG	CCAGTGCAAG	GCATCAGGGG	TTGTTAGCAT	GCGCACGTCA	GCCTGGGGTC	360
TGTCACTATG	GAACTAAACT	GGCTGCTGTC	TACGGCTGGA	GAAGAAACAG	CAAGGGAGTC	420
TGTGAAGCTA	CATGCGAACC	TGGATGTAAG	TTTGGTGAAT	GCGTGGGACC	AAACAAATGC	480
AGATGCTTTC	CAGGATACAC	CGGGAAAACC	TGCAGTCAAG	ATGTGAATGA	GTGTGGAAATG	540
AAACCCCGGC	CATGCCAACCA	CAGATGTGTG	AATACACACG	GAAGCTACAA	GTGCTTTTGC	600
CTCACTGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGBAC	ATGTGCCATG	660
ATAAACTGTC	AGTACAGCTG	TGAAGACACA	GAAGAAGGGC	CACAGTGCTT	GTGTCCTATC	720
TCAGGACTCC	GCTTGGCCCC	AAATGGAAGA	GACTGCTTAG	ATATTGAATG	ATGTGCCTCT	780
GGTAAAGTCA	TCTGTCCCTA	CAATCGAAGA	TGTGTGAACA	CATTGGGAAG	CTACTACTGC	840
AAATGTGACA	TTGGTTTDTG	ACTGCAATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
AATGAATGTA	CTATGGATAG	CCATACCTGC	AGCCACCATG	CCAATGCTT	CAATACCCAA	960
GGGTCTCTCA	AGTGTAAATG	CAAGCAGGGA	TATAAAGGCA	ATGGACTTCG	GTGTTCTGCT	1020
ATCCCTGAAA	ATTCTGTGAA	GGAAGTCTCT	AGAGCACCTG	GTACCATCAA	AGACAGAATC	1080
AAGAAGTTC	TTGCTCACAA	AAACAGCATG	AAAAAGAAGG	CAAAAATTAA	AAATGTTACC	1140
CCAGAACCCA	CCAGGACTCC	TACCCCTAAG	GTGAACCTGC	AGCCCTTCAA	CTATGAAGAG	1200
ATAGTTTCCA	GAGGGGGGAA	CTCTCATGGA	GGTAAAAAAG	GGAATGAAGA	GAAATGAAA	1260
GAGGGGCTTG	AGGATGAGAA	AAGAGAAGAG	AAGCCCTGA	AGAATGACNT	AGAGGAGCGA	1320
AGCCTGCGAG	GAGATGTGTT	TTTCCCTAAG	GTGAATGAAG	CAGGTGAATT	CGGCTTGATT	1380
CTGGTCCAAA	GGAAGCCGCT	AACITCCAAA	CTGGAACATA	AAGATTATAA	TATCTCGGTT	1440
GACTGCGAGT	TCAATGCTGG	GATCTGTGAC	TGGAAACAGG	ATAGAGAAGA	TGATTTTGAC	1500
TGGAATCCTG	CTGATCGAGA	TAAATGCTATT	GGCTTCTATA	TGGCAGTTCC	GGCCTTGCCA	1560
GGTCACAGA	AAGACATTGG	CCGATTGAAA	CTTCTCCTAC	CTGACCTGCA	ACCCCAAAGC	1620
AACTCTGTGT	TGCTCTTTGA	TTACCGGCTG	GCGGGAGACA	AAGTCGGGAA	ACITCGAGTG	1680
TTTGTGAAAA	ACAGTAACAA	TGCCCTGGCA	TGGGAGAGAA	CCACGAGTGA	GGATGAAAAG	1740
TGGAAGACAG	GGAATAATCA	GTTGTATCAA	GGAACCTGATG	CTACCAAAG	CATCATTTT	1800
GAAGCAGAAC	GTGGCAAGGG	CAAAACCGGC	GAAATCGCAG	TGGATGGCGT	CTTGCTTGTT	1860
TCAGGCCTAT	GTCCAGATAG	CCTTTTATCT	GTGGATGACT	GAAATGTTACT	ATCTTTATAT	1920
TTGACITTTG	ATGTCAGTTC	CCTGGTTTTT	TTGATATTGC	ATCATAGGAC	CTCTGGCATT	1980
TTAGAATTAC	TAGCTGAAAA	ATTGTAATGT	ACCAACAGAA	ATATTATTGT	AAGATGCCTT	2040
TCCTGTATAA	GATATGCCAA	TATTGTCTTT	AAATATCATA	TCAGTGTATC	TTCTCAGTCA	2100
TTTCTGAATC	TTTCACATT	ATATTATAAA	ATATGGAAT	GTGAGTTTAT	CTCCCTCCT	2160
CAGTATATCT	GATTGTGATA	AGTAAGTTGA	TGAGCTTCTC	TCTACAACAT	TTCTGAAAA	2220
TAGAAAAAAA	AGCAGAGAGA	AATGTTTAAC	TGTTTGACTC	TTATGATACT	TCITGGAAAC	2280
TATGACATCA	AAGATAGACT	TTTGCCCTAAG	TGGCTTAGCT	GGGTCTTTCA	TAGCCAAACT	2340
TGTATATTTA	AATCTTTTGT	AATAATAATA	TCCAAATCAT	CAAAAAAAA	AAAAAAA	

55 A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6  
 Unigene number: Hs.12844  
 Probeset Accession #: N67551  
 Protein Accession #: NP\_056322.2  
 Signal sequence: 1-21  
 Transmembrane domains: none found  
 MAM domain: 402-546  
 EGF domain: 80-259  
 Cellular Localization: secreted

65  
 70  
 75  
 80

1	11	21	31	41	51	
MPLEWSLALP	LLLSWVAGGF	GNAASARHNG	LLASARQPGV	CHYGTKLACC	YGNRRNSKGV	60
CEATCEPGCK	FGCEVGPNGC	RCFPGYTGKT	CSQDVNECGM	KRPCCQHRCV	NTGSGYKFC	120
LSGHEMLMPEA	TCVNSRTCAM	INCQYSCEDT	EEGPOCLCPG	SGRLRLAPNGR	DCILDIDECAS	180
GKVICFYNRR	CWTFGSSYYC	KCHIGFELQY	ISGRYDCIDI	NZCINDSHTC	SHHANCFTNQ	240
GSFKCKCKQG	YKNGLRCSA	IPENSVKELV	RAPGTTKDRI	KCLLAHKNRM	KKAKIKNVT	300
PEPTRPTTPK	VNLQPFNVEE	IVSRGGNSHG	GKKGNSEKMK	EGLEDEKRES	KALENDIEER	360
SLRGDVFFPK	VMEAGEFGLI	LVQRKALTSK	LEBKDLNISV	DCSEFNGICD	WKQDREDDFD	420
WNPADRDNAI	GFTNAVPALA	GERKDIERLK	LLLFDLQPGS	NFCLLFQYRL	AGDKVGKLRV	480
FVIMSNALAL	NKMTSEDEK	WKTGKIQLYQ	GTDATKSIIF	BAERGRGKTG	BIAVDGVLLV	540
SGLCFDSLLS	VDD					

80 A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Nucleic Acid Accession #: NM\_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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5 1      11      21      31      41      51
   |      |      |      |      |      |
GGGCGCAGCG GGGCCGCTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CTTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CGGAGGCCCG GGTAGCGCGT AGAGCCGCG 120
CGATGCACCT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCGGGCAC 180
CCCTGTTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAAAGAG GTGCACTCGA 240
10 GCTTCATCCA CGGCGCGCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCSC GAGATCTCT 300
CCATTTTGGG CTTCGCCAC CCGCCGCGCC CGCAGCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGGAAGTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCG 420
GCCAGGGCTT CTCTACCCC TACAAGGCCG TCTTCAGTAC CGAGGGCCCC CCTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACTCG 540
15 TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGSTTTGATC 600
TTTCAGAGAT CCGAGAAGG GAGCTGTGCA CGGACGCCGA ATTCGGATC TACAAGGACT 660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAG 720
AGCACTTGGG CAGGGAATCG GATCTCTCC TGTCTGACAG CGTACCCCTC TGGGCTCGG 780
AGGAGGGCTG CTGGTGTCTT GACATCACAG CCACGAGCAA CCAGTGGGTG GTCAATCCG 840
20 GGCACAACCT GGGCCTGCGC CTCTCGGTGG AGAGCTGGA TGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCTGATTGGG CGGCACGGCG CCCAGAACAA CGAGCCCTTC ATGTTGGCTT 960
TCTTCAAGCG CACGAGGCTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AAACAGCGCA 1020
GCCAGAACCG CTCGAAGACG OCCAAGAACC AGGAAGCCCT CGCGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGAACAG AGCGAGGCCCT GTAGAAGCA CGAGCTGTAT GTCACTTCC 1140
25 GAGACCTGGG CTGCGAGGAC TGGATCATCG CGCTGAAGG CTACGCGGCC TACTACTGTG 1200
AGGGGAGAGT TGGCTTCCCT CTGAATCCTT ACATGAAGCG CACCAACCAT GCCATCGTGC 1260
AGAGCTGTGT CCACTTCATC AACCCGGAAG CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCTGTGGCT GCCACTAGCT CCTCCAGAA TTCAGACCT 1440
30 TTGGGGCCAA GTTTTTCGCG ATCTCTCATT GCTGCGCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCTCTCCCTAT CCCCACCTTT AAGGTGTGA GAGTATTAG 1560
AAACATGAGC AGCATATGCT TTTTGTATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCTACAGCAG TGTGAGGCA AAACCTAGCA GGAAGAAAAA ACAAGCATA AAGAAAAATG 1680
GCGGGGCCAG GTCATTTGCT GGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
35 TTATGAGCAG CTACAGGCCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAACG AATGAATG

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40 **A125 Protein sequence:**  
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)  
 Unigene number: Hs.170195  
 Probeset Accession #: BE616633  
 Protein Accession #: NP\_001710.1  
 Signal sequence: 1-30  
 Pfam domains: TGFb\_propeptide [37-281]  
 Transmembrane domains: none found  
 Cellular Localization: secreted

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50 1      11      21      31      41      51
   |      |      |      |      |      |
MHVRSLEAAA PHSFVALMAP LFLRLSALAD FSLDNVHSS FIHRLRSQE RREMQREILS 60
ILGLPHERPR ELQGHNSAP MFLDLVYNAV AVERGGSPGG QGFSTPYKAV FSTQGPPLAS 120
LQDSHPLTDA DMVMSFVNLV EHDKEFFHPR YHREFRFDL SKIPGCAVT AAEFRIVQDY 180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDRSLWASE ESWLVEDIYA TSNHWVNVPR 240
HNLGLQLSVE TLDGQSINPK LAGLGRHGP QNKQPPMVAE FKATEVHFRS IRTSGSKQRS 300
QNRSKTPKNG BALRMANVAE NSSSDQRQAC KHHELYVSEF DLGWQDWIIA PBGYAAYTCE 360
60 GECAPFLNSY MNAINHAIVQ TLVHFNPET VPKPCCAPTQ LNAISVLYFD DSSNVILAKY 420
RNMVVRACGC H

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**A126 DNA SEQUENCE**  
 Gene name: integrin, beta 8  
 Unigene number: Hs.52620  
 Probeset Accession #: AA479726  
 Nucleic Acid Accession #: NM\_002214  
 Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

```

70 1      11      21      31      41      51
   |      |      |      |      |      |
CCCAGAGCGG CTTCCGCCCTG TTGCTGSCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG 60
CTGCCGACTT GTCTTTGGCC GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
GTTGCGCTTC CTGCTCACCT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180
TCCCTCTGAC CTGCGCGGCG TACCTTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
75 TAGGGTGGTT TCCGCCCGAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
CTAAGCTGAT TTATGCGGCA GAGGCCCCAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360
TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTGGCC GCGGGGCCCT 420
TGGCCGTGGA AGGAGGTGCT TCTCGCGGAG ACCCGGGGAC CGCCCGTGCC GAGCGCGGAG 480
GGCCGTAGGG GCTCTAGAT GCGAGCGGCT GCGCGGGGCC GCTTACCTGC ACCGCTTGCT 540
80 CCGAGCCGCG GCGTCCGCTT GCTAGGCCCT CGSAAADFT CTTAGCGGCA CTCGCCCCGT 600
GCGCCCGAGG TCGCCCGGGA GCGCGAGCCC GCGTCCGGA GCGAGCCAG CCGCGCGGCG 660
GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTITTACC GCTGCATTG 720
TCTGCTGCA AAACGACCGG CAGAGTCCCG CTCTGTTCTT CTGGGACGCC TGGGTGTTTT 780

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5 CACTTGTTC TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840  
 CCTGTGCCAG GTGCCCTTGG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900  
 TTTTCAAGTGA ATCAAGAAGT GAACGTGTGT ATATTGTTTC CAATTTAATA AGCAAAGGCT 960  
 GCTCAGTTGA TTTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA 1020  
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080  
 ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCTTGT GGATCTTTAT TATCTTGTG 1140  
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAA TTCCGTTGGA AACGATTAT 1200  
 CTAGAAAAAT GGCATTTTTC TCCGTTGACT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260  
 10 AAACAGTTTC ACCATACATT AGCATCCACC CCGAAGGAT TCATAATCAA TGCAGTGACT 1320  
 ACAATTAGTA CTGCTATGCT CCCCATGGAT ACATCCATGT GCTGTCTTGG ACAGAGAACCA 1380  
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACCAG 1440  
 AAGGAGGTTT TGACCGCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGTGGCGGAA 1500  
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560  
 15 GCAAATTGGC AGGCATATGT GTGCCAATG ACGGAACTG TCATCTGAAA AACACGTTCT 1620  
 ACGTCAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AATTAAATAG 1680  
 ACAACAACAT TAATGTCTAT TTTGCAGTTC AAGGAAACCA ATTTCAFTGG TATAAGGATC 1740  
 TTCTACCCCT CTTCGCCCAT ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800  
 ATATTTGGT AGTGGAGGCC TATCAGAAGC TCATTTCAGA AGTGAAGTT CAGGTGGAAA 1860  
 20 ACCAGGTATA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920  
 AGGATGACGA AGGATGACGA AACGTGACGA GCATGATGA AGTTCTTTTC AATGTAACAG 1980  
 TTCAATAGAA AAAATGTGAT GTTCACAGAG GAAAAAATA TGCATTAATC AAACCTATTG 2040  
 GTTTAATGA TGACCGCTAA ATTCATATAC ACAGAACTG CAGCTGTGAG TGTGAGGACA 2100  
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTTCCAGT 2160  
 25 GTGATGAGAA TAAATGTCTAT TTTGATGAG ATCAGTTTTC TTCTGAGAGT TGCAGGTCTC 2220  
 ACGAGGATCA GCTGTGTTGC AGTGTCTGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280  
 ACRAAATTA GCTTGGAAAA GTGTATGAAA AATACTGTGA AAGGATGAC TTTTCTTGTG 2340  
 CATATACCA TGGAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400  
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460  
 30 TCAATTCAAA GGGCCAAAGT TGCAGTGGAA GAGGCACGTG TGTGTCTGGA AGGTGTGAGT 2520  
 GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580  
 GCAAGGAAAA CTGGAATTGT ATGCAATGCC TTACCCCTCA CAATTGTCT CAGGCTATAC 2640  
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 CAGAAATGTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760  
 35 TCTGTATTGG GTTCTTAAA GTCTGTATCA TTAGACAGGT GATACACAA TCGAATAGTA 2820  
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 TGCAAGTGT TTGCACAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940  
 TGGATATCAG CAATTAATAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAAGATT 3000  
 TTAACACTT AATGGGAAAC TGGAAATGTT AATAATTGCT CCTAAAGATT AATATTTTAA 3060  
 40 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACATCGAAC 3120  
 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180  
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGTTGTA GCATTTTACT GTAATATATA 3240  
 ACTTATTTAG ACTGATAGAT AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300  
 TACCTGTTAT CCTACGCTT CCGAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360  
 45 CACTACAAGG GTACAGTAAT CCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAG 3420  
 TATATTCTAA GGTTCGCAAA CACTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480  
 ATGAAATAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAC CTTAATCTTA 3540  
 AAAGATTATT GCTTTTAAA GTGTGATGTT TTATGCATGT GTGTTTATGG TTTGCTTATT 3600  
 TTTGCAAGAT GGTACTTAAT TCAGCATTC TCTCTCTT GCCTTTATGT TTTGTTTCT 3660  
 50 TTTTACAGG ATAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720  
 TACTGCCATA AAAAATTAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780  
 GAATGTTAA

55 **A127 Protein sequence:**  
 Gene name: Integrin, beta 8  
 Unigene number: Ha.52620  
 Probeset Accession #: AA479726  
 Protein Accession #: NP\_002205.1  
 Signal sequence: 1-39  
 60 Transmembrane domains: 682-704  
 EGF domain: 552-584  
 INB domain: 54-469  
 Cellular Localization: plasma membrane

65  
 70 1 MCSSALAEFT 11 AAFVCLQNR 21 RGPASFLWAA 31 NVFSLVLGLG 41 QGEDNRCASS 51 NAASCARCLA 60  
 LGPECCWCVQ EDFISGGERS ERCDIVENLI SKGCSVDSIE YPSVHVITPT ENHINTQVTF 120  
 GEVSIQLRPG AEAHFMLKVH FLKYPVDLY YLVDVSASMH NMIEKLNSVG NDLSEKMAFF 180  
 SRDFRLGPHS YVDKTVSPYI SIHFERIHNQ CSDYNLDOMP PHGYLIVLSL TENITEFEKA 240  
 VHRQKISGNI DTPBGGFDAM LQAAVCESHI GWRKEAKRLI LVMTDQTSHL ALDSKLAGIV 300  
 VPNDGMCHLK NNVVVKSTTM EHPSLGQLSE KLIDNNINVI PAVQGEQPHW YKIDLLPLLP 360  
 75 TINGEISSKA ANLNLVVEA YQKLISEVKV QVENQVQGIY FNITAICTPD SRKPGMEGCR 420  
 NVTSNDVILF NVVTVMKKCD VTGKKNYAI I KPIGFNETAK IHIERNCSCQ CEDNRGPNGK 480  
 CVDETFLDSK CFQCDENKCH FDEDFSSBS CSHKQDPVC SGRGVVCVCGK CSCHKIKLGE 540  
 VYQKYCEKND FSCPYHNGNL CAGHGECESG RQCFSGWEG DRCCQPSAAA QSCVNSEQV 600  
 80 CSGRGTCVCG RCECTDPRSI GRPCEBCPTC YTACKENWNC MQLHPHNLIS QAILDQCKTS 660  
 CALMEQQHYV DQTEBCFSSP SYLRIFFIIP IVTFILGLLK VLIIRQVILQ WNSNKIKSSS 720  
 DYRVASAKKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETFRCMF

**A128 DNA SEQUENCE**

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942  
 ProbeSet Accession #: AA435577  
 Nucleic Acid Accession #: NM\_005756  
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

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1      |      |      |      |      |      |
10     |      |      |      |      |      |
15     |      |      |      |      |      |
20     |      |      |      |      |      |
25     |      |      |      |      |      |
30     |      |      |      |      |      |
35     |      |      |      |      |      |
40     |      |      |      |      |      |
45     |      |      |      |      |      |
50     |      |      |      |      |      |
55     |      |      |      |      |      |
60     |      |      |      |      |      |
65     |      |      |      |      |      |
70     |      |      |      |      |      |
75     |      |      |      |      |      |
80     |      |      |      |      |      |

AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
CTCGCGGTCA GGATGGTTTT CTCTGTGAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
GTTTTACTGA CGTTCAGAT ATTCCTTGTC ATCATTTGTC TTCATGTGCT TCTGGTAACA 180
TCCCTGGAAG AAGATACTGA TAATTCCAGT TTGTCAACAC CACCTGCTAA ATTATCTGTT 240
GTCAGTTTTG CCCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTTA 300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAAATCA CTATAGTAAA AACCTTCAT 360
GCTTCAGCGG TCAAAACCCA GAGAAATATC TGCAATTTGT CATCTATTTG CATGACTCA 420
GCATTTTITA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAA 480
CAACATATAA CGAATGGCAC CTTAACCTGGA GTCTGTCTCT TAAGTGAAT? AAAACGCTCA 540
GAGCTCAACA AAACCTTGCA AACCTTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660
TGTGCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTCGAC CAATGGAAAC CTCGTGCTGT 720
TCTGTGAGGA TACCTGCCCC TTCTCCECCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TTGTCTGTCT TGCTGACCAI CCACGTGGCC CACCATTTTC TTCCAGCCAA 840
TCCATCCCGG TGGTGGCTGG GGCACGTGTC CTFTCCCGAG TCCCAAAAGC TACCTCTTTT 900
GCTGAGCCTC CAGATTATTC ACCTGTGACC CACATATGTC CCTCTCCAAT AGGGAGGATT 960
CAACCCCTTT TACCCAGGCC TTCAGCTGCC ATAGCTTCCA GCCCTGCCAT TGACATGCC 1020
CCACAGTCTG AAACGATCTC TTCCCTATG CCCCCAACCC ATGTCTCCCG CACCCCACTT 1080
CCGTGAAGAG CCTCATTTTC CTCTCCACC GTGTCTGCC CAGCGAATGT CAACACTACC 1140
AGCGCACCTC CTGTCCAGAC AGACATGTGC AACACCAGCA GTATTTCTGA TCTTGAGAAC 1200
CAGTGTGTGC AGATGGAGAA GGCTCTGTCC TTGGGCAGCC TGGAGCCIAA CCTGCGAGGA 1260
GAAATGATCA ACCAAGCTCAG CAGACTCCTT CATTCGCCGC CTGACATGCT GGCCTCTG 1320
GCTCAAGATG TGCTGAAAGT AGTGATGAC ATTGGCTTAC AGCTGAACCT TTCAAACAG 1380
ACTATAAGTC TAACCTCCCC TTCTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TCAACACAA CTACCTTGTG GGCACAAGAC CTGTCAATC TTCAAGTTTC TCTGGAAC 1500
CAAGCTCCTG AGAACAGTAT TGGCACAAT ACTCTTCCT CATGCTGAT GAATAATT 1560
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTITGA AACACCTGCT 1620
TTGTTTCAGG ATCCTTCCCT GGAGAACTC TCCTGTATCA GCTACGTCAT ATCATCGAGT 1680
GTTGCAACC TGACCTCCAG GAACCTGACA AGAAACGTGA CAGTCACAT AAAGCACATC 1740
AAACCCAGCC AGGAGAGGTT AACAGTGAGA TGTGATTTT GGGACTTGGG CAGAAATGGT 1800
GGCAGAGGAG GCTGTCTAGA CAATGGCTGC TGTGTCAAG ACAGGAGATT GAATGAAC 1860
ATCTGTACCT GTAGCCATCT AACAGCTTC GCGTTCCTGC TGGACCTATC TAGGACATCT 1920
GTGCTGCCCT CTCAAATGAT GGCTCTGAGC TTCATTACAT ATATTTGGTT TGGGCTTTCA 1980
TCAATTTTC GTTCAGTGTG TCCTGTAAOC TACATAGCTT TTGAAAGAT CCGGAGGAT 2040
TACCCCTCCA AATCTCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCTGGTCTTC 2100
CTCCTGACT CTGTGATTC TCTGTATAG ATGCAGGCC TCTGCATCTC AGTGGCTGTA 2160
TTCTTCTATT ATTTCTCTT GGTCTCATC ACATGGATGG GCTTAGAAGC ATTCCATATG 2220
TACCTGGCCC TTGTCAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTGC 2280
ATTGTGGTGT TGTGAGTACC AGCTGTGTT GTGACCATCA TCCGACTPAT ATCCOCAGAT 2340
AACTATGGGC TTGATCTCTA TGGGAATTC CCCAATGGTT CACCGGATGA CTCTGTCTGG 2400
ATCAACAACA ATGCAATATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTT 2460
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TTTATTTCG GATTAACCTG GGGCTTTGCC TTCTTTGCC GGGGACCACT TAACGTGAAC 2640
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TGTGTGGCCA AAAAAATGT CAGGAAGCAA TGGAGGCGGT ATCTTTGTGT TGGAAAGTTA 2760
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GTAAACCAAG GAGTGTCCAG CTCCTCAAA TCCCTACAGT CAAGCAATTA CTCCAATAAC 2880
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TCTACAGAGA GGAATGGGT CTCCTTTAGT GTTCAGATG GAGATGTGT CCTTCAAGAT 3000
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CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240
AAGCTAATTA AGGCGGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGT 3300
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ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
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GTCAAAAATC TTACTTCTAC ATTTTITGT ATTTATTTC TACTGTGTAA ATGTATTCT 3600
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TCAAGAAATA ATGATCCAG CCAAGCTGAG AAAATGTAA CAGACAGTGC CACAGTTAGC 3780
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
TGGGTGATGG TTGTACAAAC AGAGTGAGAG ACCATATTT AGCCCCACTC ACCCTCTTGG 3900
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ACTGATGGT ACAITGTGTA TTGTTATGAC TGGTACACTC TGGCCAGGCC AGAGCTATAA 4260
TTGTTTTTGA AATGTGTCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
GGGAAGTCTC CTACACTGCT ATTGTTGCTA CATGTATCGA GCTTGTATTG CTCCDAGTAA 4380
TATACAGGCT CTAATCTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC 4440
TTATTAGGAA CATTTCAAC CCCTTTTAGT TAAGTCTTTC ACTAAGGTTCT TCTGTGATAT 4500
ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560

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CTGACTTGTC TTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT 4620  
 AAAATCAAAA ATGTTAAAAA CAATGAAATA AATTTGCAGT TAAGA

# A129 Protein sequence

Gene name: G protein-coupled receptor 54  
 Unigene number: Hs.184942  
 Protein Accession #: NP\_005747.1  
 Signal sequence: 1-38  
 GPS domain: 564-615  
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 MVFSVRQCGH VGRTEEVLLT FKIFLVIIICL HVVLVTSLEE DTDNSSLSPF PAKLSVVSEFA 60  
 PSSNEVETTS LMDVTLSELP SNETEKTKIT IVKTFNASGV KPQRNICMLS SICNDSAFRR 120  
 GEIMFYDKE STVPQNHIT NGTLTGVLISL SELKRSELNK TLQTLSETYF IMCATAEAGS 180  
 TLNCTFTIKL NMTMNACAAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240  
 VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSPAEPP DYSPVTHNVP SPIGSIQPLS 300  
 PQSPAPIASS PAIDMPQSE TISSPMPQTH VSGTPPEVKA SFSSPTVSAP ANVNTTSAPP 360  
 VQTDIVNTSS ISDLENQVLQ MEKALSLSGL EPNLAGEMIN QVSRLLHSPF DMLAPLAQRL 420  
 LKVVDDIGLQ LNFSTTISL TSPSLALAVI RVNASSENTT FVVAQDEANL QVSLETQAPE 480  
 NSIGTITLPS SLMMNLPAED MELASRVQFN EFETPALPD PLENLSLIS YVSSSVANL 540  
 TVRNLRNVT VILKELNPSQ DELTVRCVFW DLGRNGRGSG WSDNGCEVKD RRLNETICTC 600  
 SHLTSPGVLL DLSRTSVLPA QMMALTFITY IGCGLSSIFL SVTLVITYLAF EKIRRDYPSK 660  
 ILIQLCAALL LINLVFLDS WIALYKMQGL CISVAVFLHY FLLVSFTWNG LEAFHMYLAL 720  
 VKVENTYIRK YILKFCIVGW GVPVAVVTII LTISPDNYGL GSYGKFPNGS PDDPCWIDNN 780  
 AVFYITVVG YFCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG 840  
 ITNGFAFFAW GPVNVTFMYL FAIFNTLQGF FIFIFYCVAK ENVRQWRRY LCCGKLRLAE 900  
 NSDWSKTATN GLKKQTVNGG VSSSSNSLQS SSSNSTNSTL LVNNDCEVHA SGNNGMASTER 960  
 NGVSFSVQNG DVCLSDFTGK QHMFNEKEDS CNGKGRNALR RTSKRGSLEP IEQM

# A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (RG38) (LGR5)  
 Unigene number: Hs.285529  
 Probeset Accession #: AA460530  
 Nucleic Acid Accession #: NM\_003667  
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 GTGGCGGCAA CCGGCACCTC AGTCCCGGCC GCGCTTCTCC TCGCCGCCCA CCGCGTGGG 60  
 TCAGGAACGC GCGCTCTGGC GCTGCAGACG CCCGCTGAGT TGCAGAGCC CACGGAGCG 120  
 CGCCCGCGCG GCGACGGCCG GTAGCAGTCC GGTGCTGCTC TCCGCGCCG TCCGCTCT 180  
 GGGCCCTCTAC TCGGGCACCT ATGGACACCT CCGGCTCGG TGTGCTCTG TCGTCTGCT 240  
 TGCTGCTGCA CTGGGCGACC GGGGGCAGCT CTCCAGGTC TGGTGTGTG CTGAGGGGCT 300  
 GCGCCACACA CTGCTATTGC GAGCCCGACG GAGGATGTT GCTCAGGGTG GACTGCTCG 360  
 ACCTGGGCTC CTGCGAGCTG CTTTCCAACT TCAGCGTCTT CACTCTCTAC CTAGACCTCA 420  
 GTATGAACAA CATCAGTCAG CTGCTGCCGA ATCCCTTACC CAGTCTCTCC TTCCTGGAG 480  
 AGTTACGTTT TCGGGGAAAC BCTCTGACAT ACATTCCCAA GGGAGCATTC ACTGGCCCTT 540  
 ACAGTCTTAA AGTCTCTATG CTGCAGATA ATCAGCTAAG ACACGTACCC ACAGAGCTC 600  
 TGCAAAATTT GCGAAGCCCT CAATCCCTGC CTCTGGATGC TAACCAATC AGCTATGTGC 660  
 CCGCAAGCTG TTTCACTGGC CTGCATTCCC TGAGGCACCT GTGGCTGGAT GACAAATGCT 720  
 TAACAGAAAT CCGCTGCCAG GCTTTTAGAA GTTTATGGCG ATTGCAAGCC ATGACCTTGG 780  
 CCCTGAACAA AATACACCC ATACAGACT ATGCTTTGG AAGCTCTCC AGCTTGGTAG 840  
 TTCTACATCT CCATAACAT AGAATCCACT CCCTGGGAAA GAAATGCTT GATGGGCTCC 900  
 ACAGCCTAGA GCTTTAGAT TTAAATTACA ATAACCTTGA TGAATCCCC ACTGCAATTA 960  
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 AGAAGCATT TGTAGGCAAC CTTCTCTTA TTACAATACA TTTCTATGAC AATCCCATCC 1080  
 AATTGTGTG GAGATCTGCT TTTCAACATT TACCTGAAT AAGACACTG ACTCTGAATG 1140  
 GTGCTCACA AATAACTGAA TTTCTGAT TAACTGGAAC TGCAACCTG GAGAGTCTGA 1200  
 CTTTAACTGG AGCACAGATC TCATCTCTTC CTCAAACCT CTGCAATCAG TTACCTAATC 1260  
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 CTTATGCTTA CAGTGTCTGT GCATTTGGAG TGTGTGAGAA TGCTATAAG ATTTCTAATC 1680  
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 TTCAGGCTCA AGATGACACG GACCTTGAAG ATTTCTGCT TGACTTTGAG GAAGACCTGA 1800  
 AAGCCCTTCA TCCAGTCAG TGTTCACCT CCGCAGGCC CTTCAAACCC TGTGAACACC 1860  
 TGCTTATAGG CTGGCTGATC AGAATTTGGAG TGTGGACCAT AGCAGTCTCG GCACCTACTT 1920  
 GTAATGCTTT GGTGACTTCA ACAGTTTTCG GATCCCTCT GTACATTTC CCATTAAAC 1980  
 TGTAAATGG GTTCATCGCA GCAGTGAACA TGCTCACGG AGTCTCCAGT GCGCTGCTGG 2040  
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 TGCCTACTCT GGCAGCCCTG GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AATTTTGAAA 2220  
 CGAAGCTCC ATTTTCTAGC CTGAAAGTAA TCATTTTGCT CTGTGCCCTG CTGGCTTGA 2280  
 CCATGGCGCG AGTTCCTGCT CTGGGTGGCA GCAAGTATGG CGCTTCCCT CTCTGCTGCT 2340  
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 CCGTTGCTT CTTATGATG ACCATTGCTT ACACCAAGCT CTACTGCAAT TTGGCAAGG 2460

5 GAGACCTGGA GAATATTTGG GACTGCTCTA TGGTAAACA CATTGCCCTG TTGCTCTTCA 2520  
 CCAACTGCAT CCTAAACTGC CCTGTGGCTT TCTTGTCCIT CTCCTCTTTA ATAAACCTTA 2580  
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 TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAAACACCC AAGCTTGATG TCAATTAAGT 2760  
 CTGATGATGT CGAAAAACAG TCCTGTGACT CAACTCAAGC CTGGTAACC TTTACGAGCT 2820  
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 AGAGCTGCCA TCTTCTCTCT GTGGCATTG TCCCATGTCT CTAATTAATA TGTGAAGGAA 2940  
 AATGTTTTC AAGGTTGAGA ACCTGAAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000  
 10 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

# A131 Protein sequence

15 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)  
 Unigene number: Hs.285529  
 Protein Accession #: NP\_003658.1  
 Signal sequence: 1-22  
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825  
 20 Cellular Localization: plasma membrana

1 11 21 31 41 51  
 25 MDTSRRLGVLL SLPVLLQLAT GSSSPRSGLV LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60  
 PSNLSEVTSY LLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGF TGLYSLKVLN 120  
 LQNNQLRHVP TEALQNLRSL QSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180  
 AFRSLSLQA MTALNLCIHH IPTYAFGNLS SLVVLHLENN RIHSLGKKCF DGLHSLLETLD 240  
 LNVNMLDEFP TAIRTLNLIK ELGPHSNIR SIPEKAFVGN PSLITITHPYD NPIQFVGRSA 300  
 30 FOELPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNQLVLDLS 360  
 YNLLEDLPFS SVQCQLQKID LRHNEIYBIK VDTFQQLSL RSLNLAWNKI AITHPNAPST 420  
 LPFLIKLDLS SMLLSFPFIT GLHGLTHLKL TGNHALQSLI SSENFFELKV IEMPYAYQCC 480  
 AFGVCENAYK ISNQWNKGDN GEMDDLHKKD AGMFQAGDER DLEDFLLDFE EDLKALESVQ 540  
 CSPSPGPFKP CERI LDGWL RIGVNTIAVL ALTCAALVTS TVPRSPLYIS PIKLLIGVIA 600  
 35 AVNMLTGVS AVLAGVDAPT FGSFARHGAW WENGVGCEVI GFLSIFASES SVFLTLAAL 660  
 ERGFSVKYSA KPETKAPFSS LKVIILLCAL LALTMARVPL LGSSKYGASP LCLPLPFGER 720  
 STMGYNVALI LINSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC 780  
 FVAFLSPSSL IMLTIFISFV IKFILLVVPV LPACINPLLY ILFNPHFKEK LVSLRKQTYV 840  
 40 WTRSKHPSLM SINSDDVEKQ GCDSTQALVT FTSSSITYDL PPSVPSPAY PVTESCHLSS 900  
 VAFVPCFL

# A132 DNA SEQUENCE

45 Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Probeset Accession #: U25128  
 Nucleic Acid Accession #: NM\_005048  
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51  
 GCGCGGTGCG CCGGCGCCGA CCACCCGAGC TCGCGGTGCT TACTGGCCAC AAGTTGCTC 60  
 TGGGCGAGCC AAGTTGGCAA CTGGAAGCT TCTCCCGGCG TCTGGAGGAG GGTCCCTGCT 120  
 TCTCTCTACA GCGCTTCCGG GCATGCGCGG CCGTGGGCGG TCGCTCACG CTGCGGGTGT 180  
 55 GCTAATGCTC GCGAGCTGCC TCCTGGCCAG AGCCGAGCTG GATCTGTATG GCACCATTAC 240  
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300  
 AGCTCACTC CAGGAGGGAG AAGGTAATTG TTTCCTGAA TGGGATGGAC TCATTGTGTG 360  
 GCCCAGAGGA ACAGTGGGGA AATATCAGG TGTTCCATGC CCTCTTATA TTTATGACTT 420  
 60 CAACATATA GAGATTGCTT TCGACACTG TAACCCCAAT GGAACATGGG ATTTTATGCA 480  
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 CAGCATAGGA AAGCAAGAA TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600  
 CATCTCTTTT GGTTCCTTGG CTGTGGCTAT TCTCATCAT GGTACTTCA GACGATTGCA 660  
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 65 CATCTTTGTC TGGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780  
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 GATCTGTGTC GAAGTCTCT ACCTGCAATA TCTCATCTTT GTGGCTTCT TTTCGGACAC 960  
 70 CAAATACCTG TCGGGCTTCA TCTTGATAGG CTGGGGGTTT CCAGCAGCAT TTGTTGACAC 1020  
 ATGGGCTGTG GCAGGAGCAA CTCTGGCTGA TCGGAGGTGC TGGGAACCTA GTGCTGGAGA 1080  
 CATCAAGTGG ATTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAAAT TTATTCTGTT 1140  
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 75 CCGCATGCAC TGGAGCTCT TCTTCAACT CTTTCAGGCT TTCTTTGTGT CTATGCTCTA 1380  
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 CTCGTGGGAC TGAAGAAAGG CACCGCCATG TGGCAGCCGC AGATGCGGCT CAGTGTCTAC 1500  
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 80 TGGCTATGTC TGGAGTACTT CTTCAACTC CTGCTGGCCA CACTCTTTC ACGAGGAGAC 1680  
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 ATACTCTTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAAATATAGT 1920  
 TTTTAGGCTC CATGAATTGG CTCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980

5 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040  
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 GCTGTAGCTT TCTCTCATAT ATATCACCCCT AAATATAATG AAGATCTTTT AGTGTGTATC 2160  
 ATTTTCCCTT TAGAACTAG TATCTCTTA TTCTTACTT TAATGTACTT CTATCACTGC 2220  
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAATA AAATATATGG GAAGATAAAA 2280  
 GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATGTATAA AATAATGCAT 2340  
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 ACATCCCTTC TTTTGAATGG CCTCTTTGTG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460  
 10 TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCTCAGTT AGTGAGCTTG TGCTGCATA 2520  
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTTCTTG 2580  
 TTTAGCTGT TACTACATTC TACATGGCAT GTGGGATCAA TTAAAAATTT GTTTTAAAAA 2640  
 T

# **A133 PROTEIN SEQUENCE**

15 Gene name: parathyroid hormone receptor 2  
 Unigene number: Hs.159499  
 Protein Accession #: NP\_005039.1  
 Signal sequence: 1-25  
 Pfam domain: 7tm\_2 [141-420]  
 20 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419  
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51  
 | | | | | |  
 MAGLGASLHV WGLMLGSLCL LARAQLDSGG TITIEBQIVL VLKAKVQCEL NITACLQEGE 60  
 GNCFFPEWDGL ICNPGTGVK ISAVPCPPYI YDFNKGVA RHCNPNGTWD FMSLNKTWA 120  
 NYSDDLRFQ PDISTGKQEF FERLYVMYTV GYSLFSGSLA VAILLIGYFR RLECHTNYIH 180  
 MHLFVSEMLR ATSIPIVORV VHAHIGVKEL ESLIMQDDQ NSIEATSVDR SQYIGCKIAV 240  
 30 VMFIYFLATN YWHLVEGLY LHNLIPIVAF SPTKYLWGTI LIGWGFPAAF VAAWAVARAT 300  
 LADARCWELS AGDIKIWIYA PILAAIGLNF ILFLNTVRVL ATKIWNENAV GHDTRKOYRK 360  
 LAKSTLVVL VEGVYIVFV CLPHSFTGLG WDIRMHCELF FNSFQGFVYS ILYCYNGEV 420  
 QAEVKKMSR WNLSDVKKT PPGSRRRCGS VLTTVTHSTS SQSQVAASFR MVLISGKAOK 480  
 35 IASRQPDISH TLPGRVWENS BQDCLPHSFH ESTKEDSGRQ GDDILNKP6 RPMESNPDT6 540  
 GCGGETEDVL

## **A134 DNA sequence**

40 Gene name: ESTs  
 Unigene number: Hs.128899  
 Probeset Accession #: AA983251  
 Nucleic Acid Accession #: AA983251  
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51  
 | | | | | |  
 ATGCTGTCTG GCTTCTGTAT GAGTCCAGT ACCAGCACA GAGCAGTA CACTCCCGGA 60  
 GGAAGAAAC TTCCGTGGGA GGCITCCATC GGTGCGCACA CCTCCGAGG GCGAGGCGAGC 120  
 GACCGGAGA GGAAGAGCCG GCCCGAGGCT GCGGGCTCC TGTGGGACCG CACTGCAGCC 180  
 GGGAGGCGG AGAAGGGGAA CCGGGGCGAG CGCGCGGCTT GGATCCGCGC CCAGCAGCAGC 240  
 50 CCGCGGCGGC CGCCAGCTGG GCAGGCTCCC GGGAGTCCGG CTGGGGGCGC GCAGGACTCT 300  
 CGCTCTGGTC CTGGAGCTTC CCGGGGAGGG GTCCGGTTGC CAGTGAACCC TCCAGAGGCT 360  
 TCCGAGAGAC AGCCCCGGGG GCCTTCTGAC TGCAATCCGA GATTTCATC AGCAGGTGCA 420  
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480  
 GCTCTCGGAC CTAGGGCCCG GCGTCTCTCC CTCTCTGGCG TCGCGGCGA GGGGAGTGGC 540  
 55 CCGCGCGGAA AGCGCCGCGG GACAGTCAAT GACGAGGCCC GGGGGTCCGC GGGGCCACGA 600  
 CTTCCTCGAG ACCGTCTTGC GCTCTCTGGA GAGCGGCTGT CCGCGGCCAG GGTGGTCCCA 660  
 TGTGGGCGCG TCGGCTCTCG TCCGTCTCTT CATCTGGA GCGCCCTTCG CTCTGCGAGC 720  
 TGCTGTCTGG TCGCTCTCTG GCGGCGGGGG CGAGGGGCCA GCGGGGAGTA CTGCCAGCGC 780  
 TGGCTGGAAG CGGAGGCGCT CTGGCGCATC GGCCTTCAAT GTCCGAGCG CTTCGACGCG 840  
 60 GGCAGAGCCA CCATCTGCTG CCGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900  
 GCGCGCCTGG ACCAGGCGCG CTGCGCAAT GACCGCCAGC AGGGCGCTGG CGAGCTTGGC 960  
 CCGGCGGACA AAGACCGGCC CCGACGCTC GCGAGGCTT CATGCTTAG GGGTACCCAA 1020  
 GGAGACCGCG AGGGTTCGCC CCACCCCGTG AGGGCCTGGC AGCGGTGCTC CCTGGAAGGC 1080  
 65 TCCCGGAAAG GAAGGCGAGT CCTCAGGGCT TTCCCGGGGC TGCTGCCCCG TGCAGAGCGC 1140  
 CGCGGATCC CATCTTCTCC ACAGCGCGGC CCTCTCTCCC TGCAGCGGCC CGCCTTGCCT 1200  
 ATCTACGTGC CGTTCTCTAT TGTGTGCTCC GTGTTGTGCG CCTTTATCAT CTGGGGTCC 1260  
 CTGTTGGCAG CTGTGTGCTG CAGATGTCTC CGGCTTAGC AGGATCCCA GCAGAGCCGA 1320  
 GCGCCAGGGG GTAAACGCTT GATGGAGACC ATCCCATGTA TCCCGAGTGC CAGCACTCC 1380  
 CGGGGCTGCT CTTCAGGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440  
 70 GGGGCCCGGG CGCCCCAAC AAGGTACAG ACCAACTGTT GCTTGGCGGA AGGAGCATG 1500  
 AACAACTGTF ATGTCAACAT GCGCACAAAT TTCTCTGTC TGAACGTGA GCAGGCTACC 1560  
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCATCAT AGTGGGTA CACGCTGAC 1620  
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCTATG ACGGCTGCA GCTGGCTAC 1680  
 75 AGGCAGATTG AGTCCCTCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCGAGCGGTG 1740  
 ACTGTATAAC CAGAGTCAAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800  
 GATTCTCGAG GTGGAAGTCC GCACATGTCT GTGGTATTTA TGGCAGGATT CCTTTGGATG 1860  
 GCTTCATTGG CCCCCAGACT GTATGAARAC ATCTCGAAT TAGCATTTCT GATATGTTT 1920  
 CATCCAGGAT ATCATTGATT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980  
 80 TTGCTGATGA GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGAGCA 2040  
 AAGAAATTTA TAAACTGATA AATTAAAGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100  
 TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTTACTGG GACTTTTCTT 2160  
 TTTTCTTTT TTTTCTTTAA TCAGACAGGG TCTTGTCTTG TTGCCAGGC TGGAGTGCAG 2220  
 TGGTGGATC TCGGCTCACT GCACTTCTAG CCTCTGATG TCAGGCAACA CTCTGCTTCT 2280  
 AGCTCTCCAG GTGCTGGGA TTACAGGTGC CTGCCCCAT GGCATAATTT TTGATTTTCT 2340

5 TG TAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400  
 TCTGCTGTCT TCAGCCCTCCC AAGATGCTGG GATTACAGGC GTGAGCCACC GCGCCGACCC 2460  
 TGAGCCCTTTT TTTTTCCTTA ATGCATCCAA GGTAAAGGGG AAGACGCCAA TAACAGGACT 2520  
 ATCTTAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCACA GTATCCACA 2580  
 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640  
 GGGCTATTTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700  
 TAAAAAGAG ACTGAATAAA ATGTATAGT TACTTAAC TAAGAACAT TTCAGAACTC 2760  
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAAT CATCCCCCTC 2820  
 10 TTGATTGTAT CTTAATTTTC TGGCTTAAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880  
 TATATTGAAA TCATAAACTA TCACCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940  
 TGGTATAGT TTTGCGTTTC CTCTGTTTGT GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000  
 GAGTCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCTTA GATCTGATAA 3060  
 AAAAAATTTT TGTCTTAGT TATAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120  
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTA AACAGATAC GATTACTTT 3180  
 15 GCAGATCATA AGGCTTTTTA TACTCTTGT ATCAAAATG CTTATTTTTC AGGCCTAAG 3240  
 GATTGTTAAG AGAAAGCTT TTCAACGAG GATTGCCCTT CTCTCCAC ACTGTTCTTG 3300  
 ATTTCTCTC TCTTCTAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360  
 CAAATTCAG TGAATTTATT TGTGTGTTCT TTAATATAT AAAAAAGAT AACTTTAAGG 3420  
 ATGTGCAAGT ACATTTCCAA CTCTAGCAC AACAGTATT TTGTAATTA ACAATCGCT 3480  
 20 GTATGGTATG GTCTCTTACA CATTATGTC TATAGATATC TATGATCAT CTTTCTATTC 3540  
 TGTTCATGA CTGAATAATG TAAACCACT GTTGGCAATT GGTATCATCA ATGATACTCA 3600  
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660  
 TGAATAAATA AAAAAAATA AAAAAAATA

25 A135 Protein sequence  
 Gene name: ESTs  
 Unigene number: Hs.128899  
 Protein Accession #: none found  
 30 Signal sequence: 1-11  
 Transmembrane domains: 402-424  
 Cellular Localization: not determined

35 1 11 21 31 41 51  
 | | | | | |  
 MLSGFLMSPS TQHRAYTPG GKPLPWEASI GAHTSRGRGS DRERESRFEA AGLINDRAAA 60  
 GEAEKGNRGE PPAWIRAQQQ PRPPAGQAP GTAAGGAQDP RLPRGRERGR VRLPVKFPFA 120  
 SGRQFRGFD CTFPRFSASA THKAVPKGTG PPAEDGDGLG AFGPRARRRR LLGVAABEGSG 180  
 PRGKRRTGVS DEARSGPGER LLGDRPALSG DALSAPEVVP CGALAARESP HPGTPLSCSS 240  
 40 CCMRLCWRER RGPSPGEBCHG WLDAQGVNRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300  
 ARLDQGGCDN DQGGAGBEPG RADKDGPRRL GRASCLRGTD GDGEGAPPVW RAWQRCBPBG 360  
 SPFGQLLRA PFQLFRARR RGPSSPRGG PSLQRPALP IYVPLIVGS VFVAFILGS 420  
 LVAACCCRCCL RPKQDPQQR APGGNRLMET IPMIPSASTS RGSRRQSSST AASSSSSANS 480  
 GARAPPTRSQ TNCCLPEBTM NNVYVDMPTN FSVLNCQQAT QIVPHQGGYL HPPYVGTTVQ 540  
 45 HDSVFMTAVP PFMDGLQPGY RQIQSPFFHT NSEQKMPAV TV

A136 DNA SEQUENCE  
 Gene name: selectin E (endothelial adhesion molecule 1)  
 50 Unigene number: Hs.89546  
 Probeset Accession #: M24736  
 Nucleic Acid Accession #: NM\_000450  
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51  
 | | | | | |  
 ATGATTGCTT CACAGTTTCT CTGAGCTCTC ACTTTGGTGC TTCTCATTA AGAGAGTGA 60  
 GCCTGGTCTT ACACACCTTC CACGGAAGCT ATGACTATG ATGAGGCCAG TGCTTATGT 120  
 CAGCAAGGT ACACACACCT GGTTCGAATT CAAACCAAG AAGAGATTGA GTACCTAAC 180  
 TOCATATTGA GCTATTTCAC AAGTTATTAC TGGATTGGA TCAGAAAGT CAACAATGG 240  
 60 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAG CCAAGAATG GGTCCAGGT 300  
 GAACCCACCA ATAGGCAAAA AGATGAGGAC TGCCTGGAGA TCTACATCA GAGAGAAAA 360  
 GATGTGGGCA TGTGGGAATG TGAAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420  
 GCTGCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480  
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAACGT 540  
 65 ACAGCCCTGG AATCCCTTGA GCATGGAAGC CTGGTTTCCA GTCAACCACT GGGAAACTTC 600  
 AGCTACAAAT CTCTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660  
 ACCATGCAAT GTATGTCTTC TGGAGAATGG AGTGTCTCTA TTCCAGCCTG CAATGTGGTT 720  
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGA 780  
 70 AGCTTCCAT GGAACACAA CTTACATTT GACTGTGAAG AAGGATTGA ACTAATGGGA 840  
 GCCAGAGACC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900  
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960  
 CCTGCTGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020  
 TTGCAAGGAC CAGCCAGGT TGAATGCACC ACTCAAGGCG AGTGGACACA GCAATCCCA 1080  
 75 GTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCG AGCGAGGCTA CATGAATTGT 1140  
 CTCTCTAGTG CTCTGTCAG TTTCCGTTAT GGGTCCAGCT GTGAGTCTCT CTGTGAGCAG 1200  
 GGTTTTGTGT TGAAGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260  
 GAGAAGCCCA AGTGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGTTTGT 1320  
 GTGAGGTGTG CTATTCCCTC TATTGGAGAA TTCACCTACA AGTCCCTCTG TGCCTTCAGC 1380  
 80 TGTGAGGAGG CATTGTAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGAACA 1440  
 TGGACAGAAG AGTTCCTTTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCGGGA 1500  
 AAGATCAACA TGAGCTGAGC TGGGGAGGCC GTGTTTGCCA CTGTGTGCA GTTCGCCCTGT 1560  
 CCTGAAGCAT CGAGCTCAAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620  
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680  
 CTTTCTGCTG CTGACTCTC CTTCTGACCA TTAGACCAT TTCTCCTCTG GCTTCGGAAA 1740

TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800  
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

5 A137 Protein sequence:  
Gene name: Selectin E (endothelial adhesion molecule 1)  
Unigene number: Hs.89546  
Probeset Accession #: M24736  
Protein Accession #: NP\_000441  
10 Signal sequence: 1-22  
Transmembrane domains: 555-573  
C-lectin domain: 23-139  
Cellular Localization: plasma membrane

15  
1 11 21 31 41 51  
| | | | | |  
MIASQFLSAL TLVLLIKESG AMSYNTSTEA MTYDEASAYC QQRTHLVAI QNKKEIEYLN 60  
SILSYSPSY WIGIRKVMNV NVWVGTQKPL TEEAKNWAPG EPNNRQDED CVRIYIKREK 120  
20 DVGWMDERC SKKKLALCYT AACINTSCSG HGECEVETIN YTCCKDPGFS GLKCEQIVNC 180  
TALSSPEHGS LVCSEPLGNF SYNSSCSISC DRGYLPSSMS TMQCMSSGSEW SAPIPACNVV 240  
ECDAVINPAN GFVECFQNPQ SFPWNTTCTF DCEBGFELMG AQSLLQCTSSG NWDNEKPTCK 300  
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEFGM LQGPAAQVCT TOGOWTQQIP 360  
VCEAFQCTAL SNPERGYMNC LPSASGSERY GSSCBFSCEQ GFVLKGSKRL QCGPTGENDN 420  
25 EKPTCEAVRC DAVHQPPEGL VRCASPIGE PTYKSSCAPS CEQSELYGS TQLECTSQBQ 480  
WTEVPSQV VKCSSLAVFG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGRW 540  
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAFPLNLRRK CCRKAKKFVP ASSCQSLBND 600  
GSYQKPSYIL

30 A138 DNA SEQUENCE:  
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
Nucleic Acid Accession #: AA487468  
35 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
| | | | | |  
40 CGGCACCAAG AGCACTGGCC AAGTCAGCIT CTTCGAGAG AGTCTCTAGA AGACATGATG 60  
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCACAG TTCTCTCCAA CCTTGCCATT 120  
GCATATAAAA AGGAAAAGAG GCTTCTCTAG ACACCTCTCA GAGGATGGGG AGATGACATC 180  
ACTTGGGTAC AAACATTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAGGCCATTA 240  
ATGGTTATTC ATCACTCTGA GGATTGTCAA TACTCTCAAG CACTAAGAA AGTATTGGCC 300  
45 CAAATGAAG AATACAAGA AATGGCTCAG AATAAGTICA TCATGCTAAA CCTTATGCAT 360  
GAAACCACTG ATAAGAAATT ATCACTGAT GGGCAATATG TGCTTAGAAT CATGTTTGTA 420  
GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480  
TATGAGCCTC GGGATTATCC CCTATTGATA GAAAACATGA AGAAGCAATT AAGACTTATT 540  
50 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAAAGT CAAATTTTAT 600  
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAAT 660  
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720  
TCTGAAAAAA AAAAAA AAAA

55 A139 Protein sequence:  
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
Unigene number: Hs.100686  
Probeset Accession #: AA487468  
Protein Accession #: none found  
60 Signal sequence: 1-23  
Transmembrane domains: none found  
Cellular Localization: secreted

65 1 11 21 31 41 51  
| | | | | |  
MMLHSALGLC LLLVTVSSNL AIAIKKEKP PQTLSRGWED DIIVVQTYEE GLFYAQSKK 60  
PLMVEHLED CQYSQALKKV PAQNEEIQEM AQNKFIMLNL MBETTDKLS EDGQVPRIM 120  
70 FVDPSLTVRA DIAGRYSMRL YTYEPDRLPL LIENMKALR LIQSEL

A140 DNA SEQUENCE  
Gene name: TMPS33a  
Unigene number: Hs.298241  
Probeset Accession #: AI538613  
75 Nucleic Acid Accession #: AB038157  
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51  
| | | | | |  
ACCGGGCACC GGACGGCTCG GTTACTTTCG TTCTTAATTA GGTCAATGCC GTGTGAGCCA 60  
GGAAGGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGGC CTACTATCTC TTCCGTGGTG 120  
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCCGA GCCGGATGTC 180  
AGAGGTCTCG AATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA ACCCCCTTC 240

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TCATTCCGAT CGCTTTTGG CCITGATGAT TTGAAATAA GTCCGTGTGC ACCAGATGCA 300
GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATIGA AGTTTTTTCC AATCATCGTC 360
ATTGGGATCA TTGCATGTAT ATTACCACTG GCCATTGCTC TGGGCATCCA CTTCGACTGC 420
TCAGGGAAGT ACAGATGTCT CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
AAGGGTCACT ACGCAATGTG TGCCTGTGCC CAACGTGGTT TCCCAAGCTA TGTGAGTTCA 660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACACT CAGTATATGT GAGGGAGGGA 780
TGTGCCCTCG GCCACGTGGT TACCTTGCG TGACAGCCT GTGGTCATAG AAGGGGCTAC 840
AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
CTTCAGTTCC AGGGCTACCA CCTGTGGGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
ACTGTGTCAC ACTGTGTTTA TGACTGTAC CTCCCAAGT CATGGAACAT CCAGGTGGGT 1020
CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTGG TGGAGAAGAT TGTCTACAC 1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATGSCC TTATGAAGCT GCGCGGCCA 1140
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200
GATGGAAGAAG TGTGCTGGAC GTGAGGATGG GGGGCCACAG AGGATGGAG AGGTGACGCC 1260
TCCCTGTGCC TGAACCAAGC GGCCTGCTCT TTGATTCCA ACAAGATCTG CAACCAAGG 1320
GACGTGTGCG GTGGCATCAT CTCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGTGGC 1380
GTGGACAGCT GCCAGGGGGA CAGCGGGGG CCCTGTGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACCGC CTTTGGCATC GGCTGGCAG AGGTGAACAA GCCTGGGGTG 1500
TACACCGTGG AGGGCTACCA OCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTG AGGTGATGAA GACAGCCGGA 1620
TCTCTCCCTG GACTCCGCTG TAGGAACCTG CACACGAGCA GACACCTCTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CCGAAGAGG CACCTTCCA TCTGATTCCA GCACAACCTT 1740
CAAGCTGCTT TTTGTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCGAGGCTGG 1800
AGTGAGTGG CSAAATCCCT GCTCACTGCA GCCTCGCTT CCTGTGTTCA AGCGATTCTC 1860
TTCCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACCC CAACTAATTT 1920
TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTGGCCA GGTCTCTC AAACCCCTGA 1980
CCTCAATGA TGTGCTGCT TCAGCCTCCC ACAGTGTGCG GATTACAGGC ATGGGCCACC 2040
ACGCCTAGCC TCACGCTCCT TTCTGATCT CACTAAGAAC AAAAGAAGCA GCACTTGCA 2100
AGGGCGGCT TTCCACTGG TCCATCTGCT TTCTCTCCA GGGTCTTGC ABAATTOCTG 2160
ACGAGATAAG CAGTATATG ACCTCAGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAAGCC AGAAGTGCG AACTGCACTC ACTGCACTT TTCATCTTA GGGACCAAA 2280
CCAAACCCAC CCTTCTACT TCACAGACTT ATTTTCACAT GTGGGGAAGT TAATCTAGGA 2340
ATGACTCGTT TAAGGCCTAT TTTCATGAT TCTTTGTAGC ATTTGGTGCT TGAAGTATTA 2400
TTGTCTTTG ATTCCAAATA ATATGTTTC TTCCCTCAA AAAAAA AAAA 2460
AAAAAA
  
```

#### A141 Protein sequence:

Gene name: TMPS93a  
 Unigene number: Hs.298241  
 Probeset Accession #: AI538613  
 Protein Accession #: BAB20077  
 Signal sequence: none found  
 Transmembrane domains: 43-65, 239-261  
 Tryp\_SPC domain: 216-444  
 Cellular Localization: plasma membrane

1 11 21 31 41 51  
 | | | | |  
 MGENDPPAVE APFSFRLSP LDDLKISFVA EDADAVAAQI LSLPLKFFP IIVIGIALI 60  
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120  
 TAAGWKTMCS DDWKGHYANV ACAQLQFPST VSSDNLRVSS LSGQFREEPV SIDHLLPDDK 180  
 VTALHESVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240  
 LCGGSVATPL NIKTAARCVY DLYLPKSWTI QVGLVSLDN PAFSELVEKI VYHSKYKPKR 300  
 LGNDIALMKL AGPLTFMEMI QPVCLPENSE NFPDGKWCNT SGWGATEDGA GDASPVLNHA 360  
 AVPLISNKKC NHRDVGII SPSMLCAGYL TGGVDSQGD SGGPLVCQER RLWLKLVGATS 420  
 RGIGCAEVNK PGVYTRVTSF LDWIEHQMER DLKT

#### A142 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]  
 Unigene number: Hs.105484  
 Probeset Accession #: AA314779  
 Nucleic Acid Accession #: none found  
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51  
 | | | | |  
 CCAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60  
 CTGAGATCCT TGCATAGCT ACATCTCTAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120  
 CGGCTGTCTC TATGTCTGAG CTGCTGTGCC AAAACAGGAG TCTTGGGTGA TATCATCATG 180  
 AGACCCAGCT GTGCTCTCTG ATGGTITTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240  
 AAGCTGAGTA ACTGGTCTGA TGCCGAGCTC GAGTGTCACT CTTACGGAAG CGGAGCCAC 300  
 CTGGCATCTA TCTTGAGTTT AAAGGAAGCC AGCAACATAG CAGAGTACAT AAGTGCTAT 360  
 CAGAGAAAGC AGCGGATATG GATTGGCTTG CACGACCCAC AGAAGAAGCA GCAGTGGCAG 420  
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCTTGGTCTG GCAAGTCCAT GGGTGGGAAC 480  
 AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTGGAGCAG CAACGAATGC 540  
 AACAGCGGCC AACACTTCTT GTGCAGTAC CGAOCATAGA GCAGGAATCA AGATTCTGCT 600  
 AACTCTGCA CCAGCCCCGT CCTTCTCTT TCTGCTAGCC TGGCTAAATC TGCTCATTTAT 660  
 TTCAGAGGGG AAACAGTACA AACTAAGAGT GATAAGGCC CTACTACACT GCTTTTTTA 720

